applied biosystems

GeneChip™ Command Console™ (GCC) v7.0

USER GUIDE

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ThermoFisher SCIENTIFIC

Affymetrix, Inc.
3450 Central Expressway
Santa Clara, CA 95051

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Revision history: Pub No. MAN0027771

Revision	Date	Description
14	March 2023	Initial release in Thermo Fisher Scientific document control system. Supersedes legacy Affymetrix publication number 702569. v7.0 release. The About Box now displays the detected camera.
13	August 2019	Software release v6.1. Wash only option added to the Multi-Channel (MC) Instrument. Enhanced log file collection functionality.
12	March 2019	Software release v6.0. Scan only option using the GCC GeneTitan Scanner. Wash only option added to the GeneTitan System. Updated branding.
11	January 2019	Software release v5.0. Windows 10 Enterprise 2016 LTSB only. Features Thermo Fisher Cloud connectivity for monitoring instruments remotely.
10	June 2013	Documented new features for v4.0 release. Version 4.0 supports the new 384 plate format (GeneTitan Multi-Channel Instrument Control ONLY) and is now compatible with Windows 7 Professional with SP1.Minio
9	February 2013	Minor v3.2 revisions to documentation.
8	June 2011	Documented new features for v3.2 release. The Viewer now monitors the progress of array data through the workflow and updates to the GeneTitan Instrument Control software to improve reliability.
7	July 2010	Software release v3.1.1.
6	April 2010	Software release v3.1.
5	November 2009	Documented new features for v3.0 release. Version 3.0 supports the new genotyping array plate used with GeneTitan Multi-Channel (MC) Instrument. Version 3.0 also allows you to control the GeneTitan family of instruments to process array plates from hybridization to scanning.
4	November 2008	Minor 2.0 revisions to documentation.
3	October 2008	Documented new features for v2.0 release. Register plate, array, and sample data for Array Plates and control the GeneTitan Instrument to process array plates from hybridization to scanning with no user intervention.
2	March 2008	Software release v1.1.
1	August 2007	Initial release.

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Contents

1 Introduction

The development of microarray technology means that researchers can now perform more experiments and collect more data from each experiment than ever before. Researchers need to analyze and organize this mass of data, which presents new challenges for the researchers and the software they use.

GCC provides flexible and powerful tools for:

- Entering and organizing information about the sample and GeneChip probe arrays.
- Controlling the instruments used to process probe arrays and collect the intensity data.
- Tracking the progress of an array through the array processing workflow.
- Working seamlessly with other tools for downstream analysis.

There are several GCC configurations:

- GCC and GeneChip Scanner 3000 system (GCS3000 and FS450)
- GCC and GeneTitan™ system
- GeneTitan Multi-Channel (MC) Instrument
- GCC Only
- GCC and GeneTitan Scanner system
  - GeneTitan Scanner Instrument

New features in v7.0

- The About Box now displays the detected camera.

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2 Getting started

GCC provides tools that enable you to process arrays, extract the intensity data for use by the probe level analysis software, and organize the resulting sets of data files.

You can use GCC to process:

- Cartridge Arrays
- Array plates for the GeneTitan MC instrument

See "Different array types" on page 16 for more information about the differences in the arrays.

IMPORTANT! Before running GCC for a particular GeneChip Array, you must have the library files for that array type installed on your computer.

To fully use the capabilities of GCC, you need to understand:

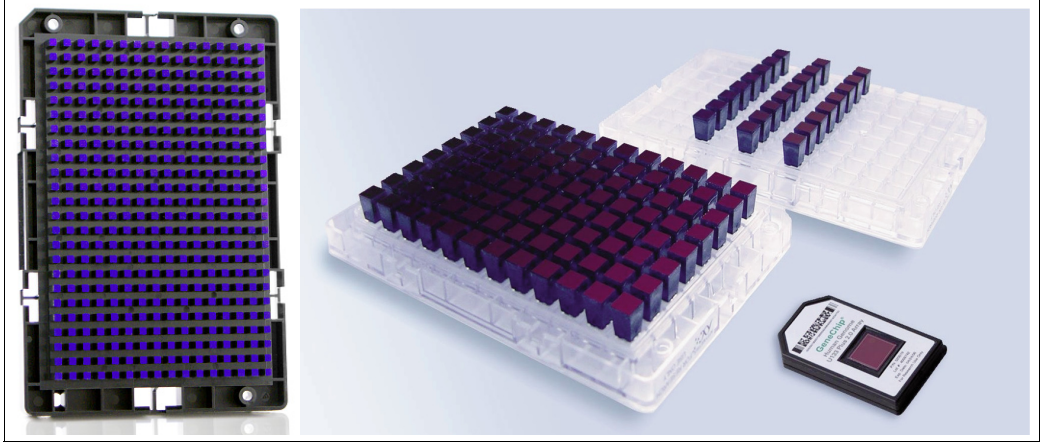
- The components of the software
- The array processing workflow that the GCC components perform
- The types of files that GCC produces and uses
- The structures and tools that GCC uses to organize the resulting data

This chapter describes the above concepts in:

Different array types

The GCC software may be used to process both cartridge arrays and array plates for the GeneTitan MC instrument.

Figure 1 384-format, 96-format, and 24-format array plates and Cartridge array



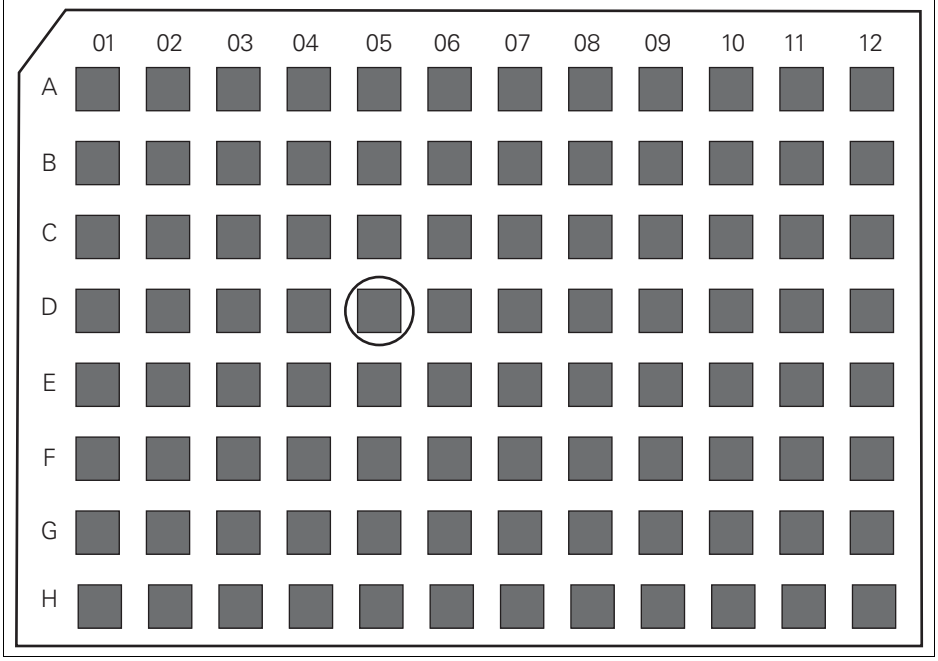
An array cartridge contains a single array, which is processed on its own through washing and staining and scanning by using the GCC Fluidics Control and GCC Scan Control with the FS-450 Fluidics Station and the GCS3000 scanner. Hybridization is performed using instruments that are not controlled by the GCC software. The array cartridge is identified by a bar code that can be scanned and used to track the array workflow.

Multiple arrays can be scanned sequentially if you use the GCS 3000 AutoLoader.

A 384 or Mini-96 format array plate can be used on the GeneTitan MC instrument. A 96-format array plate may contain 16, 24, or 96 arrays.

All the arrays on the plate are processed from hybridization to scanning using the GeneTitan MC instrument and the GCC GeneTitan Control software. This enables increased automation and consistency in processing when dealing with large numbers of samples

Figure 2 Arrangement of arrays on an Array Plate for the GTMC instrument



The array plate has a barcode for tracking. Each individual array on the plate is identified by its row and column. For example, the circled array in the figure below is array D05.

GCC components

The features and functions of GCC vary depending upon which instrument or instruments it is being used with.

GCC is comprised of the following components:

- GCC Portal: software for sample registration, data organization, and tracking the array processing workflow. GCC Portal uses a web interface for user access.
- Other GCC components are installed on your computer and run behind the scenes on your computer. These include the Indexer, a service that tracks the relationships of files in the GCC data roots. The information is used to keep track of the GCC files, for example, in the Folders and Projects views. The services typically run behind the scenes without user control, but you may need to change their configuration in some circumstances. See "GCC services" on page 35 for more information.
- GCC Fluidics Control and GCC Scan Control for processing cartridge arrays:
  - GCC Fluidics Control: Software for running the Fluidics Station 450.
  - GCC Scan Control: Software for the GeneChip Scanner 3000 (GCS 3000) and GCS 3000 with AutoLoader (AutoLoader).
- GCC GeneTitan Control and GCC GeneTitan Scanner for processing array plates:
  - GCC GeneTitan Control software for running the GeneTitan Multi-Channel (MC) instrument.
  - GCC GeneTitan Scanner for running the GeneTitan Scanner instrument.

IMPORTANT! A system used as a GeneTitan workstation requires a user account with specific privilege settings. In addition, some of the other features of Windows 10 Enterprise 2016 LTSB must be set up in particular ways or disabled to avoid causing problems when running GeneTitan IC software.

Your system has been set up for use with GeneTitan with the user account AFFXUser. This account has these privileges and features already set up.

- GCC Viewer: Software for viewing image data and workflow status and performing manual gridding.

These tools are used to install necessary files or manage other GCC functions:

- Library File Importer
- Fluidics Script Importer
- GeneTitan Library File Installer
- Data Upload Scheduler
- Email Configuration Editor

Before using GCC

Required Operating System	GCS3000/FS450 Instrument	GeneTitan MC Instrument	GeneTitan Scanner	Analysis Only Workstation
Windows® 10 Enterprise 2016 LTSB	Yes	Yes	Yes	Yes

The following prerequisites must be met:

- The necessary GCC components are installed.
- The proper Data Root is set up and selected.
- See "Adding a data root" on page 76.
- Libraries are installed for the probe array types you want to process.
- The correct fluidics scripts are installed for the probe array types you want to process.
- See "Installing protocols" on page 172.
- If using remote network data storage or linked instrument control systems, you need to perform additional configuration.

  See Appendix A, "Networking" on page 338.

  Note: GeneChip Command Console (GCC) software has been validated for use with your Operating System's built-in Windows Defender anti-virus software. Using other anti-virus software is not recommended, as it may cause incompatibility issues.

Starting the GCC launcher

IMPORTANT! GCC Launcher menu options vary, as they are based on the type of GCC software that was installed.

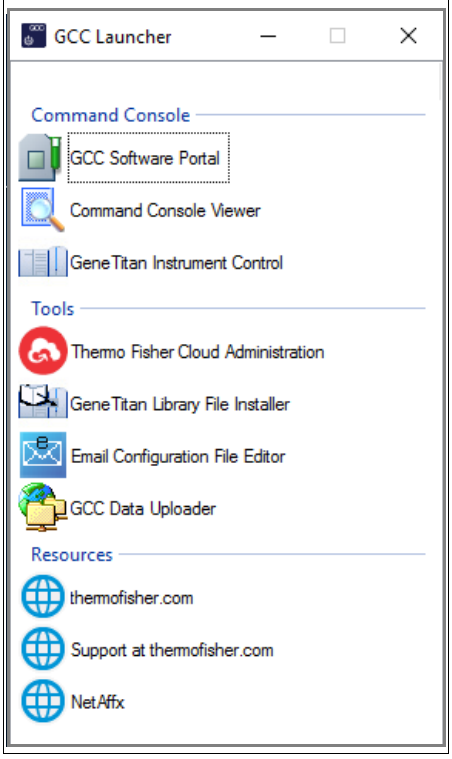
1. Click **Start** →**Thermo Fisher Scientific** → **GCC Launcher** or double-click on the **GCC Launcher** shortcut on the desktop.

   The appropriate Launcher appears:

   "GeneTitan MC" on page 20
   "GCS3000 with fluidics" on page 21
   "Analysis only" on page 22

GeneTitan MC

Figure 3 GCC Launcher menu - GeneTitan MC



Command Console

- **GCC Software Portal** (See "GCC portal home page" on page 48)
- **Command Console Viewer** (See Chapter 9, "Using the GCC viewer" on page 267)
- **Gene Titan Instrument Control** (See Chapter 8, "Controlling the instruments" on page 223)

Tools

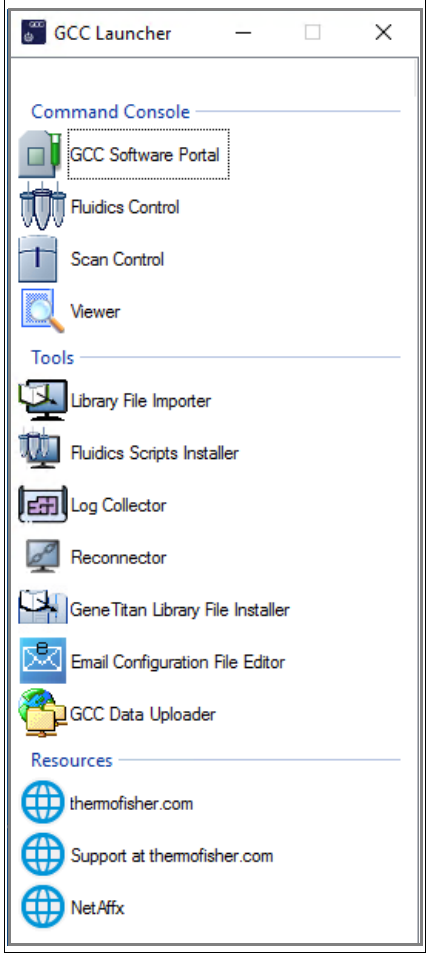
- **Thermo Fisher Cloud Administration** (See "Monitoring an instrument remotely" on page 36)
- **GeneTitan Library File Installer** (See Appendix D, "Installing library files and scripts" on page 360)
- **Email Configuration Editor** (See Appendix E, "Notification e-mails" on page 367)
- **GCC Data Uploader** (See "Scheduling auto-uploads" on page 96)

Resources

- thermofisher.com (Home page)
- Support at thermofisher.com (Services and support page)
- NetAffx (Home page)

GCS3000 with fluidics

Figure 4 GCC Launcher menu - GCS3000 with fluidics



Command Console

- **GCC Software Portal** (See "GCC portal home page" on page 48)
- **Fluidics Control** (See Chapter 6, "Controlling the fluidics station" on page 150.
- **Scan control** (See Chapter 7, "Scanning cartridge arrays" on page 179)
- **Viewer** (For more information, see Chapter 9, "Using the GCC viewer" on page 267)

Tools

- **Library File Importer** (See Appendix D, "Installing library files and scripts" on page 360)
- **Fluidics Script Installer** (See "Installing protocols" on page 172)
- **Log Collector** (See "Collecting GCS3000/FS450 log files" on page 371)
- **Reconnector** (See Appendix H, "Reconnector" on page 375)
- **GeneTitan Library File Installer** (See Appendix D, "Installing library files and scripts" on page 360.)

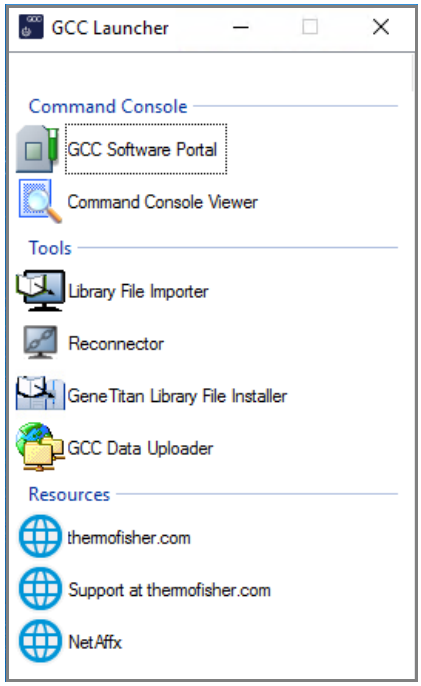
- **Email Configuration Editor** (See Appendix E, "Notification e-mails" on page 367.)
- **Data Uploader** (See "Scheduling auto-uploads" on page 96)

Resources

- thermofisher.com (home page)
- Support at thermofisher.com (services and support page)
- NetAffx (home page)

Analysis only

Figure 5 GCC Launcher menu - Analysis only



Command Console

- **GCC Software Portal** (See "GCC portal home page" on page 48)
- **Command Console Viewer** (For more information, see Chapter 9, "Using the GCC viewer" on page 267)

Tools

- **Library File Importer** (See Appendix D, "Installing library files and scripts" on page 360)
- **Reconnector** (See Appendix H, "Reconnector" on page 375)
- **GeneTitan Library File Installer** (See Appendix D, "Installing library files and scripts" on page 360.)
- **Data Uploader** (See "Scheduling auto-uploads" on page 96)

Resources

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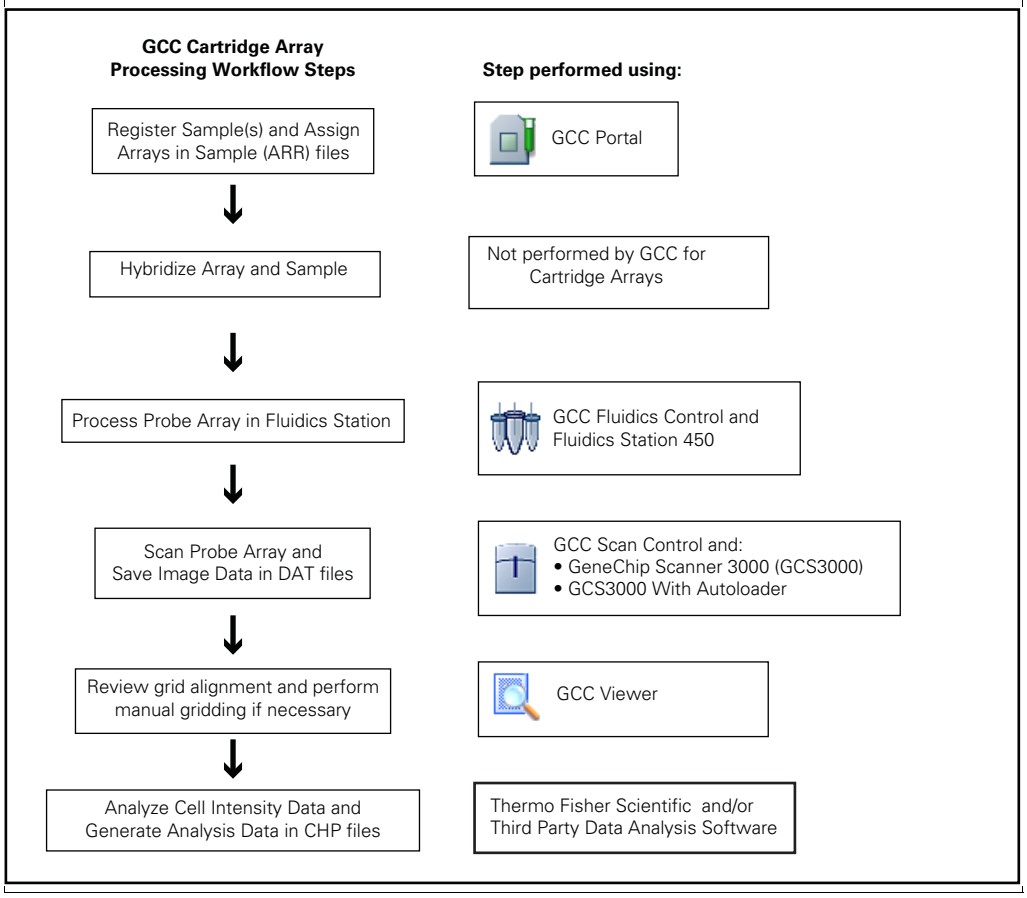
- NetAffx (home page)

Array processing workflow

GCC is used to process the arrays used in your experiment. While GCC provides several options and alternatives for processing arrays, the recommended workflows for cartridge arrays (Figure 6) and for array plates (Figure 7) enable you to include data about the sample and experiment and to easily track the processing steps for the cartridge array or array plate.

Figure 6 Processing cartridge arrays with GCC

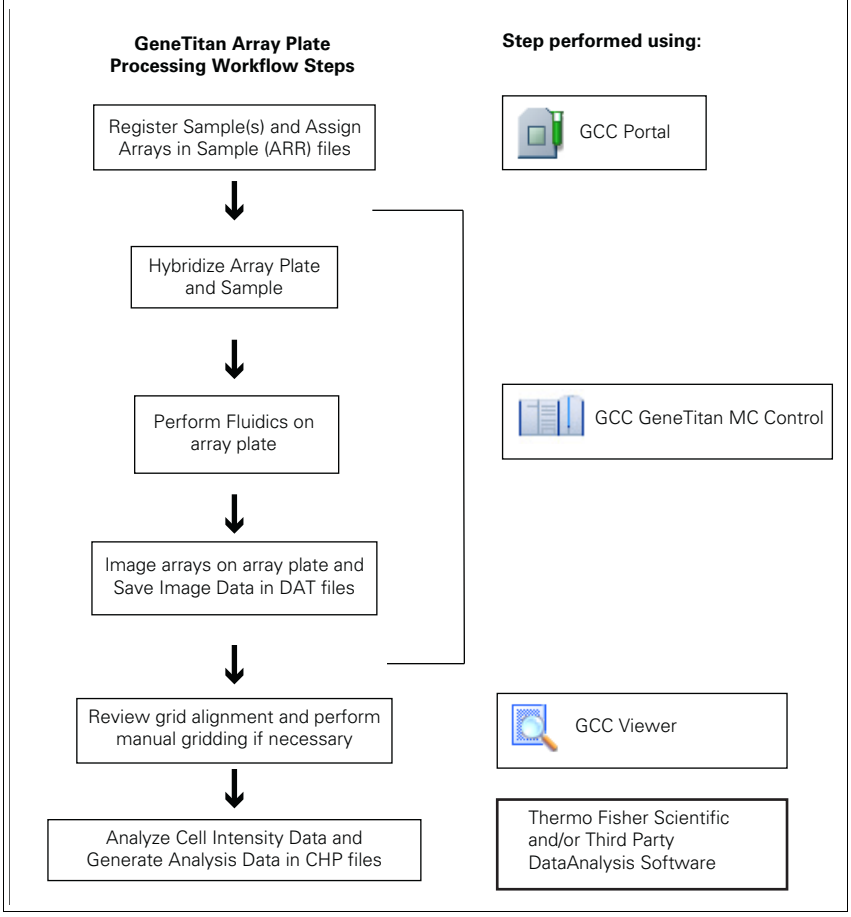


In the recommended array processing workflow for cartridge arrays, you create a sample file as the first step, assigning sample attributes and a physical array or arrays to the sample. You then:

- Hybridize the array and sample (step not controlled using GCC)
- Wash and stain the array(s)
- Scan the array(s) to create Image data (DAT) files.

After that, GCC aligns a grid on the DAT files and computes the Cell Intensity data (CEL) file.

Figure 7 Array Plate Processing Workflow in the GeneTitan MC system



In the recommended array processing workflow for Array Plates, you create sample files for all the arrays on the array plate as the first step. The Hybridization, Fluidics, and Imaging of the array plates are completed using the GeneTitan MC instrument. After that, GCC aligns a grid on the DAT files and computes the Cell Intensity data (CEL) file.

The CEL data generated in the GCC software from array plate data or cartridge data can be used by other software packages for data analysis.

The workflow steps are described in more detail in the following sections:

- "Registering samples and arrays" on page 25
- "Hybridizing arrays and samples" on page 26
- "Washing and staining the arrays" on page 26
- "Running scanners" on page 27
- "Tracking gridding and CEL file generation" on page 27

The GCC Sample and data files that are created during the workflow are described in more detail in "File types in GCC" on page 28.

Registering samples and arrays

In GCC, the Sample file is the beginning of the data chain for a given experiment. The sample information is stored in a Sample file with an ARR extension. The arrays used in analysis and data files produced by analysis are linked to this Sample File.

The information about the sample(s) and experiment(s) are collected as attributes. These attributes can then be used to locate particular Sample files in filtering and search operations.

The links between the sample and data files and the GCC tools used to generate the sample files are described in more detail below:

- "Template and user attributes" on page 25
- "Sample registration options" on page 25

Template and user attributes

There are two types of sample attributes in GCC:

- Template Attributes
- User Attributes

Template attributes

A template in GCC is a list of attributes that can be assigned to a Sample file. When you create a template, you can specify:

- The attributes included in the template.
- The data type for each attribute.
- Whether the attribute is required.
- Value options for a controlled data attribute.

After you have created a template you can assign the template to a new Sample file during Batch Registration (for cartridge arrays). This automatically adds all the attributes in the template to the Sample file. You can then enter values for each attribute. This enables you to standardize the attributes that are assigned to samples.

The template functions are described in "Working with templates" on page 328.

User attributes

User attributes are created dynamically during the registration of a sample and array. This enables you to create a quick note for a particular sample file.

User attributes are not listed in a template; they have usually been added to a specific sample file. They can be used in filtering and search operations, just like the template attributes.

Sample registration options

GCC provides multiple ways to create Sample files. To select the best one for your operation, evaluate:

- Whether you are creating sample files for cartridge arrays or array plates.
- The number of arrays you are going to be processing.
- Whether you want to enter sample attributes during registration.
- Whether you want to enter attributes at a later time.
- Whether you are creating sample files for samples that were processed in a 96-well sample prep plate.

For example:

- Batch Registration enables you to create a group of Sample files for cartridge arrays; you can assign attributes to each Sample file, along with one or more arrays.
- Detailed Registration creates a single Sample file for a cartridge array; you can assign attributes and one or more arrays to the sample file.
- Quick Registration creates multiple sample files for cartridge arrays, each with a single array and no attributes (attributes can be entered later).
- Sample Prep Plate Registration creates sample files for cartridge arrays for samples in up to two 96-well plates.
- Array Plate Registration creates the sample files for the arrays on an Array Plate for the GeneTitan MC System.
- Editing functions correct problems or add attributes to previously created sample files.

The Sample registration options are described in Chapter 5, "Creating and editing sample (ARR) files" on page 101.

In addition, the Drop and Scan feature enables you to create a sample file for an array when the array is scanned. Drop and Scan is available for:

- Cartridge arrays (see "Drop and scan" on page 206)
- Array Plates (see "Drop and scan with array plates" on page 260)

Hybridizing arrays and samples

For GeneChip cartridge arrays, hybridization is not controlled using the GCC software.

For Array Plates, the hybridization is controlled using the GCC GeneTitan MC Control software (see Chapter 8, "Controlling the instruments" on page 223).

Washing and staining the arrays

Different instrumentation and instrument control software used to process Cartridge Arrays and Array Plates.

Cartridge arrays

The Fluidics Station 450 (FS450) is used to hybridize, wash, and stain the GeneChip arrays (called arrays in this manual). The FS450 can independently process an array using a different fluidics protocol in each of four different modules.

The GCC Fluidics Control software is used to control the FS450. A workstation with GCC Fluidics Control software and a Sealevel card installed can control up to eight different fluidics stations. The software and its uses are described in Chapter 6, "Controlling the fluidics station" on page 150.

Array plates

The arrays on the Array Plate are washed and stained using the GeneTitan MC instrument, controlled using the GCC GeneTitan Control software. The software and its use are described in Chapter 8, "Controlling the instruments" on page 223.

Running scanners

Different IC software and instrumentation are used to scan:

- Cartridge Arrays
- Expression Array Plates
- Genotyping Array Plates

Cartridge arrays

The array is scanned after hybridization, washing, and staining, using one of the following scanners:

- GeneChip Scanner 3000 (GCS3000) (scans one chip only)
- GCS3000 with Autoloader (load up to 48 chips for scanning without operator attention)

The GCC Scan Control Software is used to control the scanner. The software and its use are described in Chapter 7, "Scanning cartridge arrays" on page 179.

Expression array plates

The arrays on the array plate are scanned using the GeneTitan MC instrument, controlled by the GCC GeneTitan Control software.

The software and its uses are described in Chapter 8, "Controlling the instruments" on page 223.

There are some differences in how the arrays from array plates are scanned and the data is managed, as described on "GeneTitan array plates" on page 271).

Genotyping array plates

The arrays on the genotyping array plates are scanned using the GeneTitan MC Instrument, controlled by the GCC GeneTitan Control software.

The software and its uses are described in Chapter 8, "Controlling the instruments" on page 223.

There are some differences in how the arrays from array plates are scanned and the data is managed, as described on "GeneTitan array plates" on page 271).

Tracking gridding and CEL file generation

After the array has been scanned, GCC:

- Aligns a grid on the Image (DAT) file to identify the probe cells.
- Computes the probe cell intensity data for the array and creates a CEL file.
- Generates JPG and RPT files.

The GCC Viewer enables you to track the progress of this step in the workflow and manually correct gridding problems, if necessary. The Viewer and its uses are described in Chapter 9, "Using the GCC viewer" on page 267.

File types in GCC

Different types of information are collected by GCC in different types of files:

- Information about the sample and experiment are collected in Sample files (see "Sample files", below)
- Probe array data generated during scanning and processing are collected in Data files of various types (see "Tracking files with GUIDs" on page 29).
- Audit and Log files contain information about array processing and other processes (see "Other file types" on page 31)

Globally Unique Identifiers (GUIDs) are used to track the relationships between Sample files, physical arrays, and Data Files (see "Tracking files with GUIDs" on page 29)

Sample files

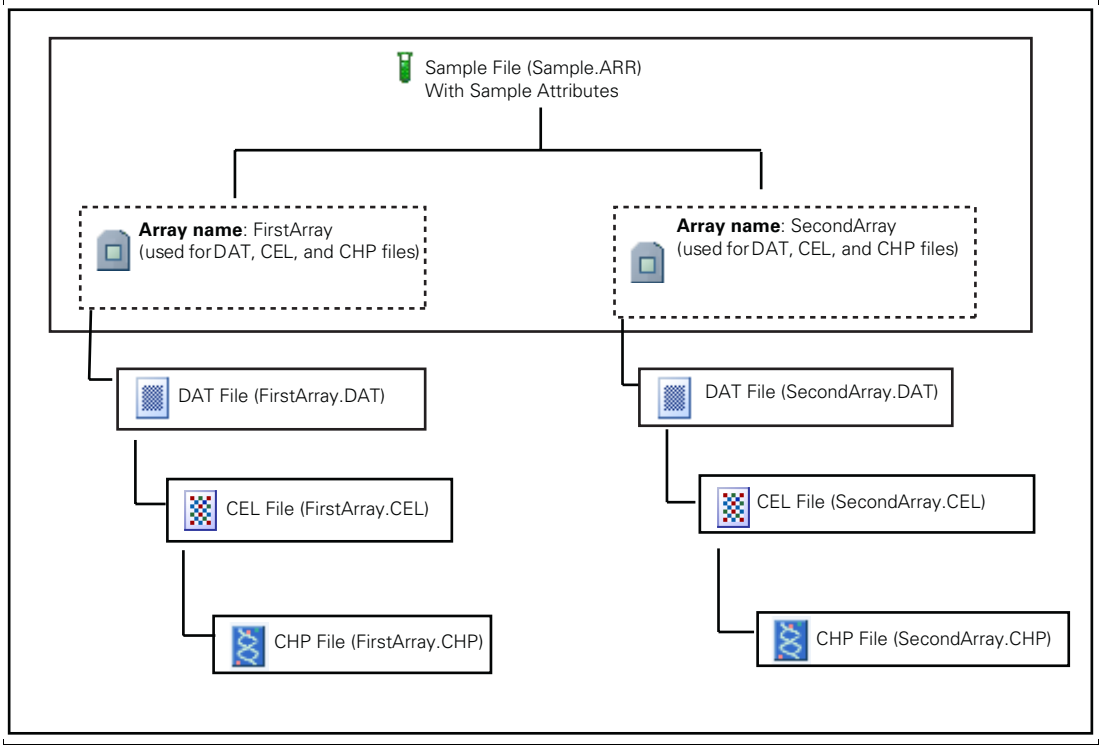
The Sample (ARR) file (Figure 8) collects two types of information:

- Sample Attributes: information that you can use to interpret the experimental data. It can include information about the sample itself, the experimental conditions, or other information you may find useful.

  You can use the attributes to search for particular files; some attributes can be used by the probe level analysis software during analysis. You can use templates to manage the attributes used for a particular experiment (see "Template and user attributes" on page 25 for more information).
- Array Information: Information about the array(s) used with the sample. More than one array can be associated with the sample. This is useful for tracking replicates; in addition, it can be used to simplify tracking data for multi-chip arrays.

  Each array is assigned an array name during registration. The array name is used to identify the DAT, CEL, and CHP data files that are generated during analysis.

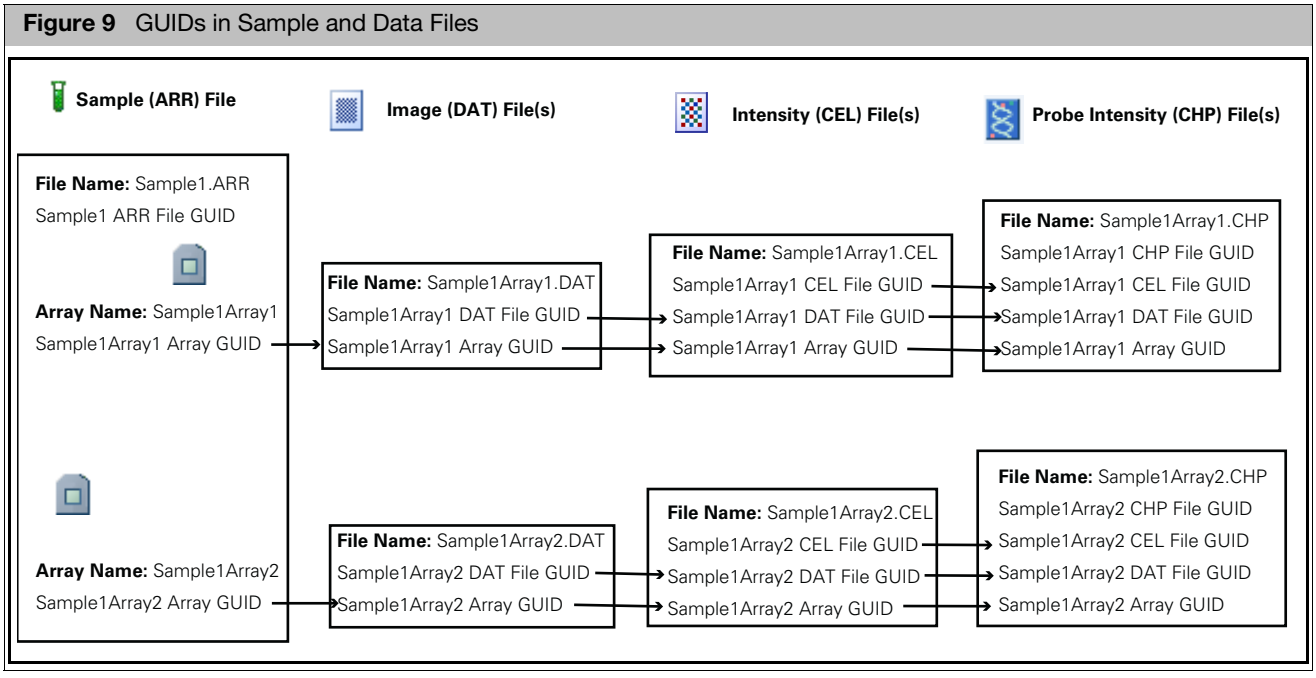
Figure 8 Sample File with associated arrays and data files



Tracking files with GUIDs

A GUID, or Globally Unique Identifier, is assigned to each file for tracking (Figure 9). GUIDs are numbers generated to track a file that are unique to that file.

Figure 9 GUIDs in Sample and Data Files



During Sample registration the Sample file is assigned a Sample File GUID. In addition, an Array GUID is provided for every array name entered.

Every data file (DAT, CEL, and CHP) generated for an array will contain the Array GUID for the array, as well as the GUIDs for each of its parent data files.

The GUIDs enable you to trace the lineage of any data file independent of the file name.

Data files

A set of data files is produced for each array in the Sample file. (Figure 9)

The data files include:

- "Image (DAT) file"
- "Intensity (CEL) data files" on page 30
- "Probe analysis (CHP) Files" on page 30

Each file is assigned a GUID, or Globally Unique Identifier, to be used in tracking the relationships between Sample files, physical arrays, and data files. See "Tracking files with GUIDs" on page 29 for more information.

Image (DAT) file

The DAT file contains pixel intensity values collected from the scanner, along with the gridding information used during feature extraction.

When a DAT file is regridded, the underlying data used by previously generated CEL files is changed. A new GUID is assigned to the regridded DAT file, breaking the link to any previously generated CEL files. The CEL files are linked with the array via array GUIDs, but not to the regridded DAT file. CEL files generated after regridding are linked to the new DAT file via the DAT file GUID and to the array by the array GUID.

Intensity (CEL) data files

The CEL file stores the results of the intensity calculations on the pixel values of the DAT file. This includes an intensity value, standard deviation of the intensity, the number of pixels used to calculate the intensity value, a flag to indicate an outlier as calculated by the algorithm and a user defined flag indicating the feature should be excluded from future analysis. This data is used by the CHP writer software to extract the actual data of interest.

JPG files

JPEG files are a copy of the DAT file in a standard image file format; they provide an image file with a reduced file size for QC inspection, archiving, and publication.

Probe analysis (CHP) Files

These files, which have file extensions ending in CHP, contain the probe analysis data for the array. They are produced by the Analysis Application software and contain the actual data of interest (SNP calls, expression data, etc., depending upon the array type).

Other file types

Audit and Log files track the tasks performed by different software components.

Audit files

An Audit file is an XML file that tracks the processing of each physical array processed by GCC. An Audit file is produced for each physical array and tracks all the processing steps that were performed on the array, including multiple scannings and regridding.

The audit file has the same root name as the physical array.

See "Viewing audit files" on page 65.

Log files

Log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and the installer.

These log files may provide useful information for troubleshooting problems.

See Appendix F, "Log files generated by GCC" on page 369 for more information.

Organizing data

To use GCC, you need to understand the structures and tools the software provides for organizing your data during and after generation.

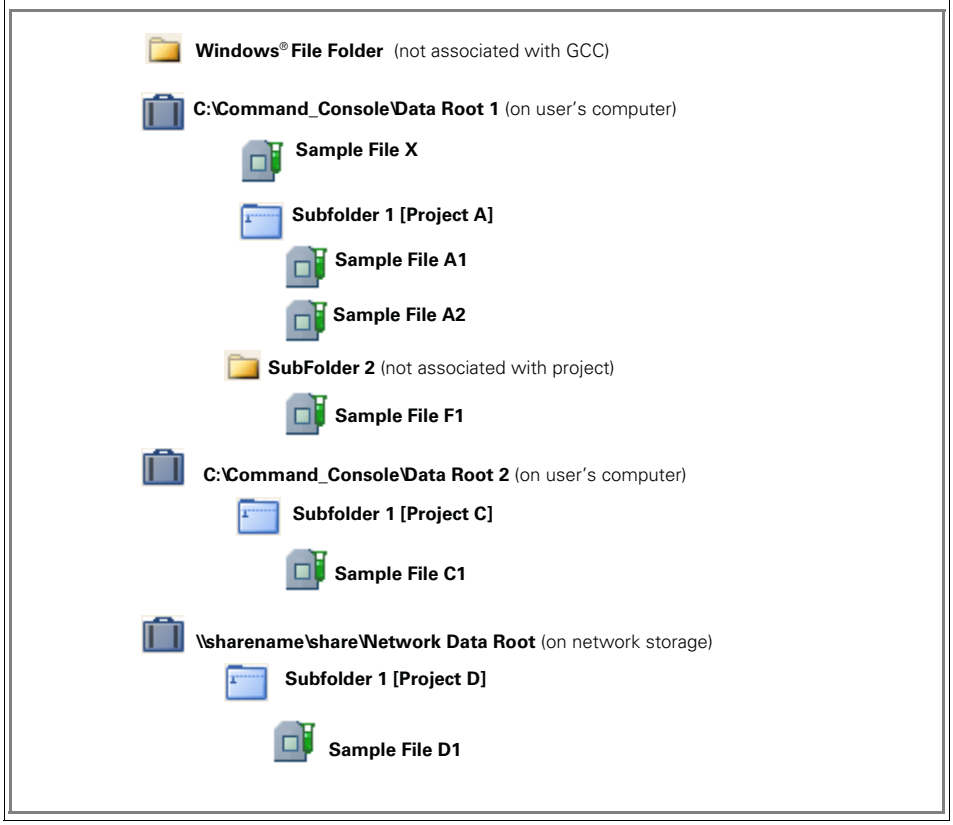
This section describes:

Folders

GCC uses the Windows file folders on your hard drive to organize your data.

Note: A folder must be designated as an GCC data root, or must be a sub-folder of a designated GCC data root, for the files in that folder to be tracked by GCC (Figure 10).

Figure 10 Organization of files in GCC



Windows file folders

These are folders that are on your hard drive, but have not been assigned to a GCC Data Root, either directly or by a parent/child relationship.

These file folders are not searched by the Indexer and the files in them are not displayed in the GCC Portal. You can copy GCC files to a system folder using different GCC Portal functions, which is useful for sharing data with other users.

Data roots and sub-folders

A Data Root is a folder that has been specified for Command Console data. Data roots are searched by the Indexer and the files in them are listed in the GCC Portal.

Note: On instrument control workstations, the default data root has to be on the local drive and cannot be a USB or an external network drive.

A default data root is created when the software is installed. You can assign other folders as data roots, too. A data root can be on the computer running GCC, or on a network data storage computer connected with a Windows network.

A data root on a local drive is indicated as a local drive path: `C:\Command_Console\Data` for example.

Data roots on networked computers are specified using Universal Naming Convention (UNC) paths as `\\server\share\filepath`.

A sub-folder is a child folder created within a data root. The sub-folder and its files are also searched by the indexer and listed in the GCC Portal.

For information about setting the data root, see "Managing data roots" on page 75.

For information about using a data root on a different computer on a Windows network, see Appendix A, "Networking" on page 338.

The data roots and sub-folders and their contents are displayed in the Folder view (see "Folder view" on page 50).

File and folder security

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly. **Work with your IT department for help in setting the permissions**.

For more information, see Appendix B, "Windows sharing and security issues" on page 348.

Default folders

A Default folder is a data root or sub-folder that has been set as a destination folder for files produced when certain operations are performed:

- Sample and data files produced when performing Drop and Scan.
- Data files for an array that is registered to a Sample file located on network data storage.

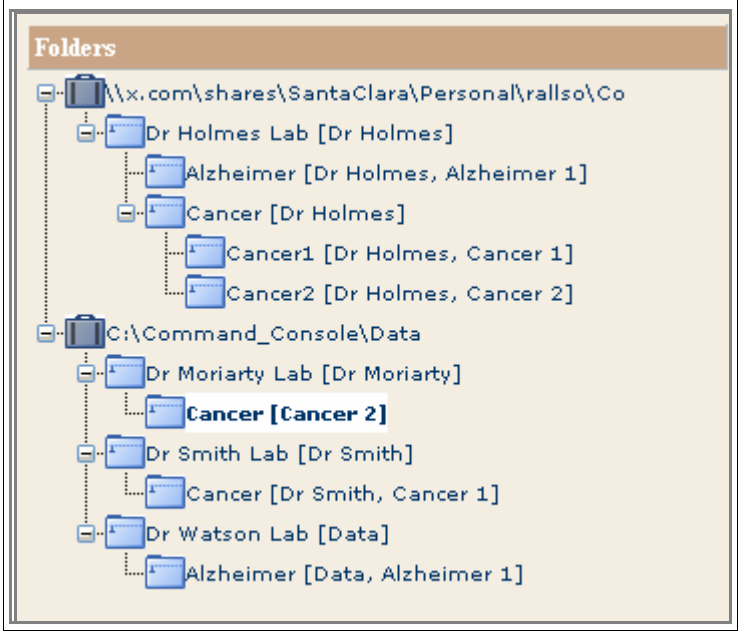
For more information, see:

- "Specifying a default folder" on page 90
- "Drop and scan" on page 206
- "Drop and scan with array plates" on page 260
- "GCC network functionality" on page 35
- "The Status window (Figure 211) displays the following information:" on page 182

Projects

A project is a label assigned to a Data Root or sub-folder; the project label can be used to organize Sample and data files. If you assign a project name to a Data Root or sub-folder, all the Sample and data files in that folder are assigned that project name. Any child sub-folders of that project folder are assigned the project name, as well.

Figure 11 Projects and folders in a data root



Projects have the following characteristics:

- Any Data Root or sub-folder can be a project.
- All sub-folders in a project folder are automatically a part of that project.
- One folder can be a member of more than one project.
- Folders in different locations can be in the same project.

After assigning a project name to a data root or sub-folder, any Sample file placed in that data root or sub-folder is assigned to the project. You can then use the project label to:

- Display file lists grouped by project
- Search on data limited to a project
- Create a spreadsheet listing the Sample (ARR) files assigned to the project with their attributes. The list can be reviewed as a summary of the project information or used to edit the Sample (ARR) file content using Batch Edit.

You can also assign a sample file to a project during its creation. This places the Sample File and the associated data files in the folder assigned to the project name.

You can move files between projects using Windows Explorer.

For more information, see "Using projects to organize data" on page 78.

Data organization tools in GCC

The data organization tools in GCC enable you to:

- View the files in data roots and folders
- Create and manage projects
- Search for files of interest by various attributes, including sample attributes entered during registration.
- Add and remove Data Roots
- Upload data to a data root

Note: To perform data management functions, you must use Windows Explorer.

See Chapter 4, "Portal and data organization" on page 47 for more information on the data organization tools.

GCC services

The following GCC Services run (in the background) on your computer:

The following GCC Services run (in the background) on your computer:

- GCCAuditLogger
- GCCIndexer.
- GCCTaskManager
- GCCWebServer
- **GCC WorkflowBroadcastService:** This service enables the instrument to notify analysis applications that data is available for analysis.
- **GCC DeepLaserService**: This service enables the instrument to send notifications and upload data to the Thermo Fisher Scientific Cloud.

Note: If using network functionality, you may need to change the configuration of these services. See "Configuring GCC services" on page 344.

Displaying GCC WebServer status

For GCC, the GCC WebServer enables the display of the GCC Portal pages; it must be running to use GCC Portal. By default, it starts when the computer boots up.

Normal operation is indicated by an icon in the right side of the Taskbar (Figure 12).

Figure 12 GCCWebServer Icon in status area of Taskbar

GCC network functionality

When GCC is installed on a system, then connected to a Windows network, it provides additional functionality with options for running the array processing workflow and organizing data. These functions include:

- Consolidating the data from multiple GCC workstations on network data storage.
- Performing different parts of the workflow for an array on different workstations while consolidating the data on a single workstation.

You may need to change the settings for some GCC Services to use the network functionality. See Appendix A, "Networking" on page 338 for more information.

3 Monitoring an instrument remotely

Creating a cloud account

Before you can access and monitor an instrument remotely, you must first create a Thermo Fisher Cloud account.

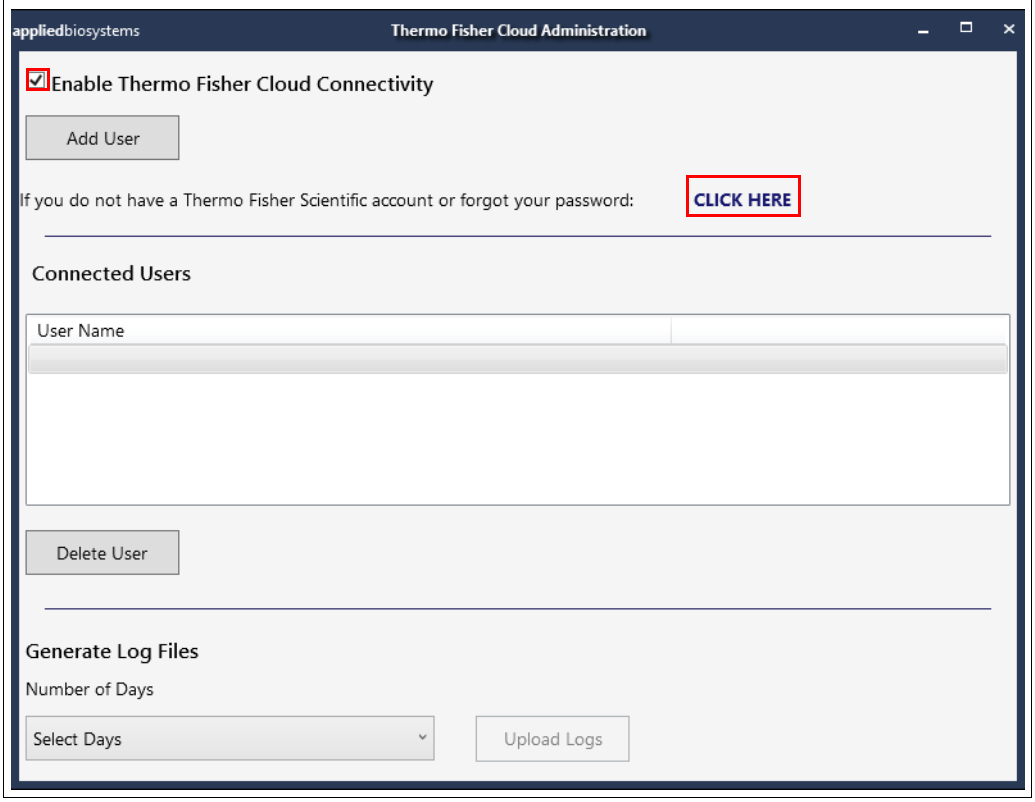
Note: The Cloud account option is ONLY available on the GeneTtian GCC Launcher.

1. Double-click on the **GCC Launcher** Desktop shortcut 

icon.
   The Launcher window appears.
2. Double-click **Thermo Fisher Cloud Administration**.
   The Cloud Administration window appears. (Figure 13)

IMPORTANT! Before signing up: a) You must have an active Internet connection. b) The **Enable Thermo Fisher Cloud Connectivity** check box must be checked, as shown in Figure 13.

Figure 13 Thermo Fisher Cloud Administration



3. Click **CLICK HERE**, as shown in Figure 13.

   The Thermo Fisher Connect web page appears.

4. Click **SIGN UP NOW**.

   A registration page appears.

5. Complete all fields, then click **Create account**.

   After a few moments, you will receive an email confirming you have been successfully added to the Thermo Fisher Cloud.

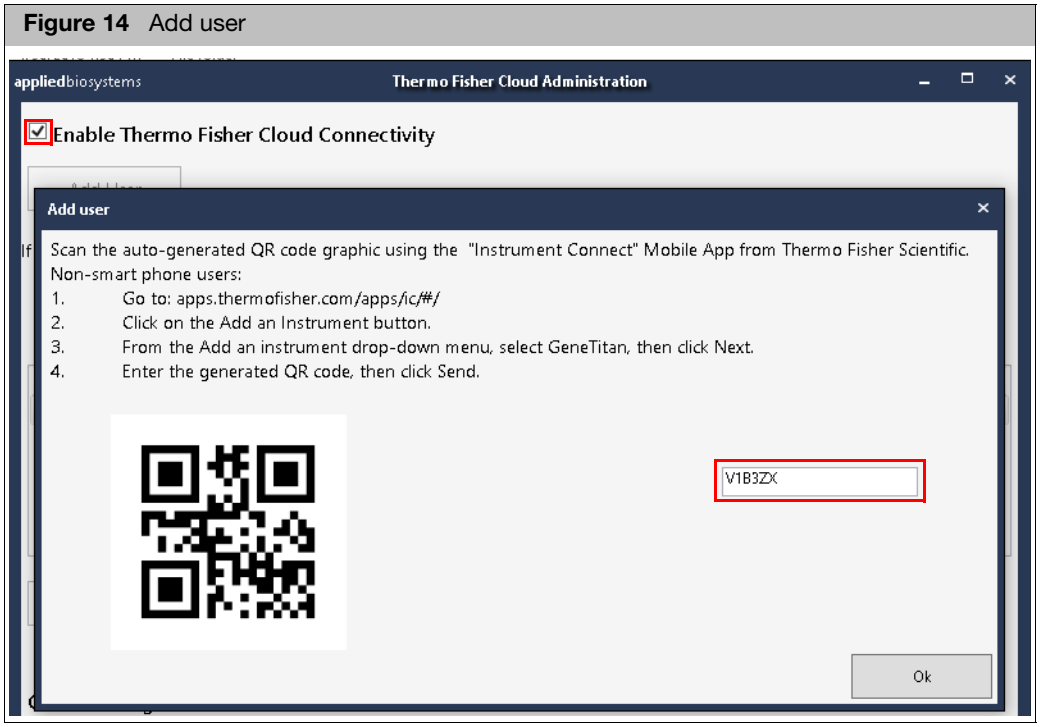
Adding users

IMPORTANT! You cannot add a user(s) while the instrument/scanner is running.

1. Click **Add User**.

   The Add user window appears with an auto-generated QR code graphic and code, as shown in Figure 14.

Figure 14 Add user



Connecting to an instrument remotely

Smart phone (Android OS 5.0+ and iOS 9.0+ only)

1. Go to your smart phone's application store and download **Instrument Connect**.
2. Install the app as you normally would, then follow the registration and/or sign in instructions.
3. Use the Instrument Connect app to scan the auto-generated QR code graphic.

Non-smart phone users

1. Go to: **apps.thermofisher.com/apps/ic/#/**

   The Instrument Connect page appears.
2. Click the **Add an Instrument** button (upper right).

   The Add an instrument window appears.
3. Click the drop-down menu, select **GeneTitan**, then click **Next**.

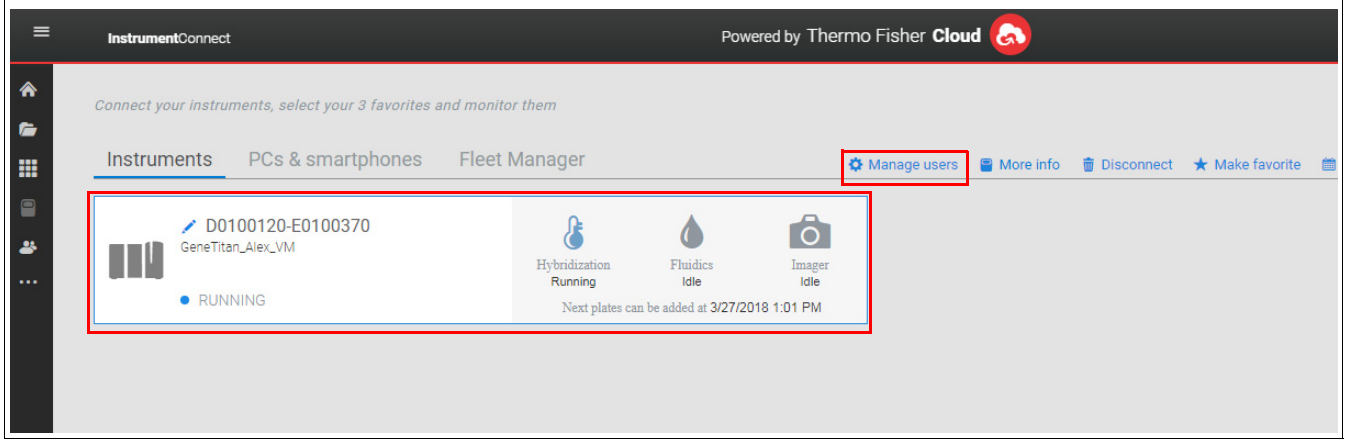
   After a few moments, you will receive an email confirming your instrument has been successfully added to your Thermo Fisher Cloud account.
4. Open the email and confirm its content coincides with the specific instrument you wanted to connect to, then click on the **Thermo Fisher Instrument Connect** hyper-link.

   Your browser opens to a Thermo Fisher Scientific/Returning Customer web page.
5. Enter your User Name and Password, then click **Sign In**.

   A Thermo Fisher Cloud Terms of Use window appears.
6. Review and acknowledge the terms, then click **Accept**.

   The Instrument Connect web page appears (Figure 15) and you are now remotely connected to the instrument.

Figure 15 Instrument Connect web page



The Instrument Connect page features the Instrument's custom tile (Figure 15) that displays the current operational status of the instrument.

- **Idle** - Instrument is on standby and ready for use
- **Running** - Instrument is in use.
- **Unknown** - Instrument has stood idle for more than 24 hours.

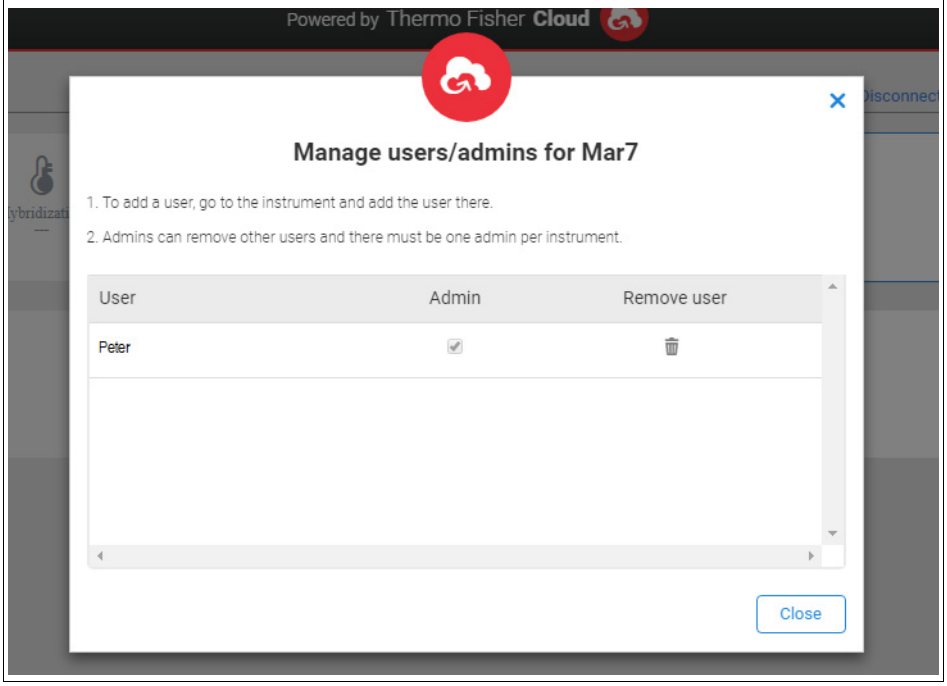
Managing users (optional)

If you are the Administrator or the first to log into the instrument, the **Manage users** link (Figure 15) is enabled (shown in blue).

1. Click on **Manage users**.

   The Manage users window appears. (Figure 16)

Figure 16 Manage users window



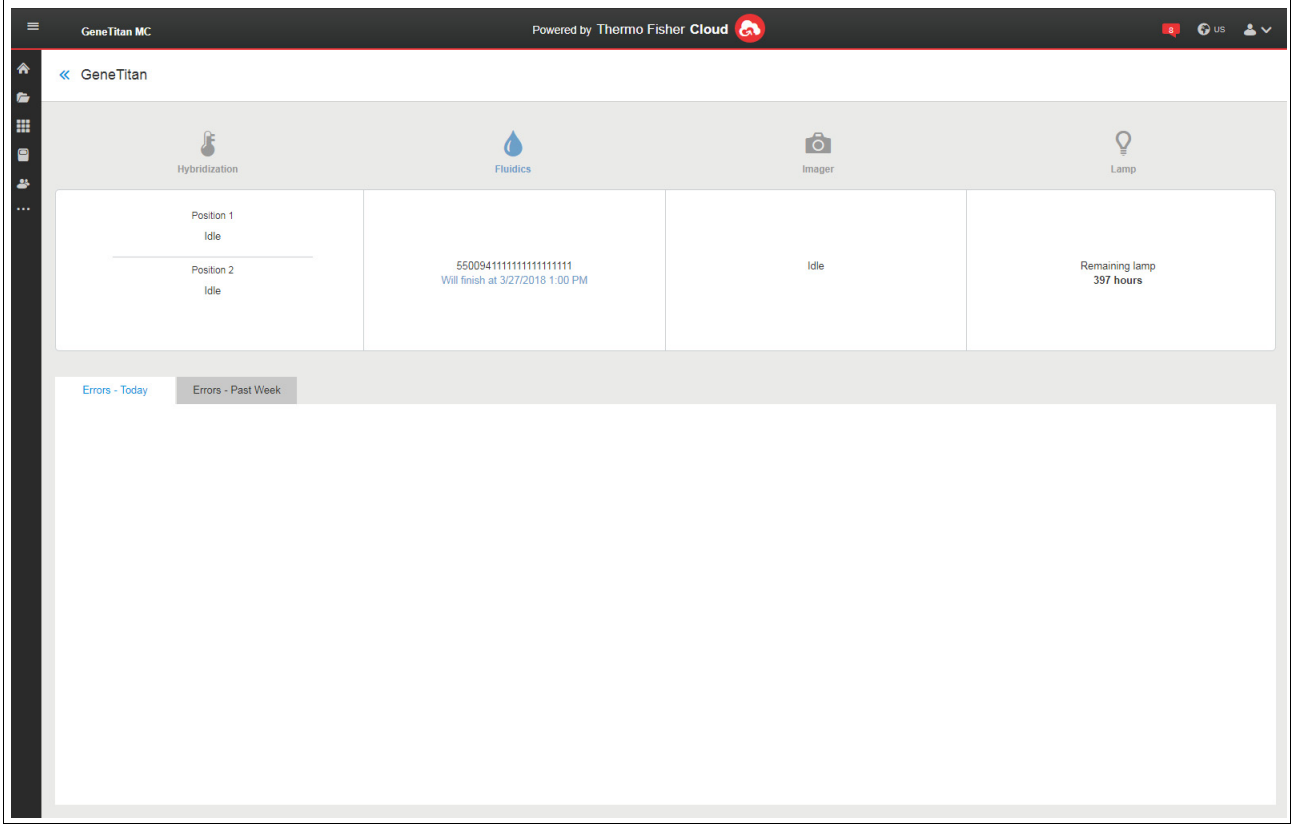
   - To add a user, return to the Thermo Fisher Cloud Administration window. (Figure 13 on page 36)
   - To remove a user, click to highlight the user you want to remove, then click on the trash can icon.
   - Click **Close** to close the window.

Viewing the instrument status in detail

1. Double-click on the Instrument's custom tile.

   The details page appears. (Figure 17)

Figure 17 Instrument Connect web page



The details page displays:

- While the instrument is running, plate position information and ending time for a plate to finish its step is displayed.
- Remaining lamp life hours.
- Error log window tabs. Any reported errors for the current day and/or past week are retained inside these window tabs for your review.

Error logs

If needed, you can send instrument error logs to your support representative using your Thermo Fisher Cloud account or by emailing a zip file of your log files.

Using your cloud account

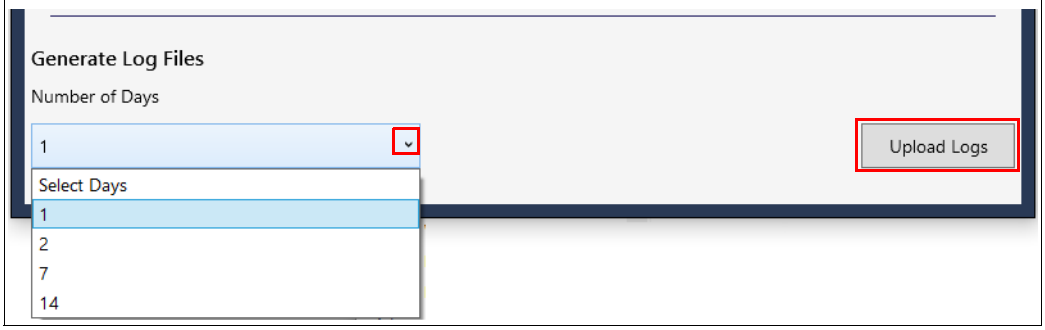
1. Double-click on the **GCC Launcher** Desktop shortcut 

icon.
   The Launcher window appears.
2. Double-click **Thermo Fisher Cloud Administration**.
   The Cloud Administration window appears.

IMPORTANT! Before accessing the cloud: a) You must have an active Internet connection. b) The **Enable Thermo Fisher Cloud Connectivity** check box must be checked.

3. Click the **Select Days** drop-down menu to choose the number of logged days you want to collect.
4. Click the **Upload Logs to Thermo Fisher Cloud** check box, then click **Gather Logs**. (Figure 18)

Figure 18 Generate and gather log files



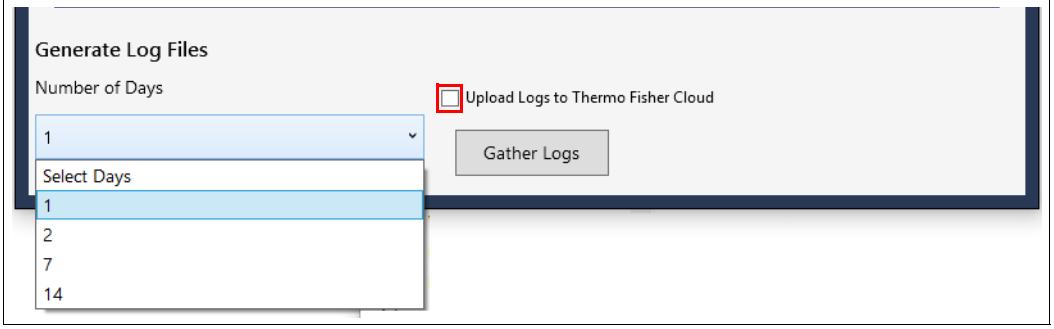
   A percentage of completion wheel graphic appears (lower right), followed by a *Logs uploaded successfully* message.
5. Click **OK** to acknowledge the message.
   The error log file(s) now reside on the cloud and are ready for your support representative to review.

Using the email option

1. Double-click on the **GCC Launcher** Desktop shortcut 

icon.
   The Launcher window appears.
2. Double-click **Thermo Fisher Cloud Administration**.
   The Administration window appears.
3. Click the **Select Days** drop-down menu to choose the number of logged days you want to collect. (Figure 19)

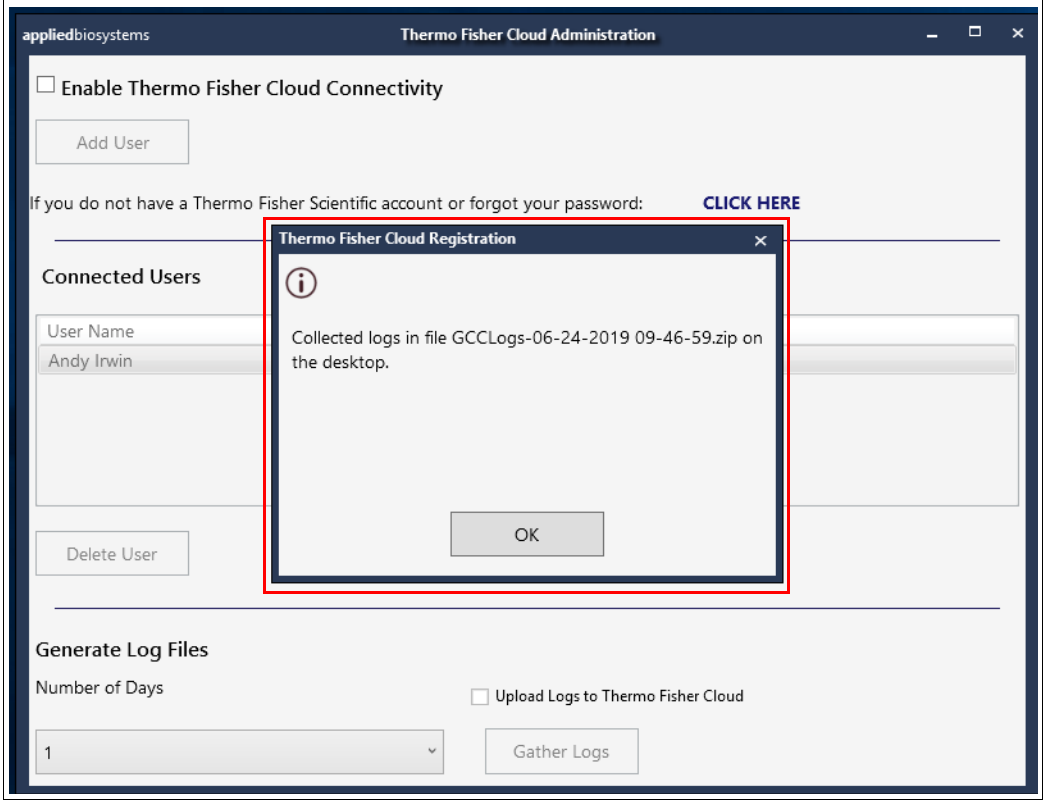
Figure 19 Generate and gather log files



4. Make sure the **Enable Thermo Fisher Cloud Connectivity** and **Upload Logs to Thermo Fisher Cloud** check boxes are unchecked, then click **Gather Logs**.

   A percentage of completion wheel graphic appears (lower right). After a few moments, a message appears stating your logs have been collected and converted to a zip file on your Desktop. (Figure 20)

Figure 20 Logs collected message



5. Click **OK** to acknowledge the message.
6. Compose an email to your support representative, attach the Log Files zip file, then send the email as you normally would.

Uploading data manually

You can also manually upload your data results to your current cloud folder or sub-folder, including failed data that has been successfully re-gridded and/or re-scanned.

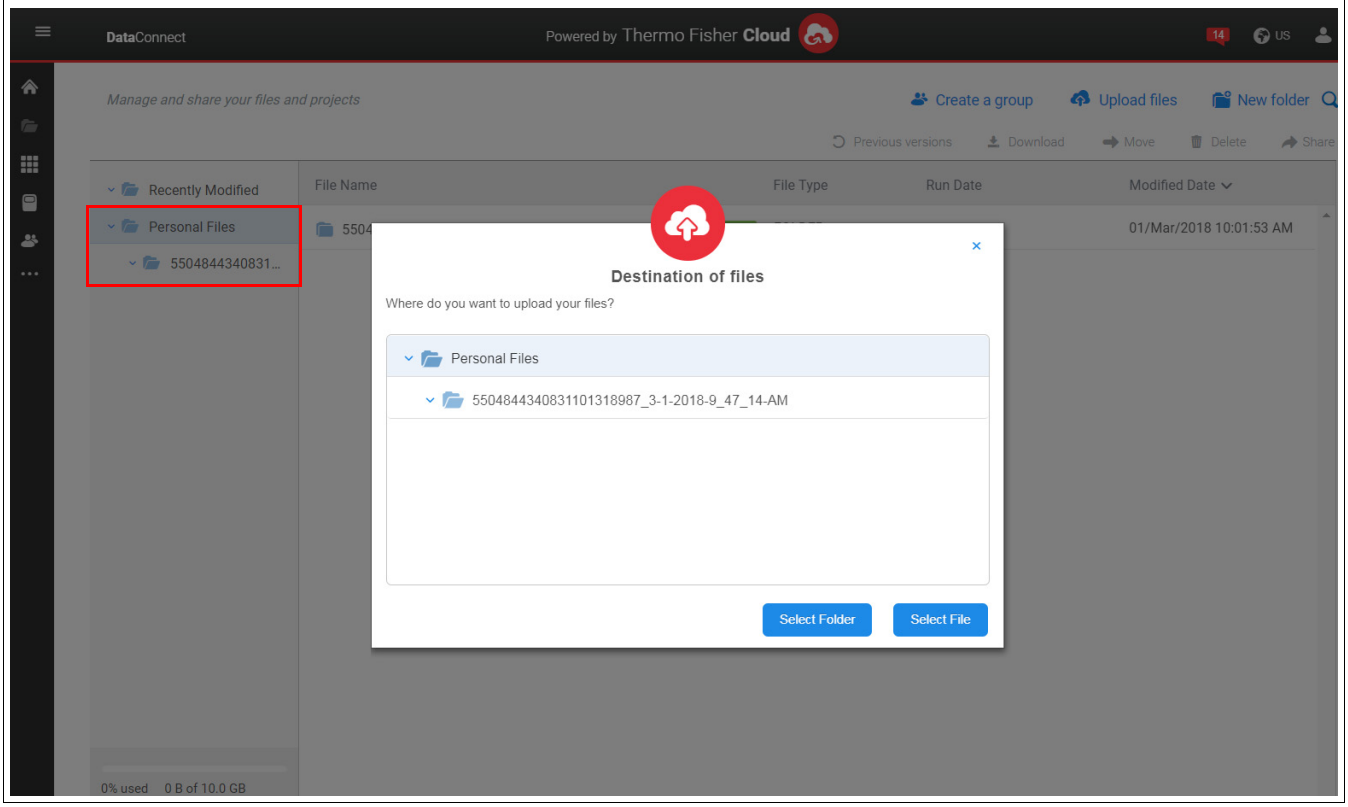
IMPORTANT! Uploading data with unresolved scanning or gridding failures is not recommended.

Manually uploading data to the cloud

1. From the Data Connect web page, click Upload files .

   A **Destination of files** window appears. (Figure 21)

Figure 21 Data Connect web page



Uploading a folder

1. Click **Select Folder**

   A Browse for Folder window appears.

2. Navigate to your folder's location, click to highlight it, then click **OK**.

   An **Uploading Files** status window appears (lower right), followed by a **Your files have been uploaded** window.

3. Click **X** to close this window.

   Your manually uploaded folder and its contents now resides in your cloud folder. (Figure 21) To share the folder, see "Using the cloud to share data results".

Uploading a file

1. Click **Select File**.

   An Explorer window appears.

2. Navigate to your file's location, click to highlight it, then click **Open**.

   An **Uploading Files** status window appears (lower right), followed by a **Your files have been uploaded** window.

3. Click **X** to close this window.

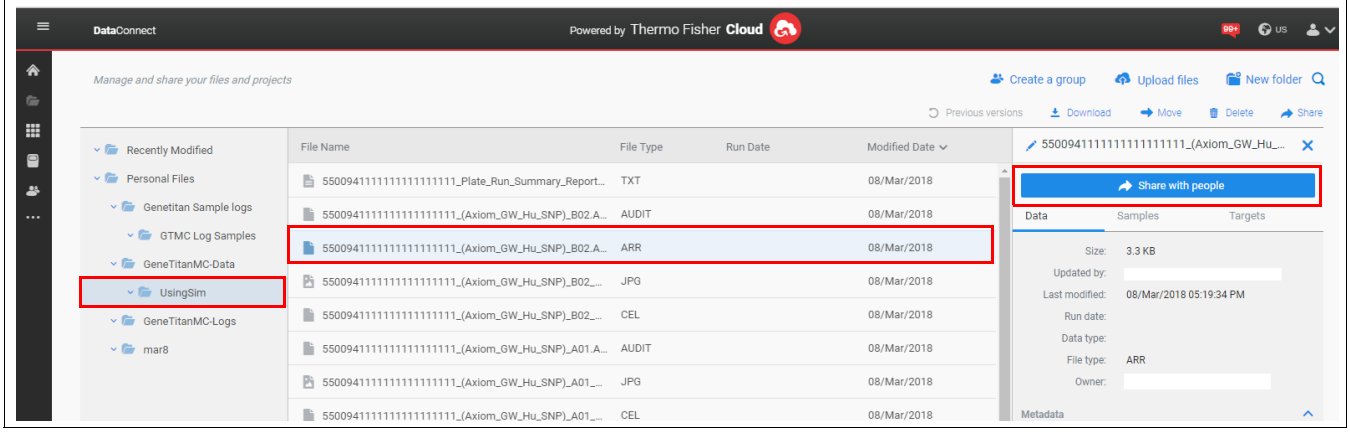
   Your manually uploaded file now resides in your cloud folder. (Figure 21)
   To share the file, see "Using the cloud to share data results".

Using the cloud to share data results

While connected to the cloud, you can share your uploaded data results.

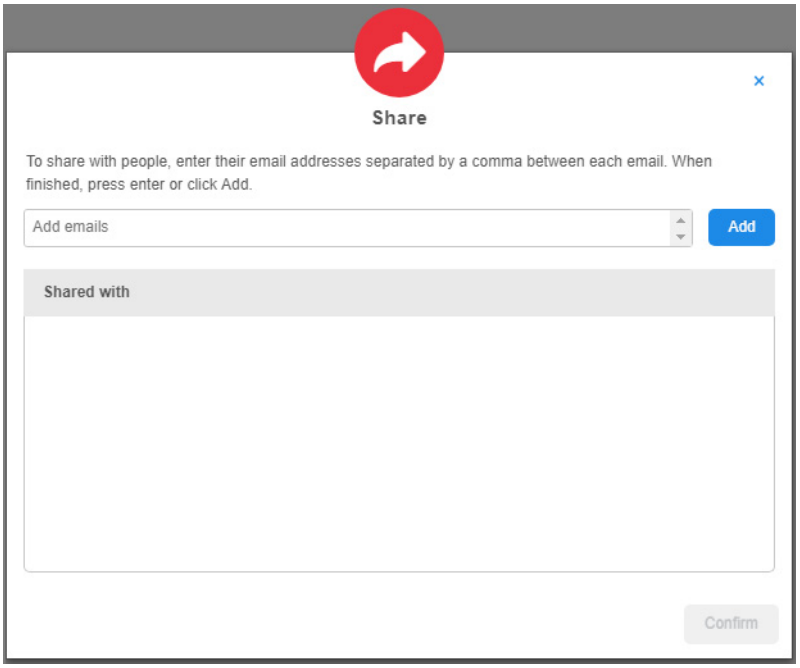
1. Click the **Data Connect**  icon.
   The Data Connect window appears.
2. From the folder list (left pane), click to select a data folder you want to share.
   Any applicable sub-folders appear.
3. Click to select the appropriate folder.
   The middle pane populates.
4. From the middle pane, click to highlight the folder or file you want to share, then click the **Share with people** button. (Figure 22)

Figure 22 Data Connect web page



A Share window appears. (Figure 23)

Figure 23 Share window



5. In the **Add emails** field, enter the recipient's email address, then click **Add**.

   The email is now populated in the **Shared with** pane and is retained within the Add emails drop-down selection during your next session.

6. Click **Confirm**.

   An email (with a hyper-link to your data) is sent to your recipient(s).

   To delete an email/recipient from the Shared with list, click its adjacent **remove** option.

4 Portal and data organization

The data organization functions enable you to organize your data and copy files from place to place. The functions are described in:

Disabling fast user switching

Fast user switching is an option in Windows that enables multiple active sessions on the console.

This option must be disabled on computers with GCC Portal installed, because it may cause a user to take actions under a different user ID and ultimately lock the first user from their data.

Refer to your Windows 10 Enterprise 2016 LTSB documentation on how to disable Fast user switching.

Starting GCC portal

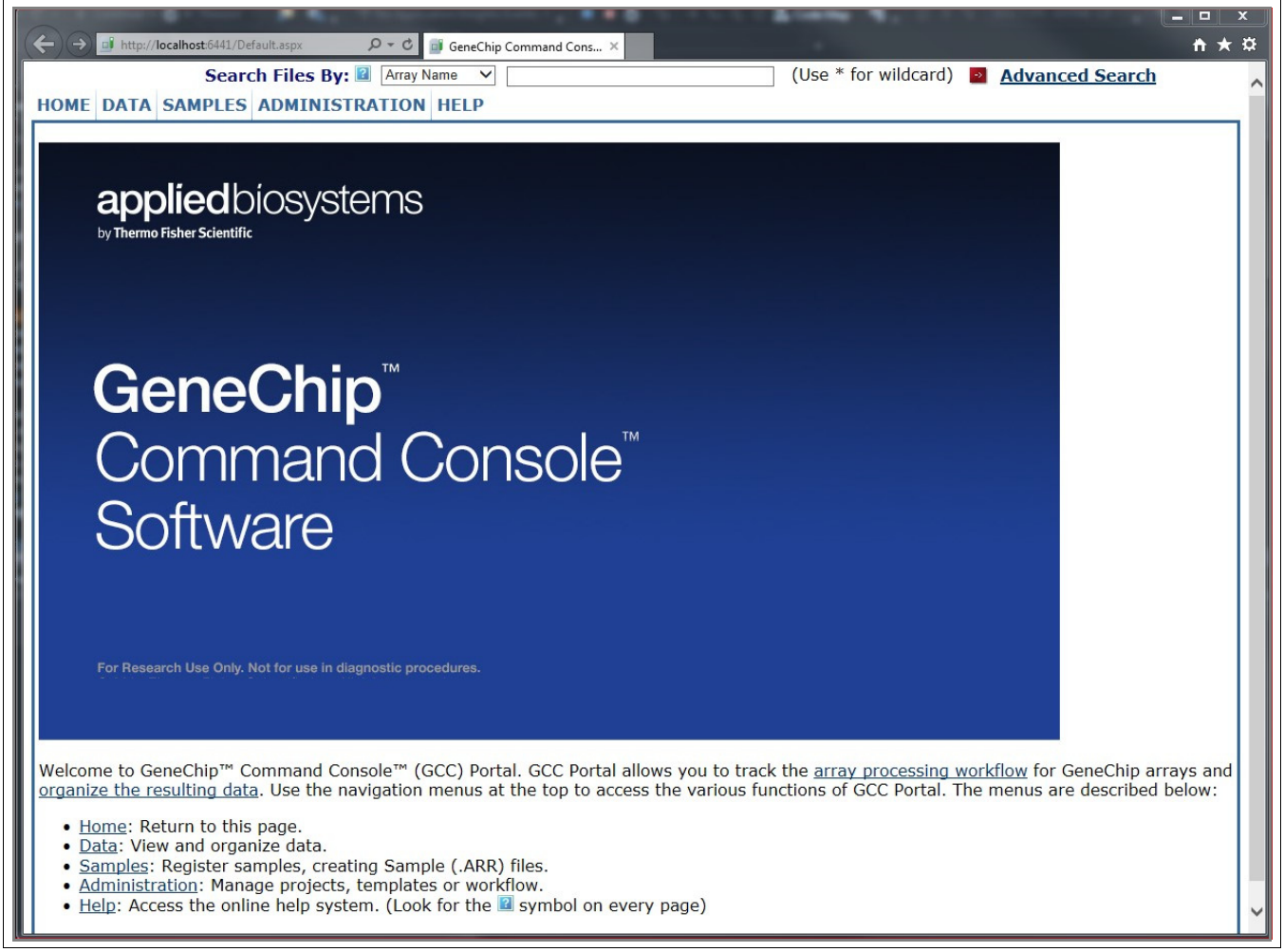
1. Open the GCC Launcher.
2. Click **GCC Portal**.

   The Home page appears. (Figure 24)

GCC portal home page

The GCC Home page (Figure 24) is your entry point to the GCC Portal functions.

Figure 24 GCC Portal Home Page



Home page features

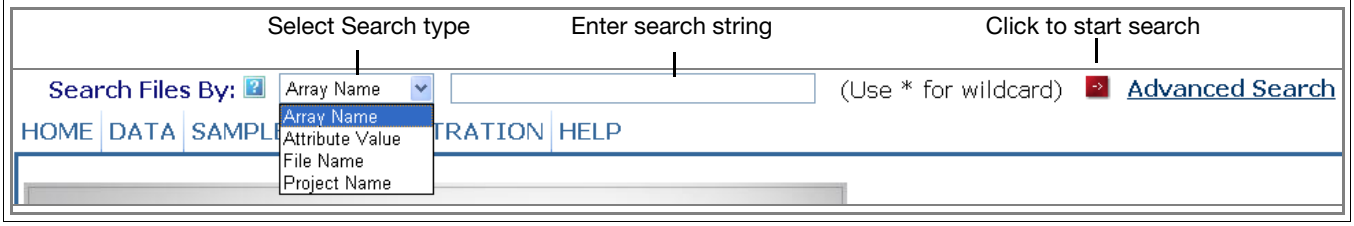
- Menu Bar (see below)
- Search Functions (see "Searching for files" on page 66)

Home page	• GCC Home Page • Web site and Support links • NetAffx Analysis Center
Data	• Folder View • Project View • Data Management functions (see Chapter 4, "Portal and data organization" on page 47).
Samples	• Sample Registration functions (see Chapter 5, "Creating and editing sample (ARR) files" on page 101).
Administration	• Project functions (see "Using projects to organize data" on page 78). • Template functions (See "Working with templates" on page 328). • Workflow Monitor (see "Tracking the workflow" on page 336).
Help	Online help

The Basic Search Function (Figure 25) enables you to search for files by:

- Array Name
- Attribute Value
- File Name
- Project Name

Figure 25 Search controls



For more information about the search options, see "Searching for files" on page 66.

Viewing the data organization

You have two different options for viewing the organization of data in GCC Portal:

- The Folder View displays a list of all the Data Roots in the GCC system, along with a list of the Sample, Data, and other files in a selected Data Root or sub-folder (see "Folder view" on page 50).
- The Project View displays the Sample and Data files associated with a selected project, showing parent and child relationships between the Sample and Data files (see "Project view" on page 63).

See "Organizing data" on page 32 for more information about the way data is organized in GCC.

Windows Security issues can impact your ability to view files and data. See Appendix B, "Windows sharing and security issues" on page 348 for more information.

Folder view

The Folder View displays a list of all the Data Roots in the GCC system, along with a list of the content of a selected data root or sub-folder.

Using the folder view

1. Click View **Folder View**.

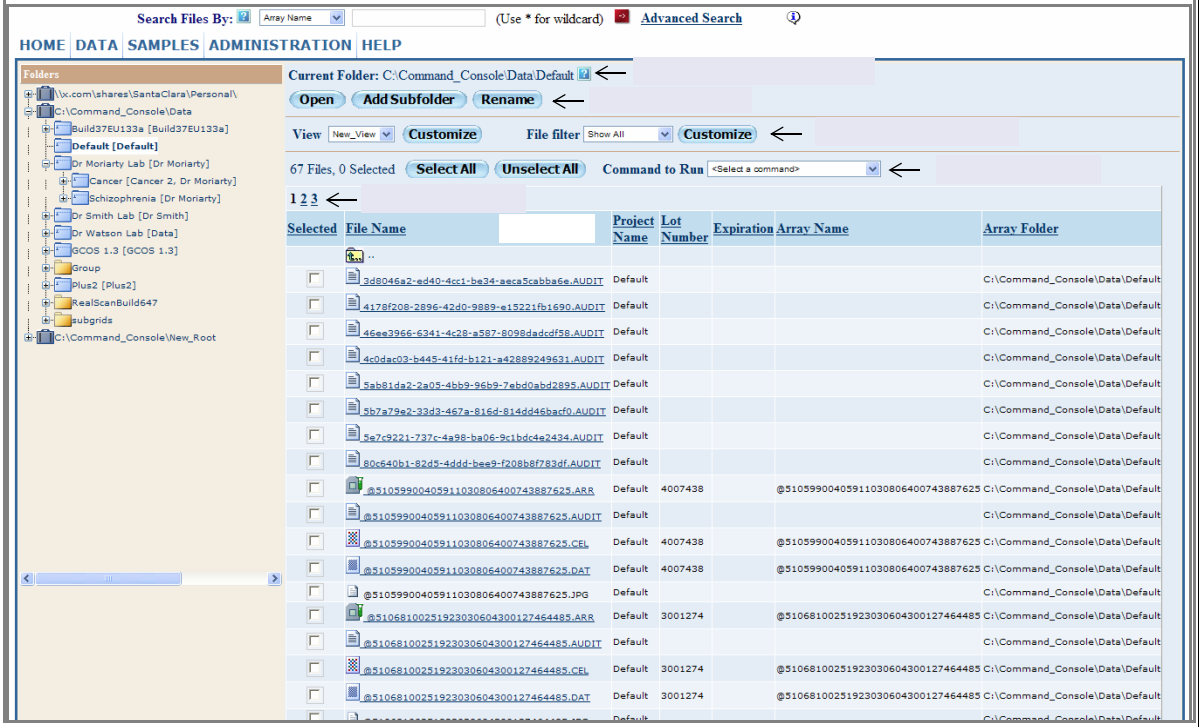
   The Folder View appears (Figure 26).

   The left side of the page displays the Folders list.

   The right side displays the following items:

   – Path to the selected folder
   – Folder controls: used to open, add, and rename sub-folders
   – Display controls: used to control the display of attributes and file types
   – File List with Select controls: used to select files and perform operations on the selected files

Figure 26 Folder view

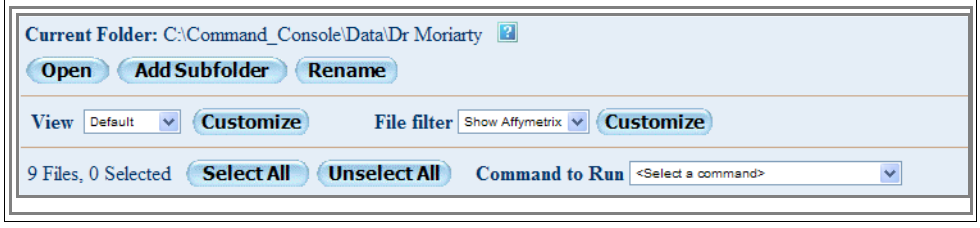


The data roots and project folders are displayed in the Folders list (see below). The contents of the data roots and project folders are displayed in the File list (see "File list" on page 55).

For a description of the file hierarchy used to organize GCC files, see "Organizing data" on page 32.

The page links enable you to go to additional pages of data.

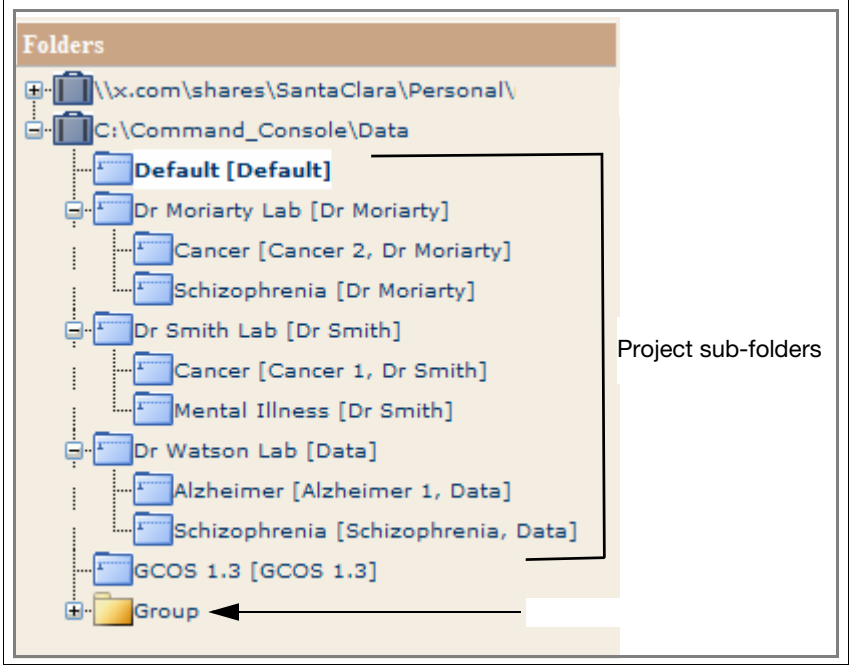
Figure 27 Folder view controls



Folders list

The Folders list (Figure 28) shows the data roots, folders, and projects used to organize data.

Figure 28 Folders list



The Folders lists displays the folder names and project names for sub-folders.

Click on a folder to display its contents in the File list (see below).

The Folders controls enable you to:

- Add a folder (see "Adding folders and projects", below).
- Rename a folder (see "Renaming folders" on page 54).
- Open a selected folder in Explorer (see "Opening folders" on page 55).

  Note: You can add or rename a folder using Windows explorer in addition to the GCC Portal functions.

Adding folders and projects

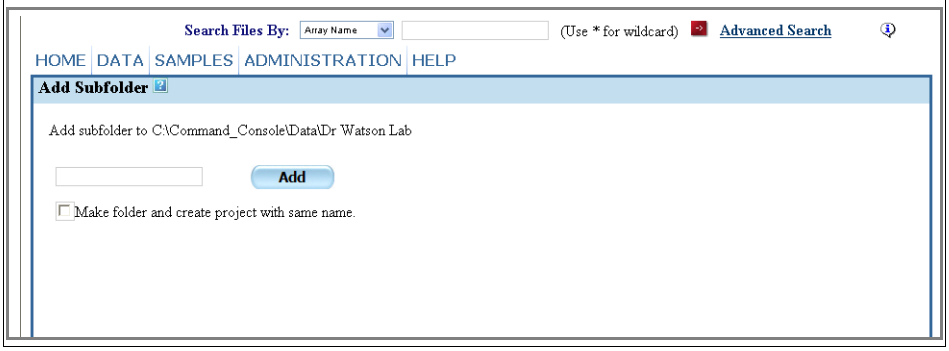
You can add a new sub-folder in a selected data root or sub-folder using the Add Folder button. You can optionally assign the folder to a project of the same name when you create the folder.

1. Select the data root in the Folders list in which you want the new folder to be created.
2. Click the **Add sub-folder** button in the Folder controls (Figure 29).

Figure 29 Folder controls

The Add Subfolder window opens (Figure 30).

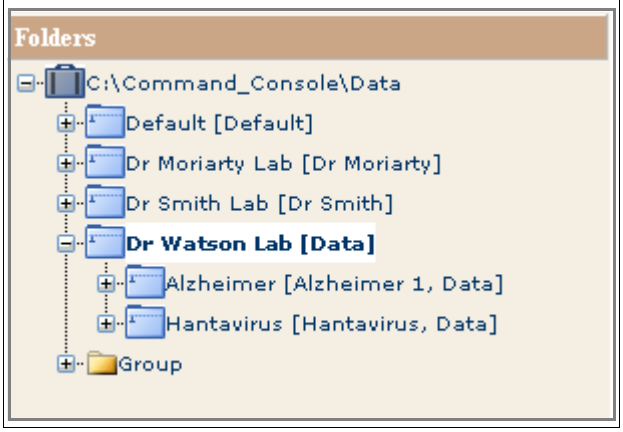
Figure 30 Add Subfolder window with folder name entered



3. Enter the new folder name in the box.
4. Select the **Make folder and create project with same name** check box to create a project in GCC with the same name as the folder.
5. Click **Add Folder**.

   The Folder View page opens with the new folder and project displayed.

Figure 31 New folder



Renaming folders

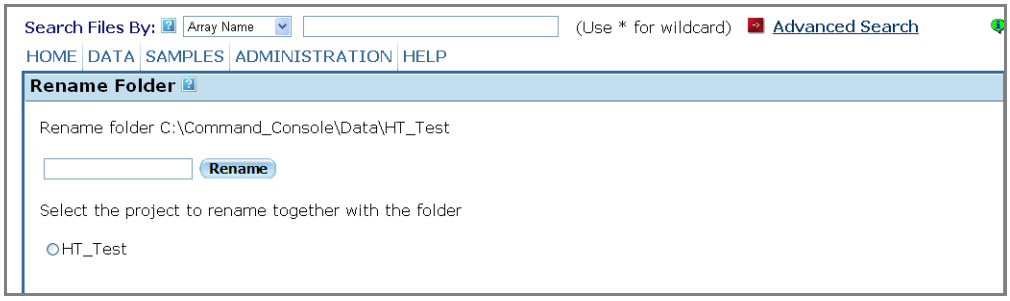
You can rename a folder using the Rename Folder link.

For information on changing the name of a project, see "Managing Projects" on page 78.

1. Select the folder to be renamed.
2. Click the **Rename** button in the Folders controls (Figure 29).

   The Rename Folder page opens (Figure 32).

Figure 32 Rename Folder page

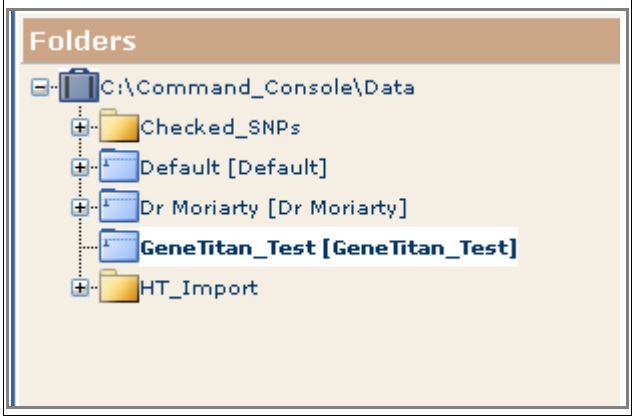


3. Enter the new folder name in the box.

   Select the radio button if you want to change the project name, too.
4. Click **Rename**.

   The Folder View page opens with the renamed folder (Figure 33).

Figure 33 Folder View with renamed folder

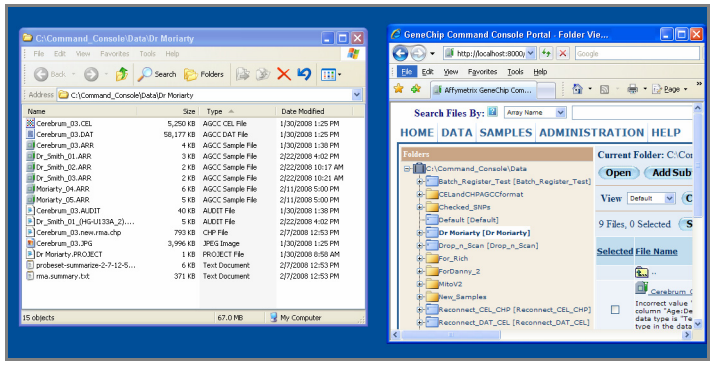


Opening folders

1. Select the folder to be opened.
2. Click the **Open** button in the Folders controls (Figure 29).

   An Explorer window opens displaying the contents of the folder. The GCC Portal browser shrinks to make room for the window (Figure 34).

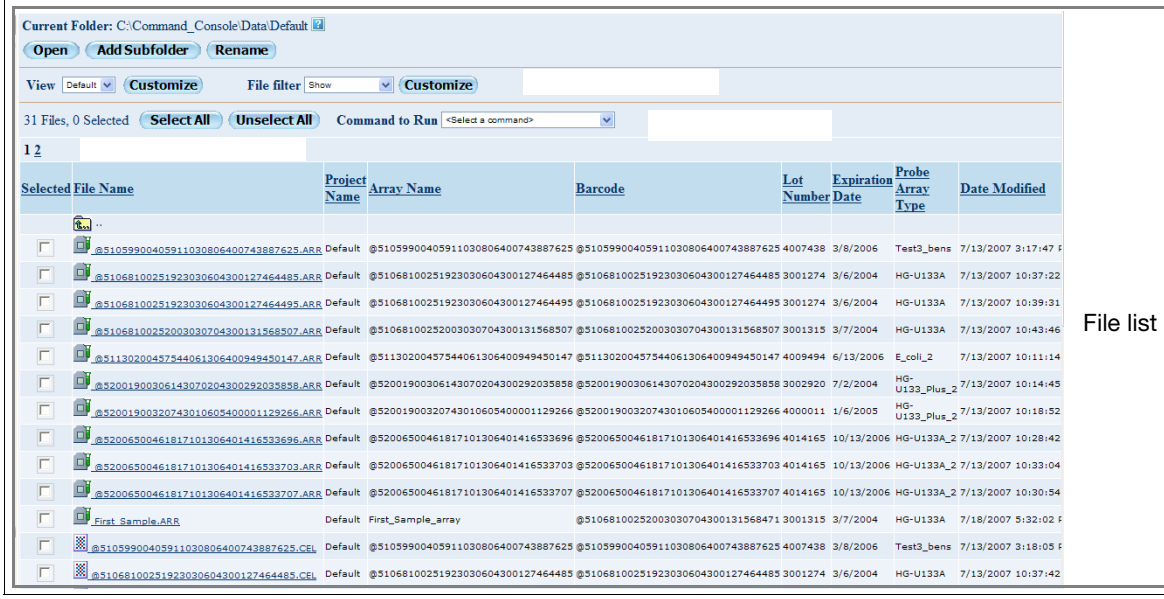
Figure 34 Explorer window with reduced GCC Portal browser



File list

The file list displays a list of the files and folders in the selected folder (Figure 35).

Figure 35 File List



The Display controls, at the top, allow you to change the display of attributes and files.

The select controls allow you to select files for various operations.

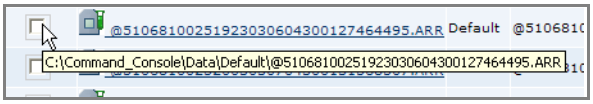
The numbered links below the Select controls enable you to switch from page to page of the File list. They are displayed only if the number of files in the selected sub-folder exceeds the display limit.

By default the File list displays a table of files with the following columns:

Select Use the check box to select a file for different operations:
- Copy Selected Files (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Copying files" on page 86).
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

See "Selecting files" on page 57 for more information.

Placing your cursor over the Select check box displays the full path and file name in a popup:



FileName The name of the file or folder.

In some cases the file name is a link. Click on the link to open the following file types:
- Folder: displays the contents of the folder in the file list.
- Sample File: opens the Sample/Array Attributes page (see "Detailed sample registration" on page 104).
- Image file (DAT) and Intensity File (CEL): opens the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).
- Audit file (AUDIT): opens the Audit File Viewer (see "Viewing audit files" on page 65)

You cannot use the Action link to open the other file types displayed in the File list. These file types can be opened using a text editor (AUDIT, RPT, GRD) or the GCC Viewer (CEL, JPG).

Project Name The name of the project that contains the file.

Array Name Name assigned to the array during registration.

Barcode Barcode of probe array (may be an Applied Biosystems or a custom barcode).

Lot Number Manufacturer's lot number for the array (only displayed with Applied Biosystems barcodes).

Expiration Date Expiration date for the array (only displayed with Applied Biosystems barcodes).

Probe Array Type Model number of probe array.

Date Modified Last date the file was modified.

You can conceal some of these columns and display selected attributes in other columns. For information about displaying and concealing columns, see "Selecting attributes for the file list" on page 57.

Sorting the file list by any column

- Click on the column header.

File types

There are several different types of files in the File List:

- Sample files (ARR)
- Image files (DAT)
- Intensity Data Files (CEL)

- Probe Analysis Files (CHP)
- JPG files (JPG)
- Audit Information files (AUDIT)
- Grid Data files (GRD)
- Project files (PROJECT)
- Report files (RPT)

For more information about the different files, see "File types in GCC" on page 28.

See "Selecting file types for display" on page 61 for more information about displaying different file types.

Note: Other file types, such as PARAM, may not be displayed in the list or the folders.

Selecting files

You can use the check boxes in the File list to select files for different operations:

- Copy Selected Files (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85).
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145).
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 36 Select Files controls

The Select Files controls allow you to select files and operations. The number of displayed and selected files are also displayed.

Selecting/Deselecting files

- Click the check box next to the file name; or click the **Select All** button.
- Click the **Unselect All** button to deselect selected files.

Selecting attributes for the file list

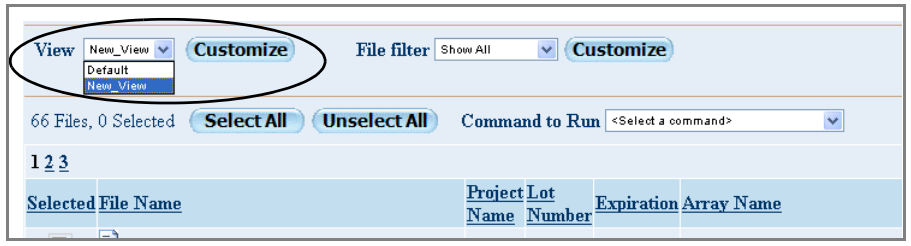
You can add or delete attributes for display in the File List using the Folder View feature. The Folder view enables you to create and edit lists of attributes to be displayed, called views. You can then select a view for display to customize the attributes in the File list.

Note: When cartridge users upgrade, the default folder view does not have well position (Pos) in the default folder view. If they have GeneTitan Array Plate data and want to see this attribute in the folder view, they will either need to add it to the default folder or create a custom view with that attribute. The Pos attribute is part of the standard fields.

Selecting a previously created view

- In the File controls, Click the View drop-down to select a view. (Figure 37)

Figure 37 File list with View controls

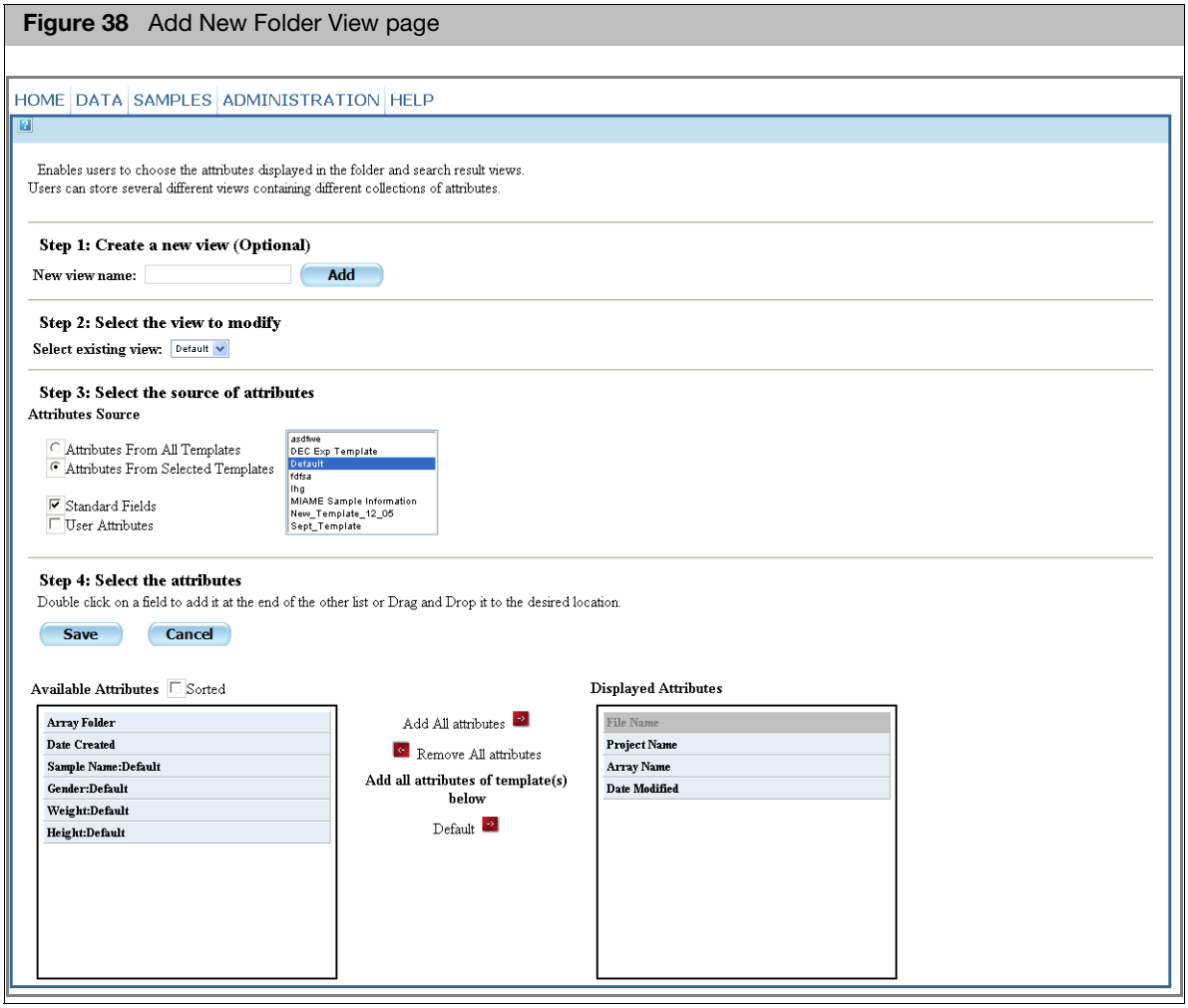


The selected View is displayed.

Adding a new view

1. Click the **View Customize** button. (Figure 37)
   The Customize page opens. (Figure 38)

Figure 38 Add New Folder View page

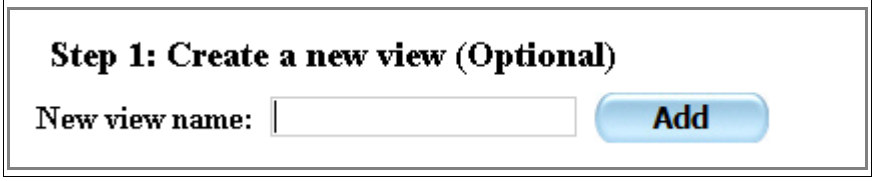


There are three steps in creating a new view:

a. Enter a name for the view.
b. Select the source of attributes.
c. Select the attributes and saving the view.

2. Enter a name for the view in the New View Name box and click the **Add** button. (Figure 39)

Figure 39 New View Name

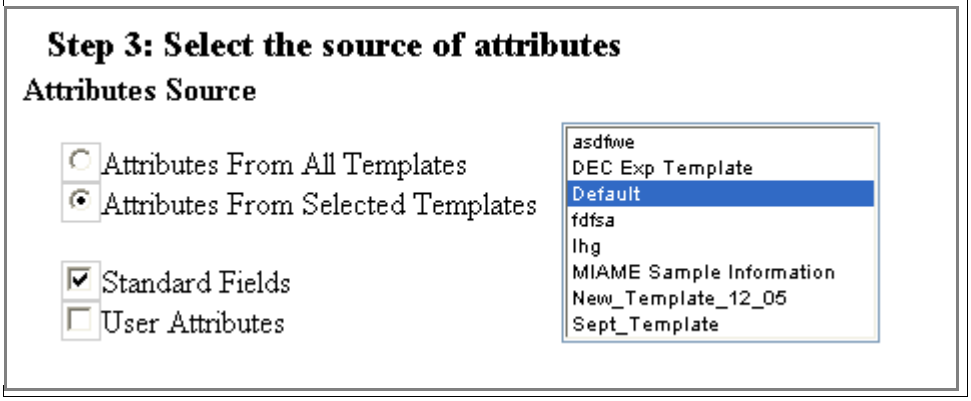


The view name is displayed in the Select Existing View drop-down box. (Figure 40)

Figure 40 New view name in the Select Existing View drop-down box.

In this step, you select the sources of the attributes. (Figure 41)

Figure 41 Select Source controls



You have several options for doing this:

- You can limit the display to attributes that are organized in templates.
- You can display user attributes which have been created by the user for individual sample files.

- If you want to use standard fields, you can display the fields from all templates, or display attributes from templates you select in the Attributes Source list.

3. Select the attributes options and templates

   The selected attributes are displayed in the Available Attributes list.

   - The **Available Attributes** list displays the attributes (with template names) that are not being currently displayed.
   - The **Displayed Attributes** lists displays the attributes that are currently being displayed in the Folder view.
   - The File Name attribute is required and cannot be hidden.

4. Select and deselect the items you want to display and conceal.
   - You can double-click on an item in one of the lists to move it to the other list or click and drag it over.
   - You can also use the center controls to add and remove attributes in groups.
   - Select the Sorted check box to display the available attributes in alphabetical order.
5. After selecting the attributes, click **Save**.

   The Folder View is displayed with the newly created view selected in the View drop-down box.

Editing a created custom view

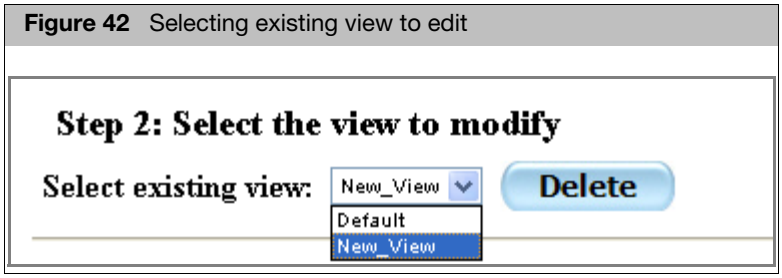
1. Click the **View Customize** button.

   The Customize page opens.

2. Select the view you want to edit from the **Select existing view** drop-down box. (Figure 42)

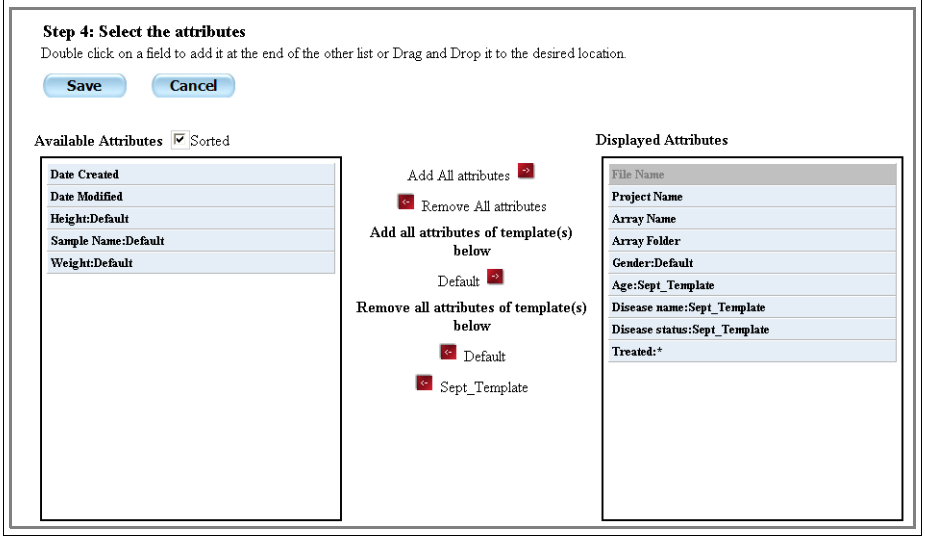
   You can click the **Delete** button to delete the selected view.

Figure 42 Selecting existing view to edit



The attributes in the view are displayed in the Select Attributes section. (Figure 43)

Figure 43 Selecting attributes



3. Select templates and attributes as described on page 58.
4. After you have selected and arranged the attributes, click **Save**.
   You can click **Cancel** to cancel the changes.
5. The View is displayed in the Folders list with the new attributes selected.

Selecting file types for display

The File Filter enables you to exclude or include particular file types in the File list.

You can:

- Use a previously created filter
- Create a new file filter.
- Edit a previously created filter

Using a previously created filter

- In the Filter controls, select the **File filter** from the drop-down list.

Figure 44 Folder list with File Filter controls

The filtered files are displayed.

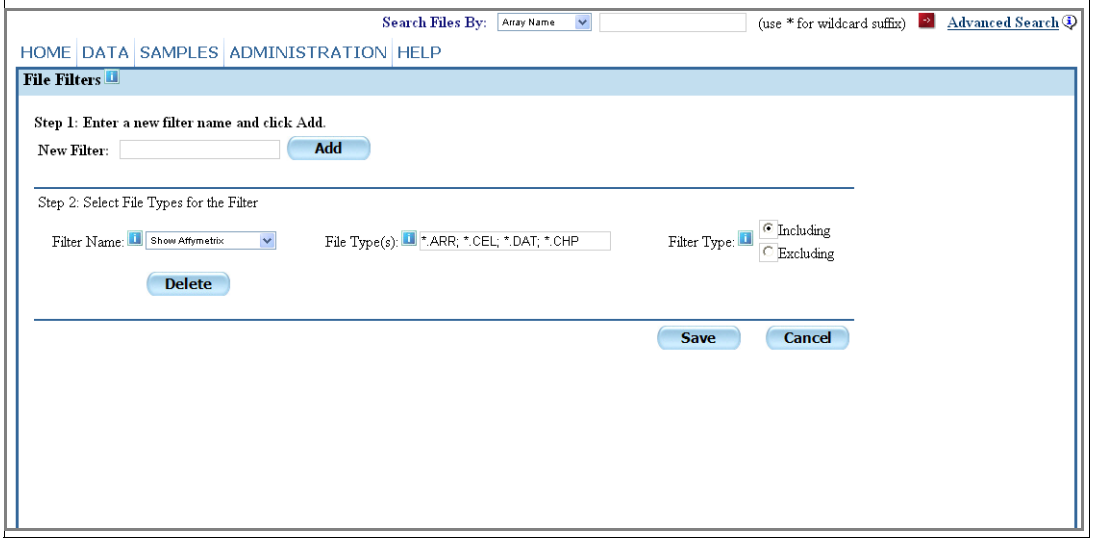
Creating a new file filter

1. In the top of the File list, click the **File Filter Customize** button (Figure 45).

Figure 45 Folder list with File Filter controls

The File Filters page appears (Figure 46).

Figure 46 File Filter page



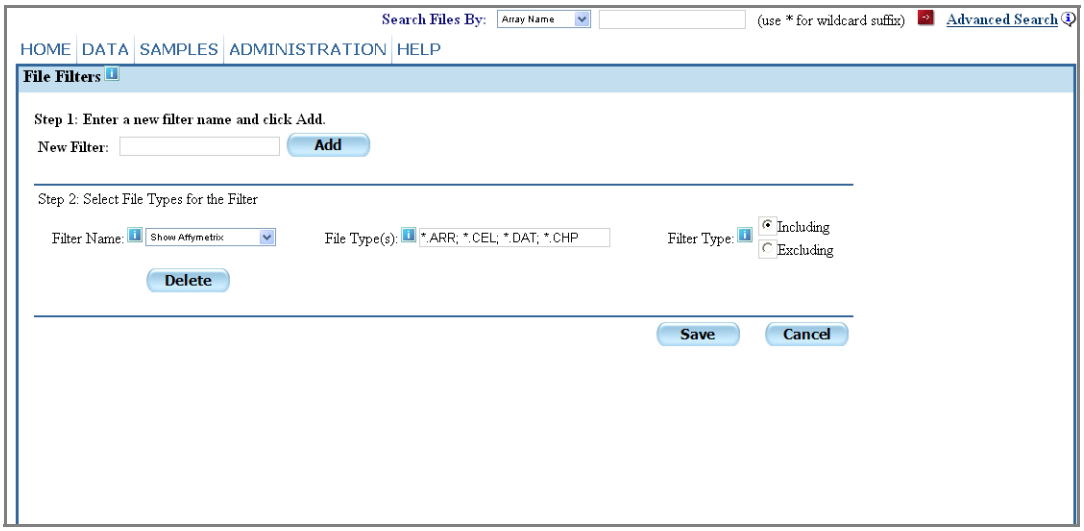
2. Enter a name for the new filter in the new Filter list.
3. Click **Add.**
   The new filter name appears in the Name box.
4. Enter the file types you want to exclude or include in the Patterns box.
   Format: ***.file** extension, (* = wildcard).
   Enter multiple file types separated by semicolons (**;**).
5. Select whether you want to exclude or include the specified file types.
6. Click **Save**.
   The Folder View appears with the edited filter selected.
   The displayed files are filtered.

Editing a file filter

1. In the top of the File list, click the **Customize** button (Figure 44).

   The File Filters page appears (Figure 47).

Figure 47 File Filter page



2. Select the filter you want to edit from the **Filter Name** drop-down list.
3. Enter the file types you want to exclude or include in the Patterns box.

   Format: *.file extension, where * is a wildcard.

   Enter multiple file types separated by semicolons (;).
4. Select whether you want to exclude or include the specified file types.
5. Click **Save**.

   The Folder view appears with the edited filter selected.

   The displayed files are filtered.

Project view

The Project View displays the Sample and Data files associated with a selected project, showing parent and child relationships between the Sample and Data files:

- Array name(s)
- Image (DAT) file(s)
- Intensity Data (CEL) file(s)
- Probe Level Summarization (CHP) file(s)

The Project view also displays basic information about a selected file, and will allow you to open and view Sample, DAT, and CEL files.

Viewing the Sample and data files associated with a project

1. Click **View** → **Project View**.

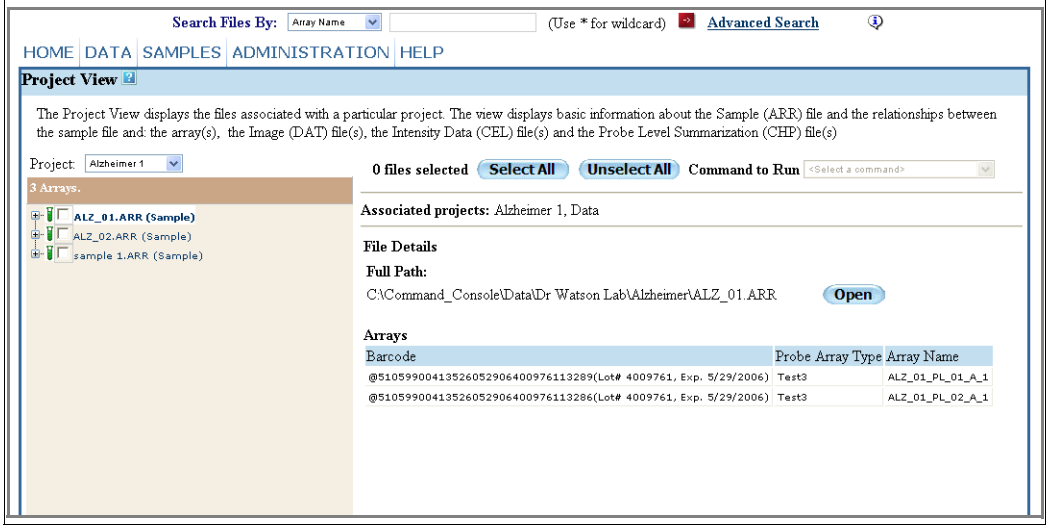
   The Project View pages opens.

2. Select a project from the Project list.

   A list of the Sample files associated with that project is displayed. (Figure 48)

   You can expand the file structure by expanding and contracting nodes in the tree.

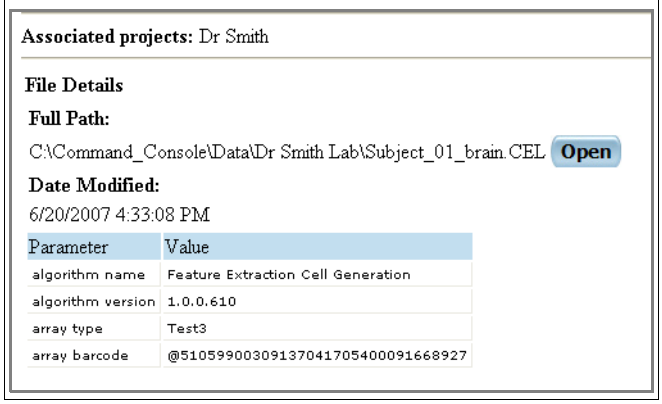
Figure 48 Project view page with sample files list



3. Click on a file to display more information about the file in the right side of the page.

   Different information is displayed for different files, as shown in Figure 49.

Figure 49 Information for selected CEL file



4. For certain files, you can click the Open button to display the file:
   - Sample files: Opens the Detailed Registration Page (see "Detailed sample registration" on page 104).
   - DAT and CEL files: Opens the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).

Selecting files

You can use the check boxes in the Project data tree to select files for different operations:

- Copy Selected Files (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85).
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145).
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 50 Select Files controls

The Select Files controls allow you to select files and operations. The number of selected files are also displayed.

Selecting files

1. Click the check box next to the file name; or

   Click the **Select All** button.

   Click the **Unselect All** button to un select selected files.

   When you select a parent file, all its child files are also selected. If you only want to select the parent file, deselect its child files after selecting the parent file.
2. Select an operation from the **Command to Run** drop-down.

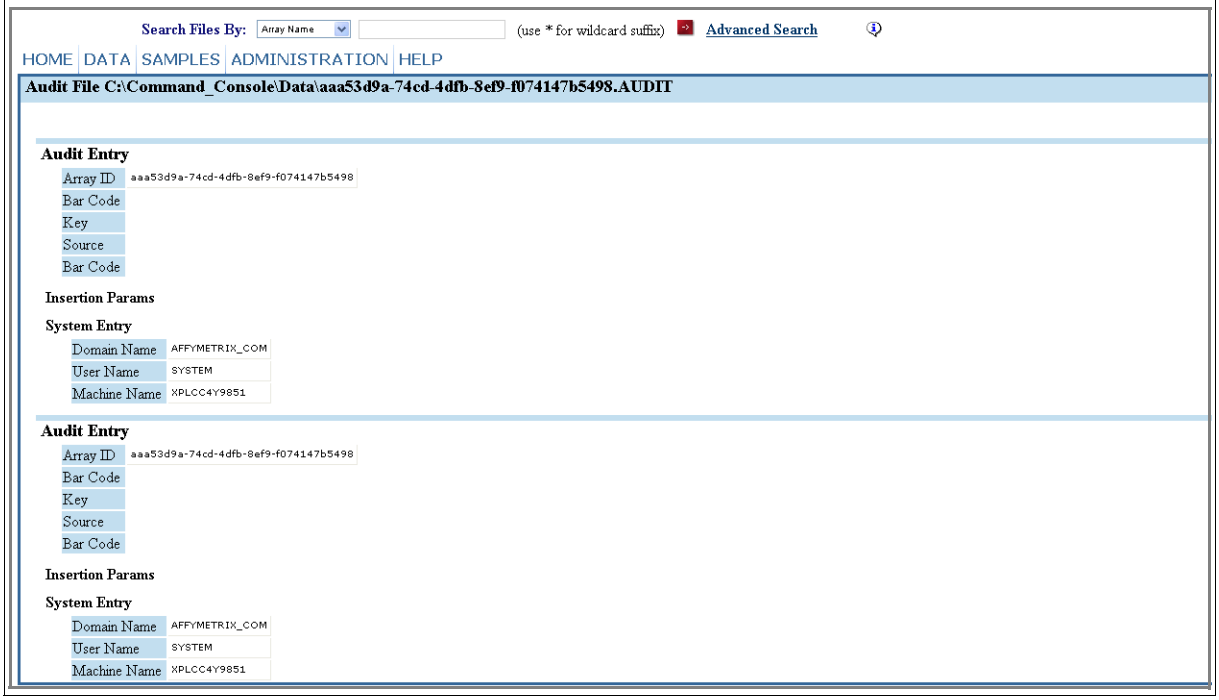
Viewing audit files

Audit files provide a record of the processing done to an array.

Opening an audit file

1. Click on the link in the File List
2. The Audit File page opens. (Figure 51)

Figure 51 Audit File page



The Audit File displays information about the processing steps the array has gone through, including the instruments and computers used in processing.

Searching for files

You have two options for locating files in GCC:

- "Basic search", below
- "Advanced search" on page 67

The results are displayed in the Search Results page (see "Search results page" on page 74).

Note: Windows Security issues have an impact on the search function. for more information, see Appendix B, "Windows sharing and security issues" on page 348.

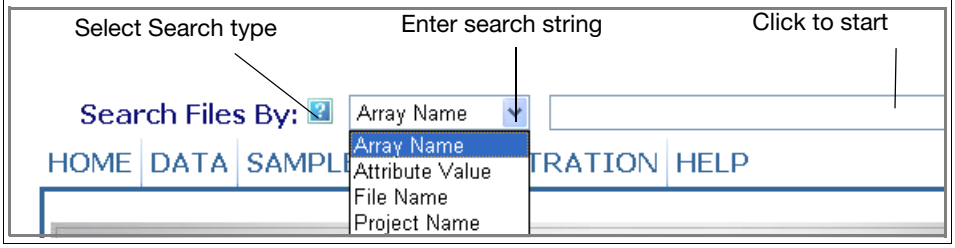
Basic search

The Search Function (Figure 52) enables you to search for files by:

- Array Name
- Attribute Value

  Note: Searching by Attribute Value returns any file with any attribute with a value that matches the search string. To search for a particular attribute, use the Advanced Search.
- File Name
- Project Name

Figure 52 Search controls



Searching for a file

1. From the **Search Files By** drop-down list, select your search criteria.
2. Enter a search string in the text box.

   You can perform special searches by using the "*" symbol and "OR" operator

   "*" Serves as a wild card function. Using `searchstring*` will return all arrays that contain an attribute that starts with the search string. Using `*searchstring` will return all arrays that contain an attribute that ends with the search string.

   Using the "OR" operator between items (`searchstring1 OR searchstring2`) will return all arrays that contain an attribute that matches any of the search strings.
3. Click the **Search** button .

   Files or Projects that match the search string are displayed in the Search Results page (see "Search results page" on page 74).

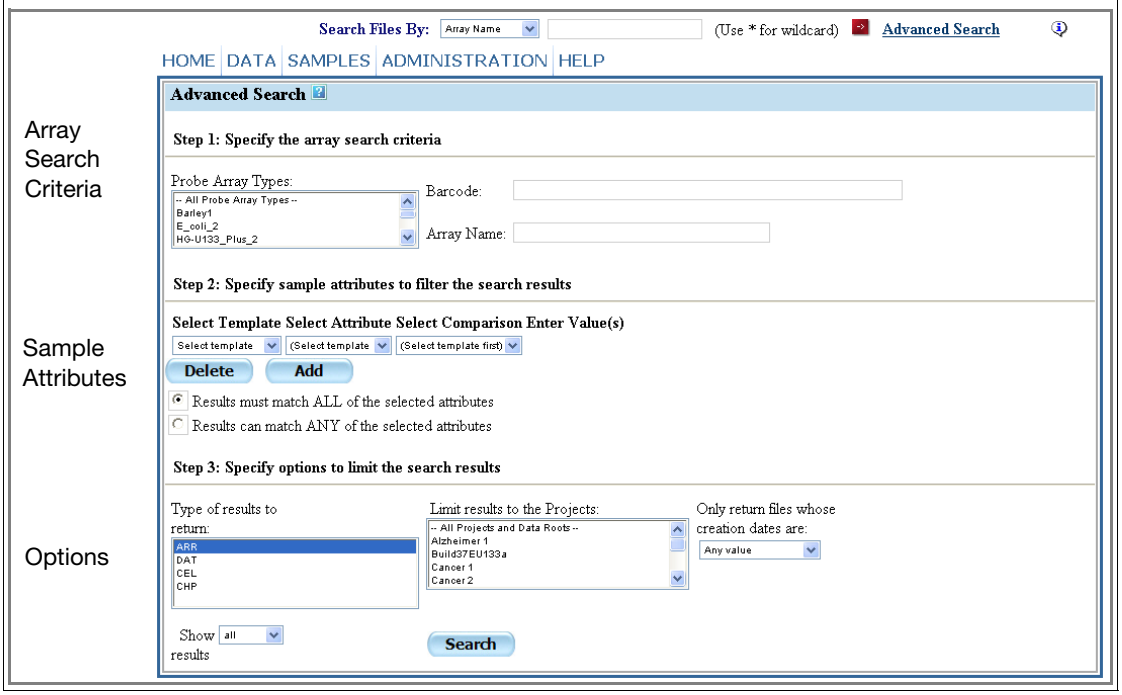
Advanced search

The Advanced search provides several ways to refine your search.

1. Click **Advanced Search** in the Search controls.

   The Advanced Search page opens. (Figure 53)

Figure 53 Advanced Search page

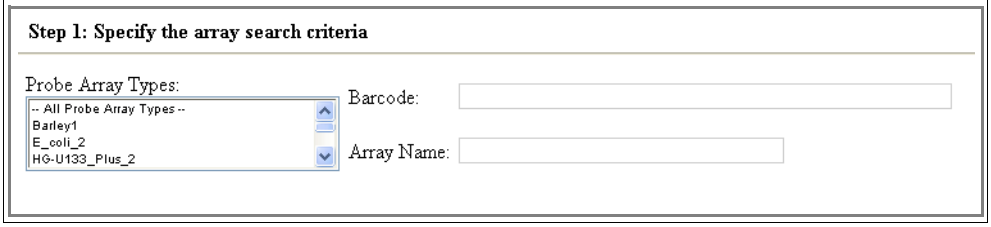


You create a search in three steps:

"Step 1: Specify Array Search Criteria"
"Step 2: Specify Sample Attributes" on page 69
"Step 3: Select Options" on page 72

Step 1: Specify Array Search Criteria

Figure 54 Array Search Criteria



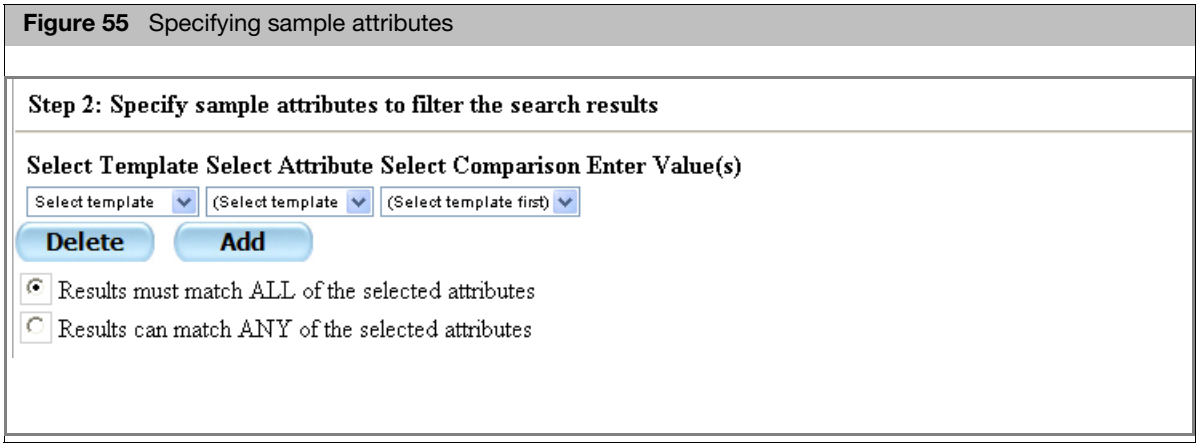
This section enables you to search for arrays that match:

- Barcode
- Probe Array Type
- Array Names

2. Enter the criteria for the information you want to find.

Step 2: Specify Sample Attributes

Figure 55 Specifying sample attributes



This section (Figure 55) enables you to specify attributes used to describe the sample and experiment. Depending upon how the search is set up, the search may return:

- Samples with any of the specified attributes.
- Samples that match all of the specified attributes.

Four things have to be selected or entered to specify an attribute:

- the source of the attribute (template name or user attribute)
- the attribute name
- the type of comparison
- the value for the attribute

When the Advanced Search page first opens, the sample attributes has three drop-down lists:

- Select Template
- Select Attribute
- Select Comparison

The Enter Value(s) box does not appear until you have selected a template and attribute.

To select an attribute:

3. From the Select Template drop-down list, select a template or other option.

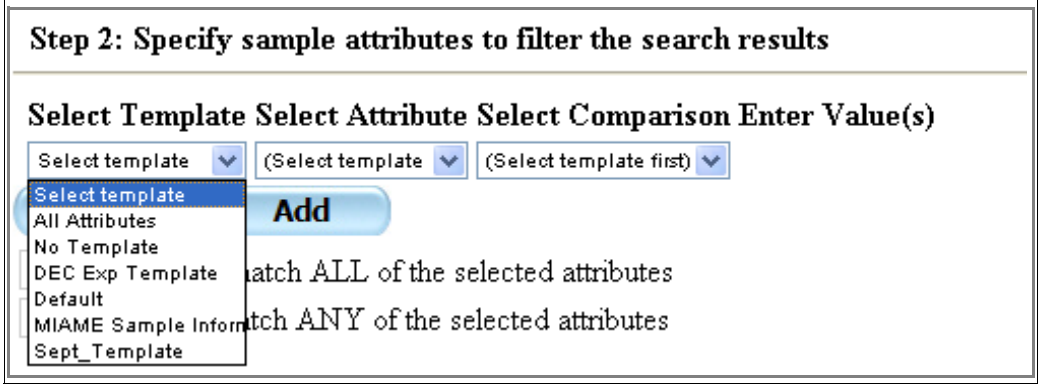
   Note: The Sample Attribute Conversion function may impact your selection of templates and attributes. For more information, see "Sample attributes conversion" on page 115.

   The Select Template list displays a list of the templates used by the files in GCC. You can also select:

   - All attributes: Enables you to perform a blanket search over every attribute in the Sample files, both from templates and from user attributes.

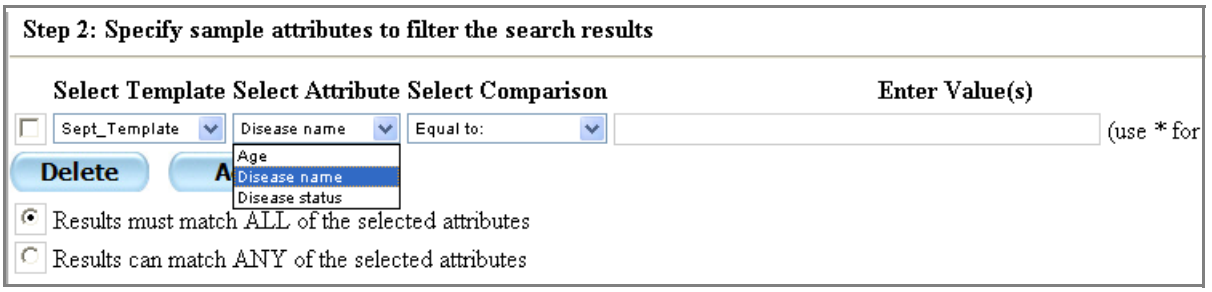
     See "Performing an all attributes search" on page 74 for more information.
   - No Templates: Enables you to select from user attributes, used in a Sample file but not included in a template.

Figure 56 Selecting a template



4. After selecting the template, a list of attributes appears in the Select Attributes drop-down list. (Figure 57)

Figure 57 Select attribute from list



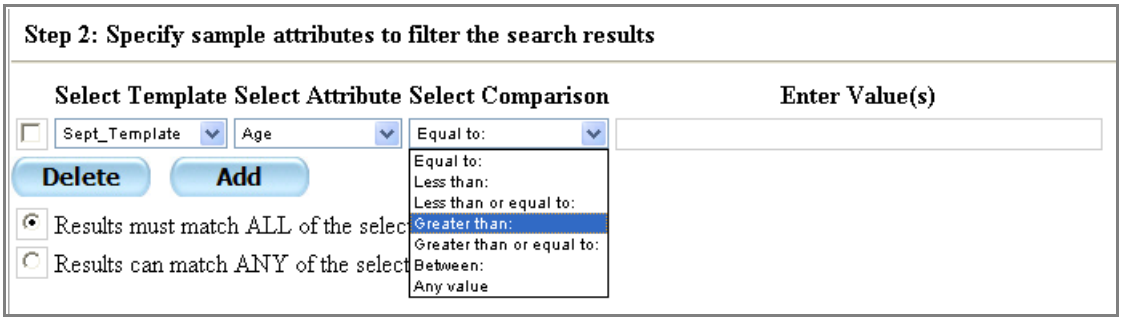
5. Select the attribute you want to search on.

   You can perform different types of comparisons for the search.

   If you select a numerical attribute, you can select from the following limits (Figure 58):

   - Equal to
   - Less than
   - Less than or equal to
   - Greater than
   - Between (displays two entry boxes for the range limits).
   - Any value

Figure 58 Comparisons for numerical attributes



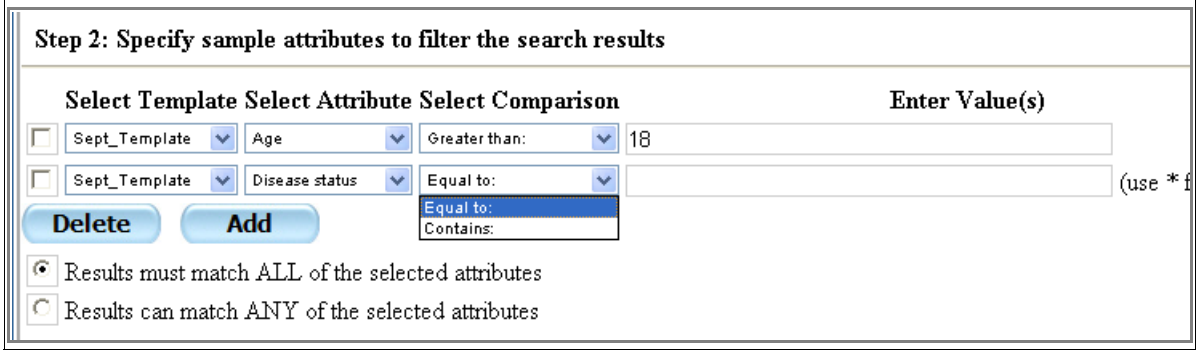
For date attributes, the comparisons are:

- Equal to today
- Within the last week
- On a specific date: (required)
- Before date: (required)
- After date: (required)
- Between dates: (required)
- Any value

For text string or SingleSelect attributes, the comparisons are (Figure 59):

- Equal to: exact match to the search string
- Contains: text string containing the search string

Figure 59 Comparisons for text string attributes



6. Select the appropriate comparison for the attribute.

   You can use comparisons with user attributes that have the data type specified, as well as sample attributes.

7. Enter a string for the attribute in the Enter Value(s) box.

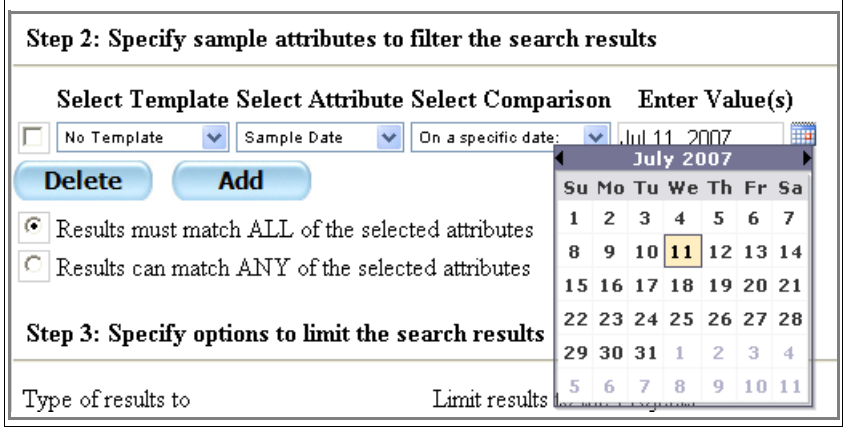
   You can perform special searches by using the “*” symbol and “OR” operator when searching for Text attributes.

Note: [*] serves as a wild card function. Using `searchstring*` will return all arrays that contain an attribute that starts with the search string. Using `*searchstring` will return all arrays that contain an attribute that ends with the search string.

Using the "OR" operator between items (`searchstring1 OR searchstring2`) will return all arrays that contain an attribute that matches any of the search strings.

For date attributes, click on the Calendar icon and select the date from the calendar that appears. (Figure 60)

Figure 60 Selecting dates



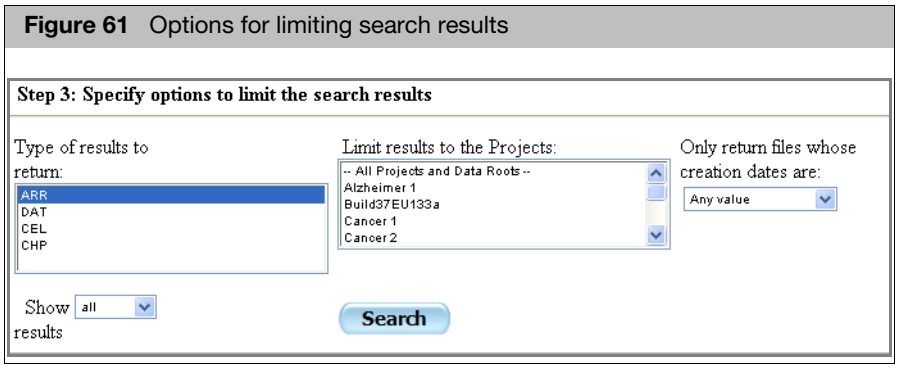
Click the < and > buttons to display a different month.

8. Click the **Add** button to add another attribute and repeat Step 3 through Step 7.
9. Select how the searches are to be combined:
   - Results must match ALL of the selected attributes.
   - Results can match ANY of the selected attributes.

   After you have finished specifying the attributes, you can select other options.

Step 3: Select Options

Figure 61 Options for limiting search results



This section enables you to search for files that match other criteria:

Type of results to return	Specify one or more of the following types of files: • ARR • CEL • CHP • DAT
Limit results to the Projects	Projects to be searched. Selecting none runs the search through all the files in the main data folder and in all the project folders. You can limit your search to one or more project folders using this box.
Creation Dates	Date of file creation: • Equal to today • Within the last week • On a specific date: (requires date value) • Before date: (requires date value) • After date: (requires date value) • Between dates: (requires date value) • Any value
Show results	Limit on the number of results to be returned.

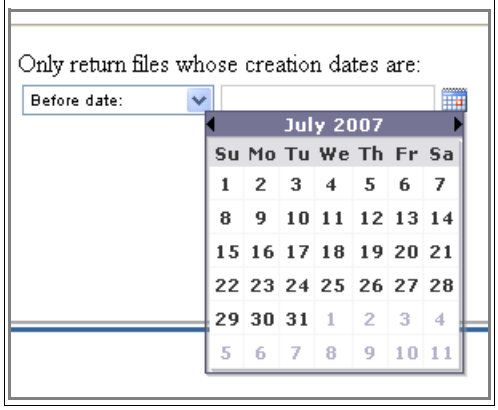
10. Select or enter the options for the information you want to find.

    You can select multiple items in the Type of Results and Projects list by holding down the Shift key and clicking on the items.

    You can deselect a project by holding down the Ctrl key and clicking on the project.

    For date attributes, click on the Calendar icon and select the date from the calendar that appears. (Figure 62)

Figure 62 Select date



    Click the **<** and **>** buttons to display a different month.

11. Click **Search**.

    The files that match the search criteria appear in the Search Results list.

Performing an all attributes search

The **All Attribute** search enables you to search across all attributes of the following types:

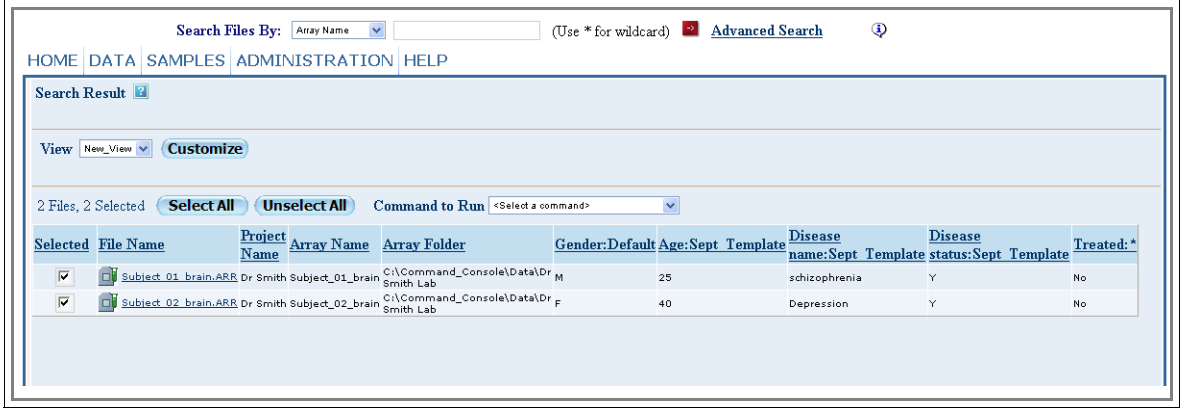
- Date
- Number
- Text

If you use the All Attributes search, it will return any file that has any attribute with a value that matches the search string.

Search results page

The Search Results page lists the files that meet the criteria specified in your search. (Figure 63)

Figure 63 Search Results list

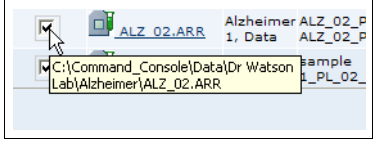


You can:

- Change sort order of the list by clicking at the head of the column you want to sort by.
- Change the attributes displayed in the list with the View controls (see "Selecting attributes for the file list" on page 57).
- Use the Select controls to select files for various operations.

  Placing your cursor over the Select check box displays the full path and file name in a popup (Figure 64):

Figure 64 Popup showing path and name



Selecting files

You can use the check boxes in the Selected column to select files for different operations:

- Copying Selected Files to a different location (see "Copying files" on page 86).
- Create Report from Sample files in List (see "Generating reports for selected sample files" on page 85). The Report can be used to review the file attributes.
- Create Batch Edit file from Selected ARR Files in List (see "Creating the batch edit file" on page 145)
- Change Probe Array Type (see Chapter 10, "Probe array types" on page 325).

Figure 65 Select Files controls

The Select Files controls allow you to select files and operations. The number of selected files are also displayed.

1. Click the check box next to the file name; or

   Click the **Select All** button.

   Click the **Unselect All** button to unselect selected files.
2. Select an operation from the **Command to Run** drop-down.

Managing data roots

A data root is a folder used to contain data files for GCC. The folder and files are displayed in the Folder View of Command Console. A default data root at C:\Command_Console\Data is created during installation, but you can create additional data roots to help you organize data from different researchers or for other purposes.

IMPORTANT! Each workstation has its own data roots. Setting the data root on one station does not add the data root on other machines.

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Thermo Fisher Scientific file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

For more information about data roots, see "Folders" on page 32.

You can:

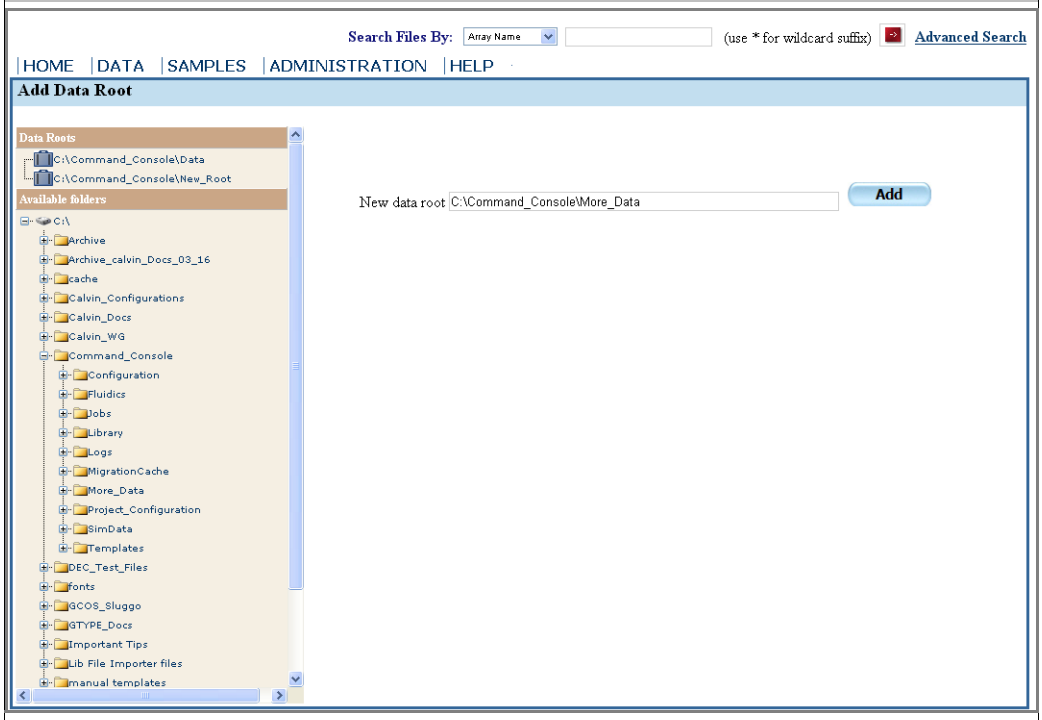
- Create a data root (see "Adding a data root", below)
- Remove a data root (see "Removing a data root" on page 77)

Adding a data root

1. From the Data menu, select **Data Roots Add**.

   The Add Data Roots page opens (Figure 66).

Figure 66 Data Root page



   The Data Root page displays a list of the data roots currently assigned in GCC and the folders that can be selected as data roots. Expand the tree to view and select child folders.

2. Select a folder for the new data root from the Data Root list; or

   In the **Add a New Data Root** box, enter the full path name and the name of the new data root.

   Data roots on networked computers are specified using Universal Naming Convention (UNC) paths as `\\server\share\filepath`.

IMPORTANT! To select a data root on a networked computer, you must configure the GCC Services to permit access. See "Configuring GCC services" on page 344 for more information.

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Applied Biosystems file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

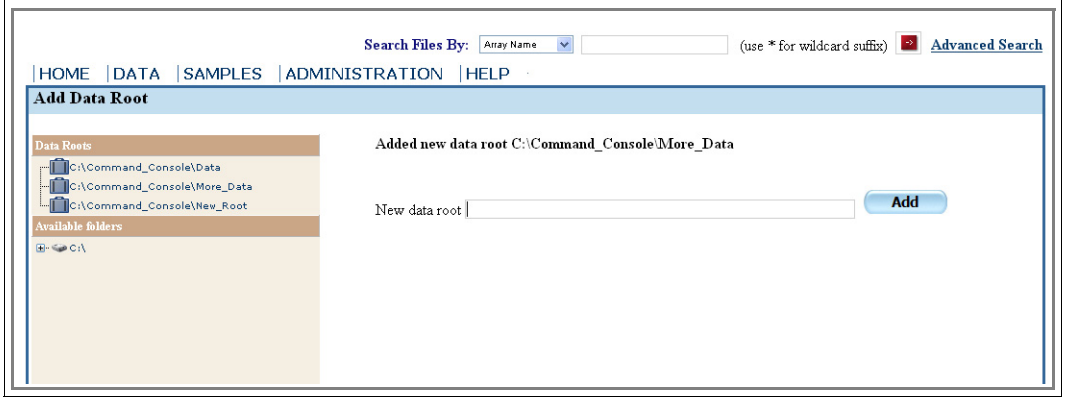
   The folder cannot be:

   - In the Windows directory
   - In the Program Files directory
   - In a root directory

3. Click **Add**.

   The list displays the new data root (Figure 67).

Figure 67 New data root added



The new data root is also visible in the Folder View (see "Folder view" on page 50).

Removing a data root

1. From the Data menu, select **Data Roots Remove**.

   The Remove Data Root page opens (Figure 68).

Figure 68 Remove Data Root page

The Remove Data Root page displays a list of the data roots available to GCC.

Note: You cannot delete the default data root. You must assign default status to another data root before deleting the current default data root. For more information, see "Specifying a default folder" on page 90.

2. Select the radio button next to the data root.
3. Click **Remove**.

IMPORTANT! Deleting a data root in GCC does not delete the actual root directory or data files in Windows.

Using projects to organize data

A project is a label assigned to a Data Root or sub-folder that can be used to organize Sample and data files. If you assign a project name to a Data Root or sub-folder, all the Sample and data files in that folder are assigned that project name. Any child sub-folders of that project folder are assigned the project name, as well. A project name can be assigned to multiple Data Roots or sub-folders, in order to group data on multiple folders together.

Project folders enable you to organize your data. After organizing data into projects you can:

- Display data grouped by project
- Search on data limited to a project
- Create a spreadsheet listing the Sample (ARR) files assigned to the project. The list can be reviewed as a summary of the project information or used to edit the Sample (ARR) file content using Batch Edit.

The Projects functions provide tools for:

- "Managing Projects"
- "Copying files"

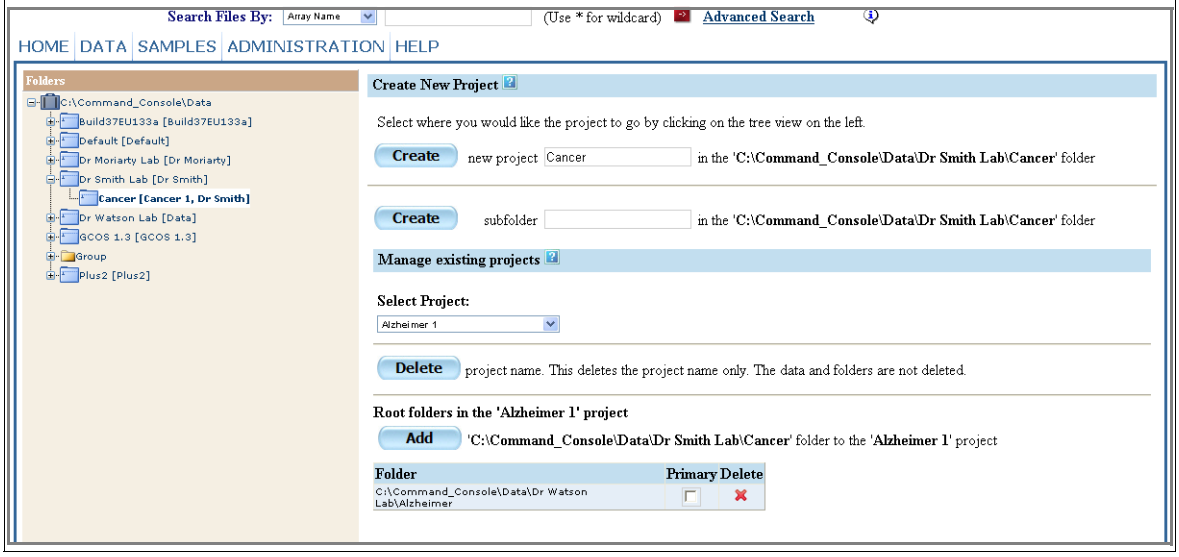
Managing Projects

Opening the Manage Projects page

- From the Administration menu, select **Project Manage**.

  The Manage Projects page opens (Figure 69).

Figure 69 Manage Projects page



The page has a folders list on the left side, similar to the one in the Folder View page.

The work area on the right has controls that allow you to:

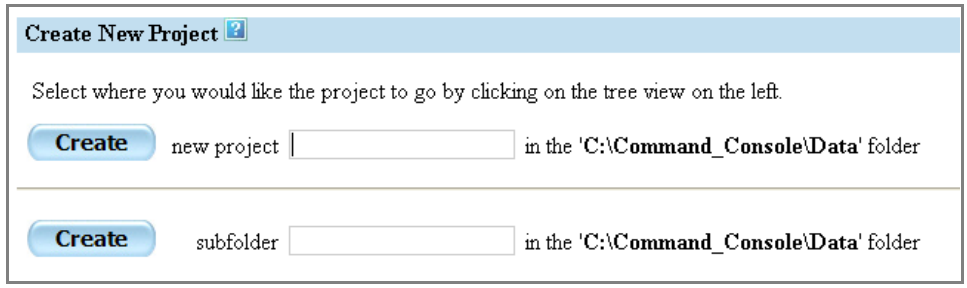
- Create a new sub-folder.
- Assign a project name to a folder.
- Designate a primary folder for a project.
- Add or delete folders for a project.

Creating a project

The Create New Project controls of the Manage Projects page enables you to:

- Assign a previously created Data Root or sub-folder to a project
- Create a sub-folder and assign it to a project.

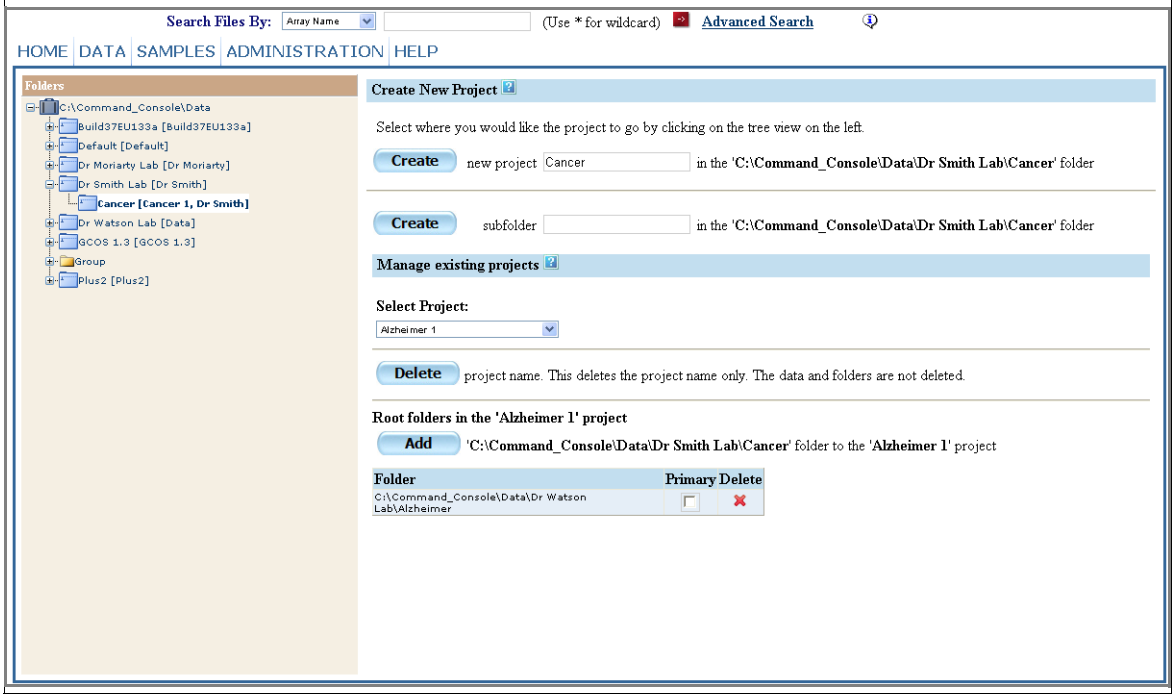
Figure 70 Create New Project controls



Creating a sub-folder and project

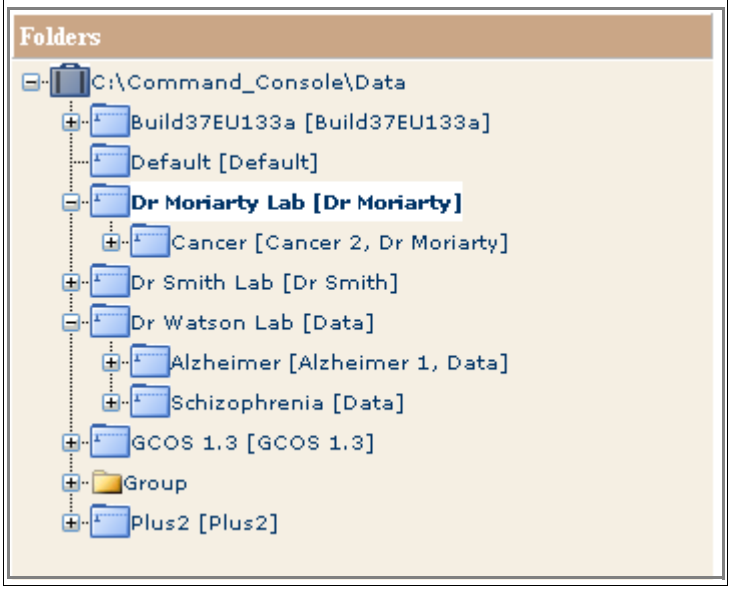
1. From the Administration menu, select **Project Manage**.
   The Project Management page opens. (Figure 71)

Figure 71 Manage Projects page



2. In the Folders tree, select the Data Root or sub-folder where you want to create the new sub-folder and Project. (Figure 72)

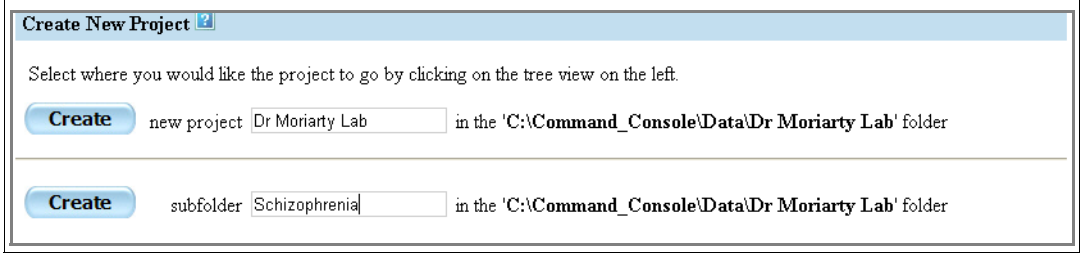
Figure 72 Folder selected as location for new sub-folder



3. Enter a sub-folder name in the Create Subfolder window (Figure 73), then click **Create**.

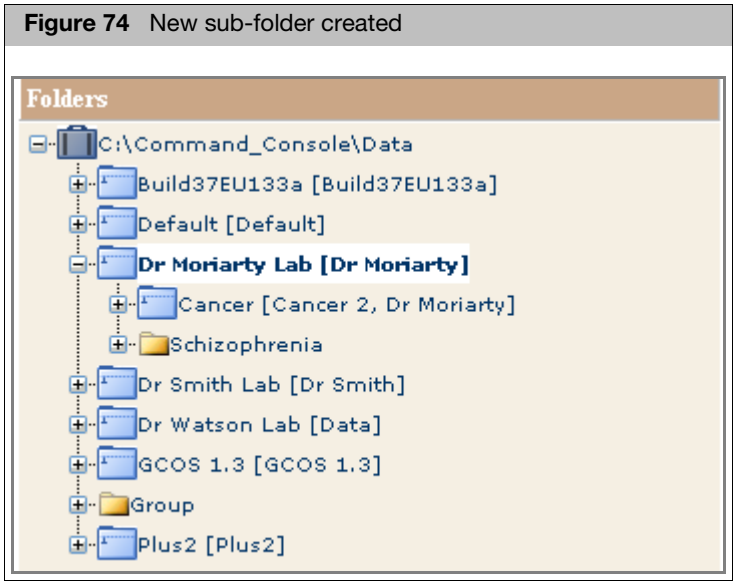
Note: The name of the location folder is entered automatically in the New Project text box. Ignore this if you do not want to use the same name for folder and project.

Figure 73 Entering name of new sub-folder



The new sub-folder appears in the Folders list (Figure 74).

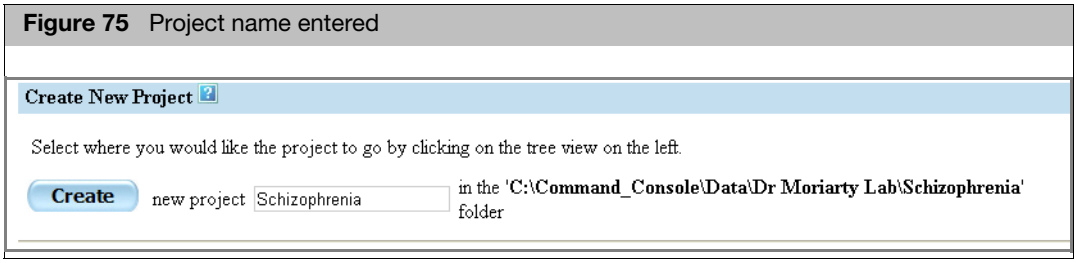
Figure 74 New sub-folder created



4. Select the folder that you created in the previous steps in the Folder list.

   The folder name appears in the New Project box and the path to the folder appears. (Figure 75)

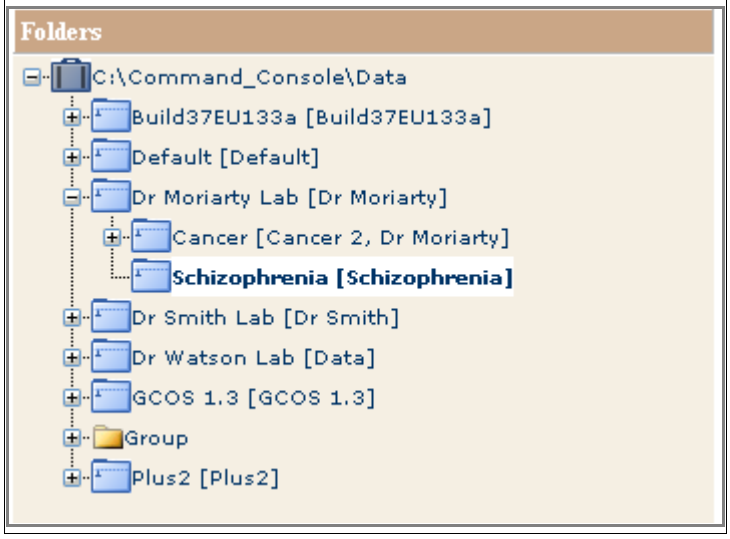
Figure 75 Project name entered



5. Enter a new project name, if desired, and click **Create.**

   The selected sub-folder has a project label assigned to it. (Figure 76)

Figure 76 New sub-folder with project label assigned



You can also assign a project label to a previously created sub-folder by:

1. Selecting the sub-folder in the Folders list
2. Entering a Project name in the New Project box and clicking the **Create New Project** button.

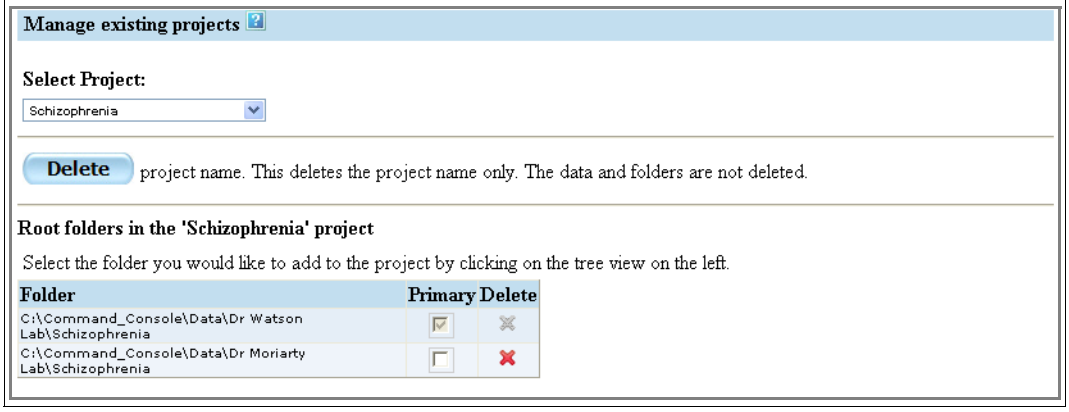
Managing existing projects

The Manage Existing Projects controls of the Manage Projects page (Figure 77) enables you to:

- Add an existing sub-folder to a previously created project.
- Specify a Primary sub-folder for a project with multiple sub-folders. A Primary sub-folder functions as the default folder for the project. The Primary sub-folder cannot be deleted.
- Delete sub-folders that are not Primary sub-folders.
- Delete a selected Project.

  Note: This deletes only the Project label. The sub-folders and files are not deleted.

Figure 77 Manage Existing Projects controls



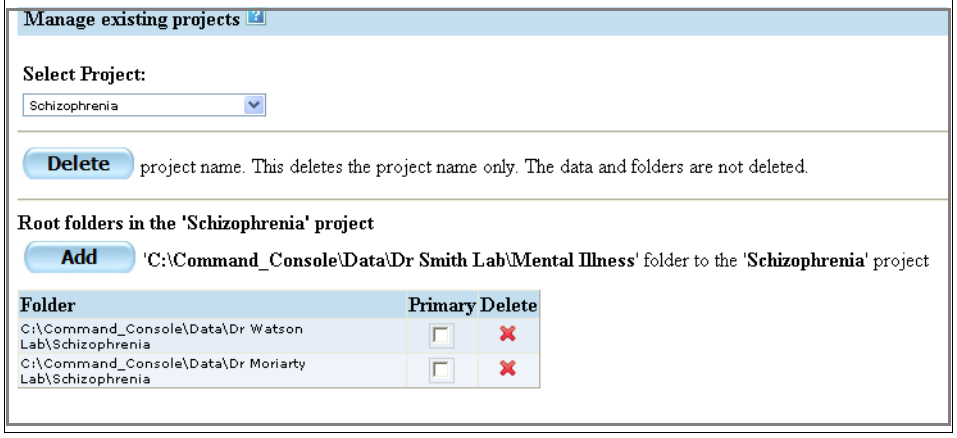
Adding an existing sub-folder to a previously created project

1. Select the project from the Select Project drop-down list (Figure 77).
2. Select the sub-folder to be added in the Folders list.

   Note: You can assign a sub-folder to more than one project.

   The Add button appears with the path of the selected folder (Figure 78).

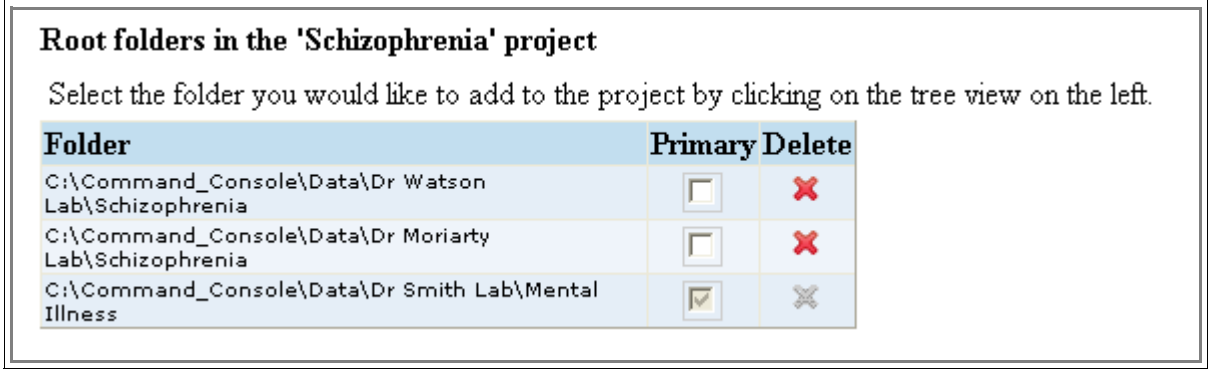
Figure 78 Add button with path



3. Click **Add**.

   The selected sub-folder is added to the Projects Folder list (Figure 79).

Figure 79 Folder added to Projects Folder list



Projects with multiple folders will have one folder specified as the primary folder. When files are assigned to the project during registration, they are placed in the Primary folder for the project. The Primary folder cannot be removed from the project; you must designate another folder as the Primary or delete the entire project.

Designating a primary sub-folder for a project

1. Select the project from the Select Project drop-down.

   The folders associated with the project are displayed in the Project Folder list (Figure 79).

2. For the folder you want to designate as primary, click the Primary check box.

   The folder is designated as the primary folder.

Removing sub-folders from a project

1. Select the project from the Select Project drop-down.

   The folders associated with the project are displayed in the Project Folder list (Figure 79).

2. Click the red **X** for the folder you want to remove.

   The sub-folder is removed from the project.

   Note: You cannot remove primary folders from the project using this method. Designate another folder as primary or delete the entire project, as described above.

Deleting a project

1. Select the project from the Select Project drop-down.

   The folders associated with the project are displayed in the Project Folder list (Figure 79).

2. Click the Delete Project Name button.

   The project is deleted.

   Note: This deletes only the Project label. The sub-folders and files are not deleted.

Generating reports and summaries

You can generate:

- Reports for selected Sample Files.
- A summary report file for the Sample files in a Project.

Generating reports for selected sample files

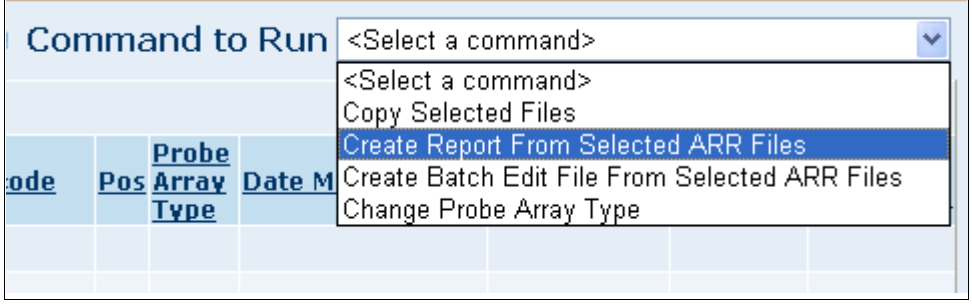
You can generate a report file in a tab-delimited text format on selected Sample (ARR) files, which you can then view in a text editor or spreadsheet program.

You can also create a Batch Edit file for the selected sample (ARR) file. See "Creating the batch edit file" on page 145 for more information.

Generating a report for selected Sample files

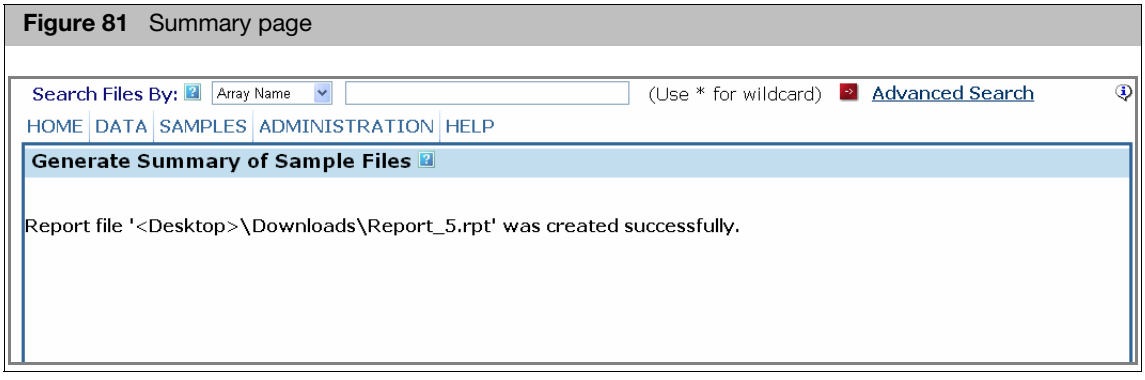
1. Select the Sample files from the:
   - Folder view page
   - Project view page
   - Search Results page
2. From the Command to Select drop-down (Figure 80), select **Create Report from Selected Arr files** link.

Figure 80 Create Report command



The report is created and the Summary page opens (Figure 81).

Figure 81 Summary page



The page displays the location and file name of the report.

The report file can be viewed in a text editor or spreadsheet program.

Generating a project summary

You can create a report for the Sample (ARR) files in a project.

The report can be used to review data.

Generating a Project Summary

1. From the Administration menu, select **Projects** → **Summary**.
   The Generate Summary page opens.
2. Select the project you want a report on from the drop-down list.
3. Click the **Create** button.
   The Summary page displays the name and location of the generated report.
   The report file can be viewed in a text editor or spreadsheet program.

Copying files

The Copy Files function enables you to select files and place a copy of those files to a new location.You can select:

- The Sample (ARR) files in a project.
- Selected Sample (ARR) files in:
  - Folder view page
  - Project view page
  - Search Results page

This can be useful for giving other users access to data.

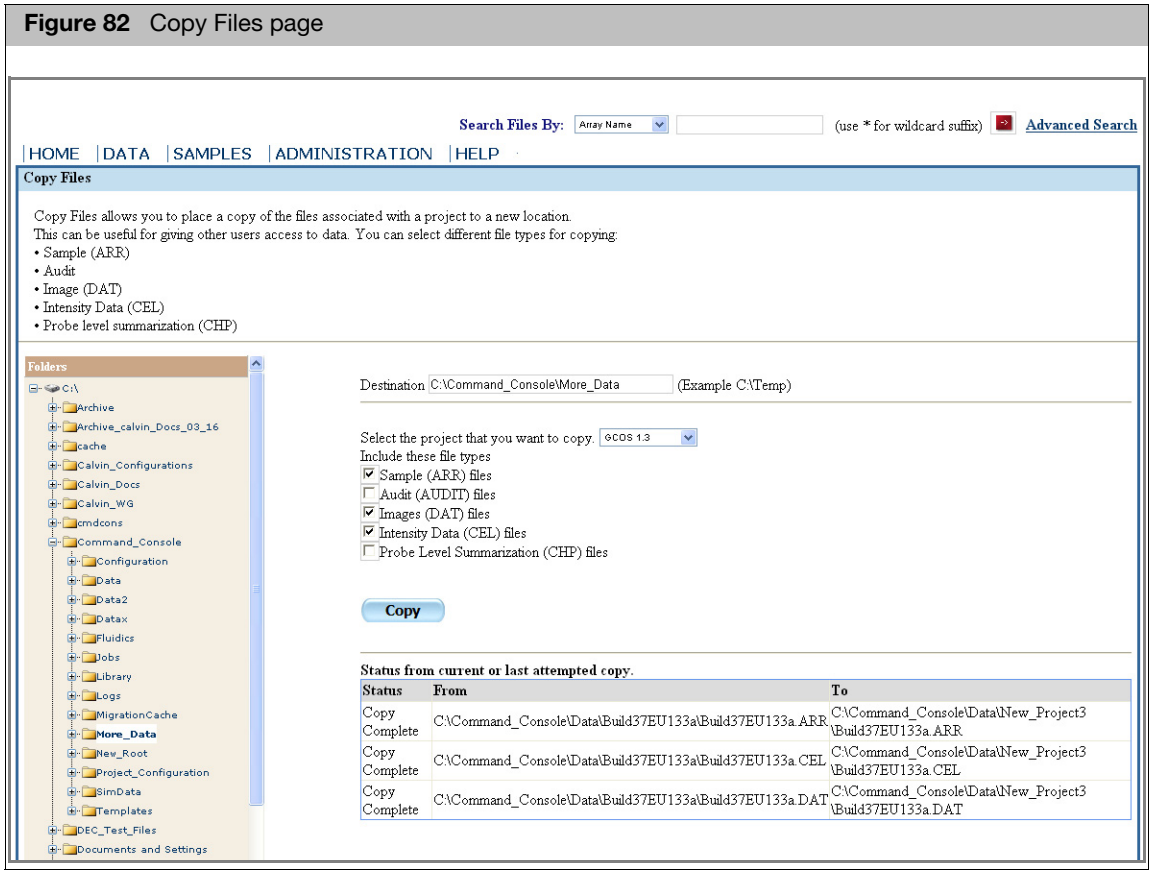
Projects are described in "Using projects to organize data" on page 78 of this manual.

Note: You can copy to any folder you have access to, as you are not limited to copying files only to a Data Root or sub-folder.

Copying files associated with a project

1. From the Data menu, select **Copy Project**.
   The Copy files page opens. (Figure 82)

Figure 82 Copy Files page

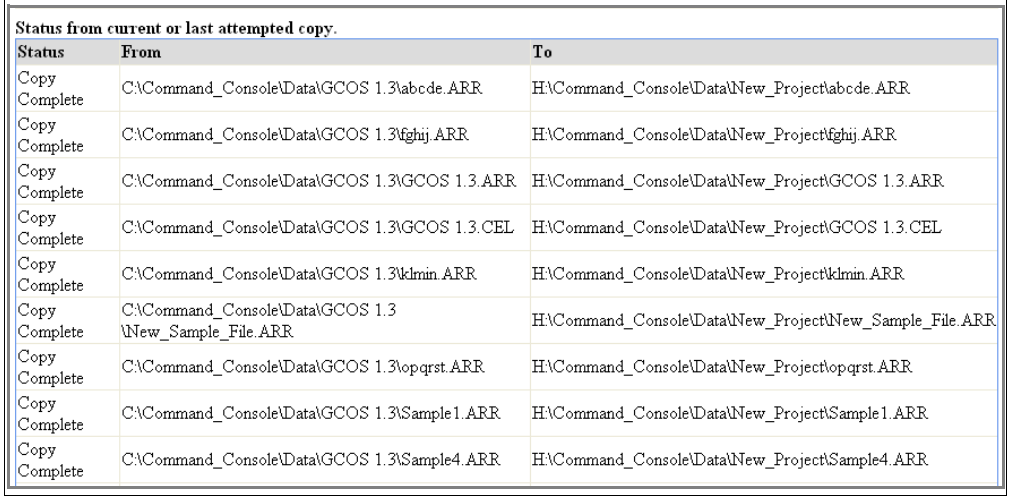


2. Select a destination folder from the Folders List, or

   Enter the path to the destination folder in the Destinations box.
3. Select a project for copying from the Projects drop-down.
4. Select the file types you want to copy:
   - Sample (ARR)
   - Audit
   - Image (DAT)
   - Intensity Data (CEL)
   - Probe level summarization (CHP)
   - The file types are described in "File types" on page 56.
5. Click **Copy**.

   The progress of the transfer is displayed in the Status window.

Figure 83 Status window



Status from current or last attempted copy.

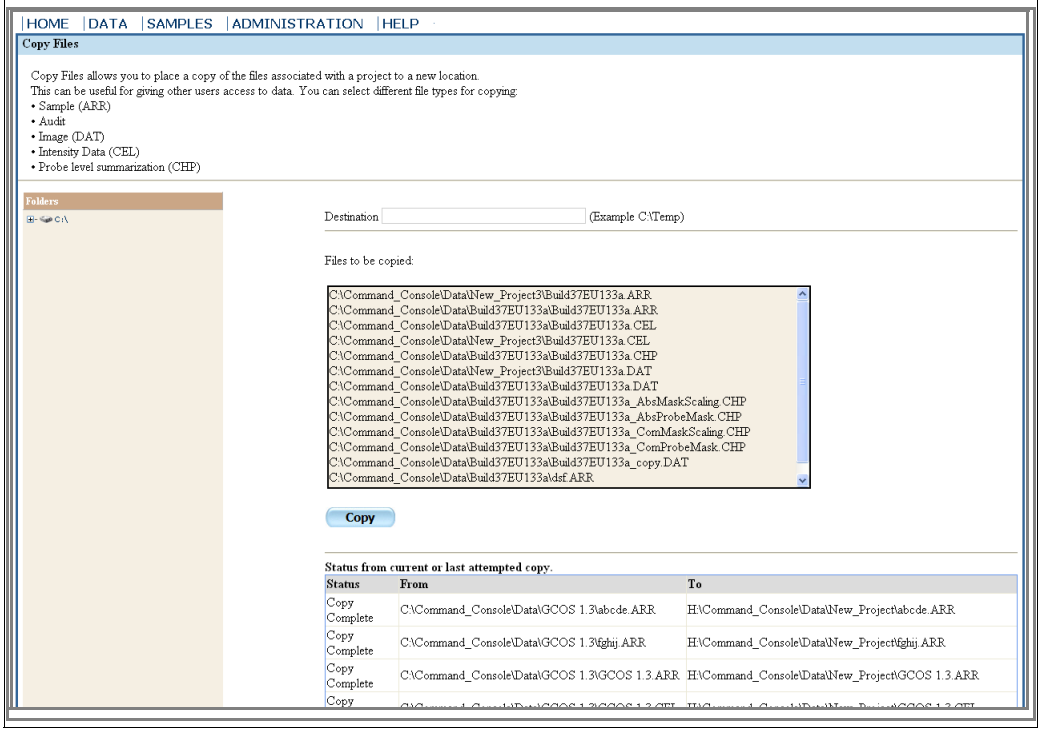
Status	From	To
Copy Complete	C:\Command_Console\Data\GCOS 1.3\abcde.ARR	H:\Command_Console\Data\New_Project\abcde.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\fghij.ARR	H:\Command_Console\Data\New_Project\fghij.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.ARR	H:\Command_Console\Data\New_Project\GCOS 1.3.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.CEL	H:\Command_Console\Data\New_Project\GCOS 1.3.CEL
Copy Complete	C:\Command_Console\Data\GCOS 1.3\klmin.ARR	H:\Command_Console\Data\New_Project\klmin.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3 \New_Sample_File.ARR	H:\Command_Console\Data\New_Project\New_Sample_File.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\opqrst.ARR	H:\Command_Console\Data\New_Project\opqrst.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample1.ARR	H:\Command_Console\Data\New_Project\Sample1.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample4.ARR	H:\Command_Console\Data\New_Project\Sample4.ARR

Copying selected files

1. Select the Sample files from the:
   - Folder view page
   - Project view page
   - Search Results page
2. From the Command to Select drop-down, select **Create Report from Arr files in List** link.

   The Copy files page opens (Figure 84).

Figure 84 Copy Files page



3. Select a destination folder from the Folders List, or

   Enter the path to the destination folder in the Destinations box.
4. Review the Files to be copied list.
5. Click **Copy**.

   The progress of the transfer is displayed in the Status window (Figure 85).

Figure 85 Status window

Status from current or last attempted copy.

Status	From	To
Copy Complete	C:\Command_Console\Data\GCOS 1.3\abcde.ARR	H:\Command_Console\Data\New_Project\abcde.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\fghij.ARR	H:\Command_Console\Data\New_Project\fghij.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.ARR	H:\Command_Console\Data\New_Project\GCOS 1.3.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\GCOS 1.3.CEL	H:\Command_Console\Data\New_Project\GCOS 1.3.CEL
Copy Complete	C:\Command_Console\Data\GCOS 1.3\klmin.ARR	H:\Command_Console\Data\New_Project\klmin.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3 \New_Sample_File.ARR	H:\Command_Console\Data\New_Project\New_Sample_File.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\opqrst.ARR	H:\Command_Console\Data\New_Project\opqrst.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample1.ARR	H:\Command_Console\Data\New_Project\Sample1.ARR
Copy Complete	C:\Command_Console\Data\GCOS 1.3\Sample4.ARR	H:\Command_Console\Data\New_Project\Sample4.ARR

Specifying a default folder

The Default folder is used as a destination folder for data when:

- Performing Drop and Scan.
- Scanning data for an array for a Sample (ARR) file located on another computer, connected through a network.

See Appendix A, "Networking" on page 338 for more information on the Network functionality of GCC.

When GCC is installed, `C:\Command_Console\Data\Default` is used for the default folder.

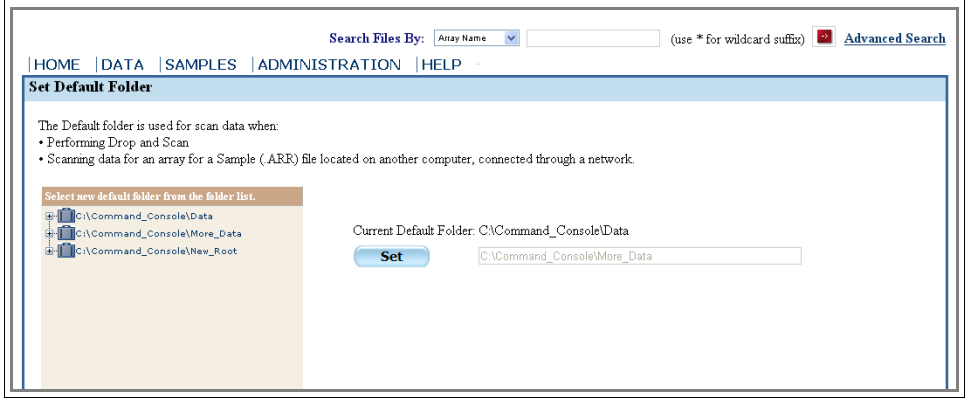
You can change the Default folder if you want.

Changing the Default folder

1. From the Data menu, select **Default Folder**.

   The Set Default Folder page appears. (Figure 86)

Figure 86 Set Default Folder



   A Folder list is displayed on the left side of the page. The right side displays the current default folder and the selection controls.

2. Select a folder from the Folder list. You can select a data root or a sub-folder.
3. Click **Set**.

   The selected folder is used for the Default folder.

Uploading data to network data storage

You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage. However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the Default folder on the local computer. This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.

The Upload Data function can be used to automatically transfer DAT, CEL, and other files from the Default folder to the network data storage where the Sample (ARR) file is located. Upload Data is useful when you want to consolidate data from different workstation computers onto one network data storage site.

The use of the Data Upload function is explained in:

- "Uploading data manually" on page 94
- "Scheduling auto-uploads" on page 96

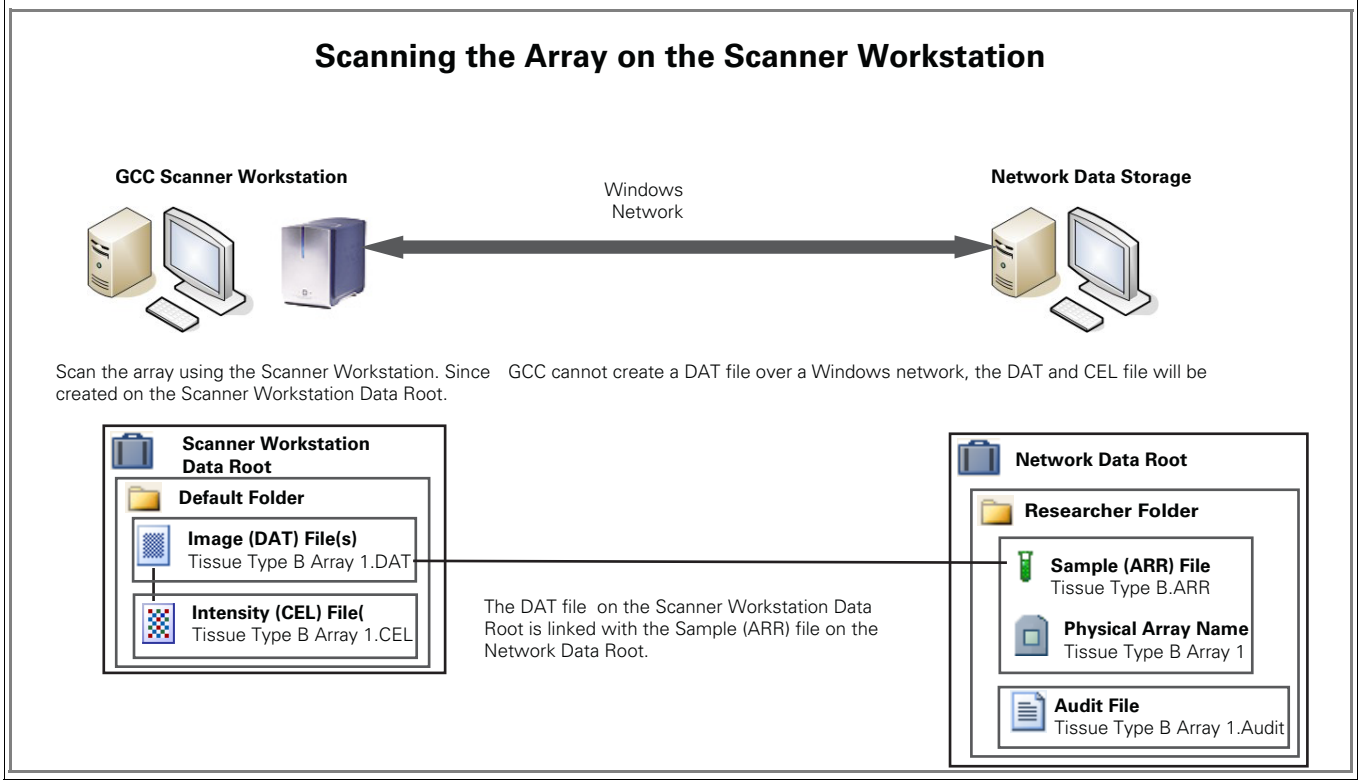
The Overview section below provides information on why you may want to use the Upload Data function.

Overview

You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage.

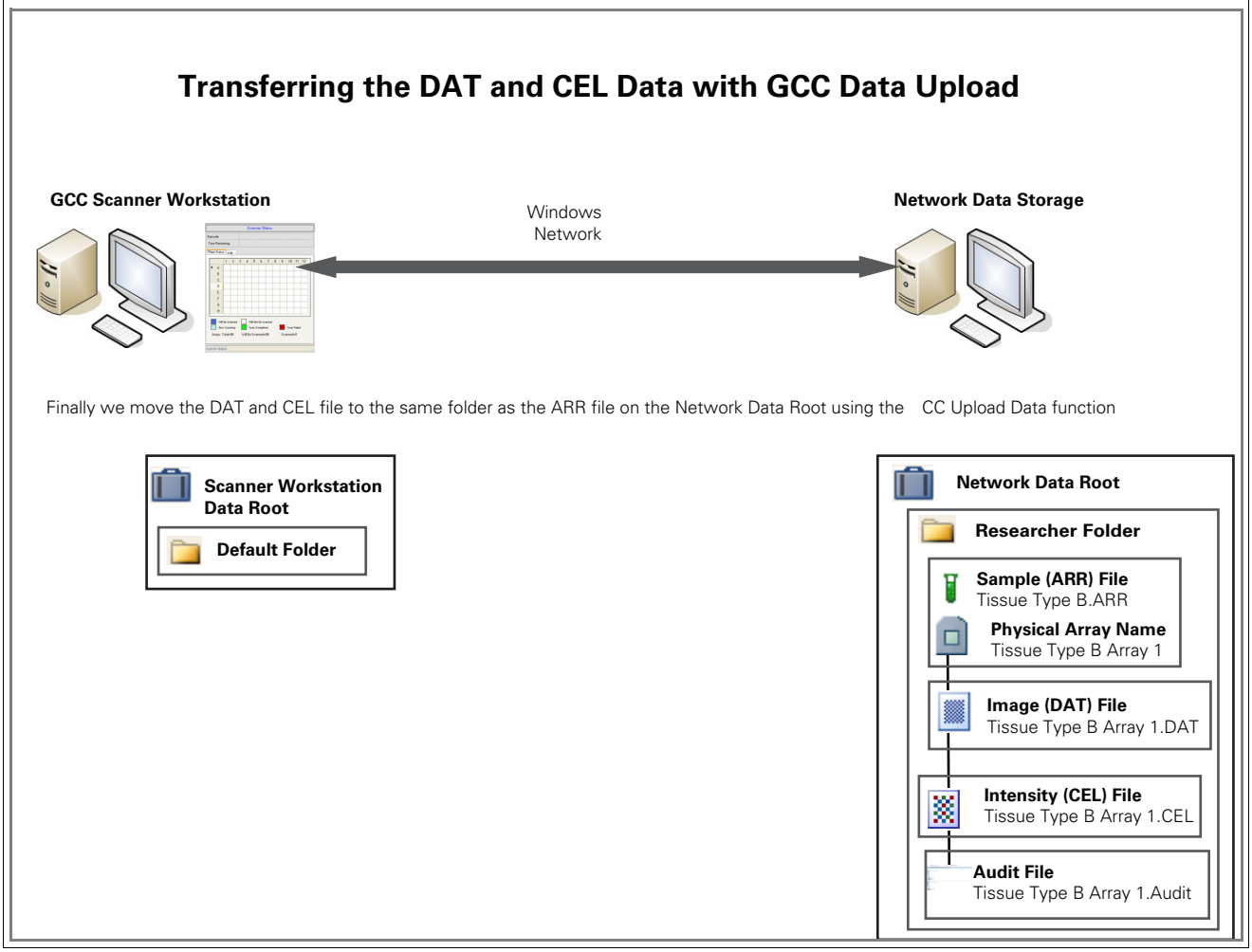
However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the Default folder on the Scanner Workstation computer (Figure 87). This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.

Figure 87 Creating DAT and CEL files on the Scanner Workstation Default Folder



The Upload Data function can be used to automatically transfer DAT and CEL files from the Default folder to the network data storage where the Sample (ARR) file is located (Figure 88). Upload Data is useful when you want to consolidate data from different workstation computers onto one network data storage site.

Figure 88 transferring the DAT and CEL files using the GCC Upload Data function

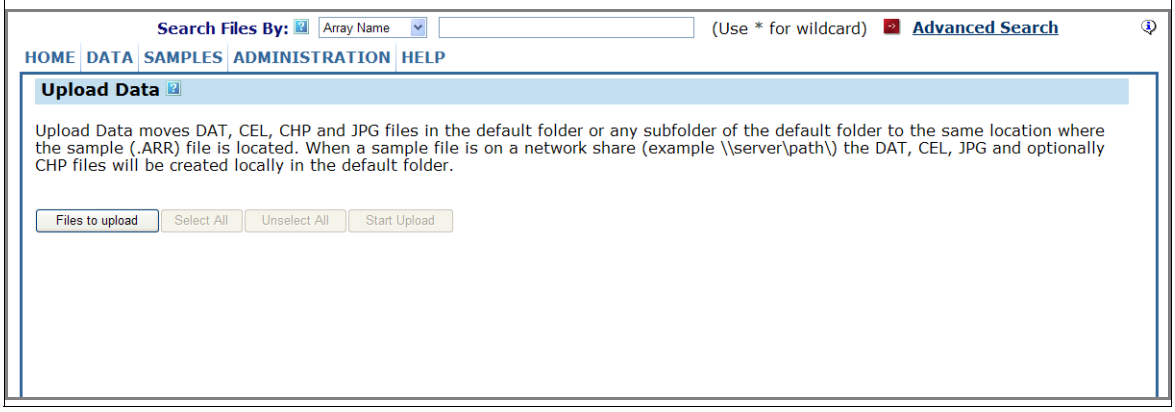


Uploading data manually

1. From the Data menu, select **Upload Data.**

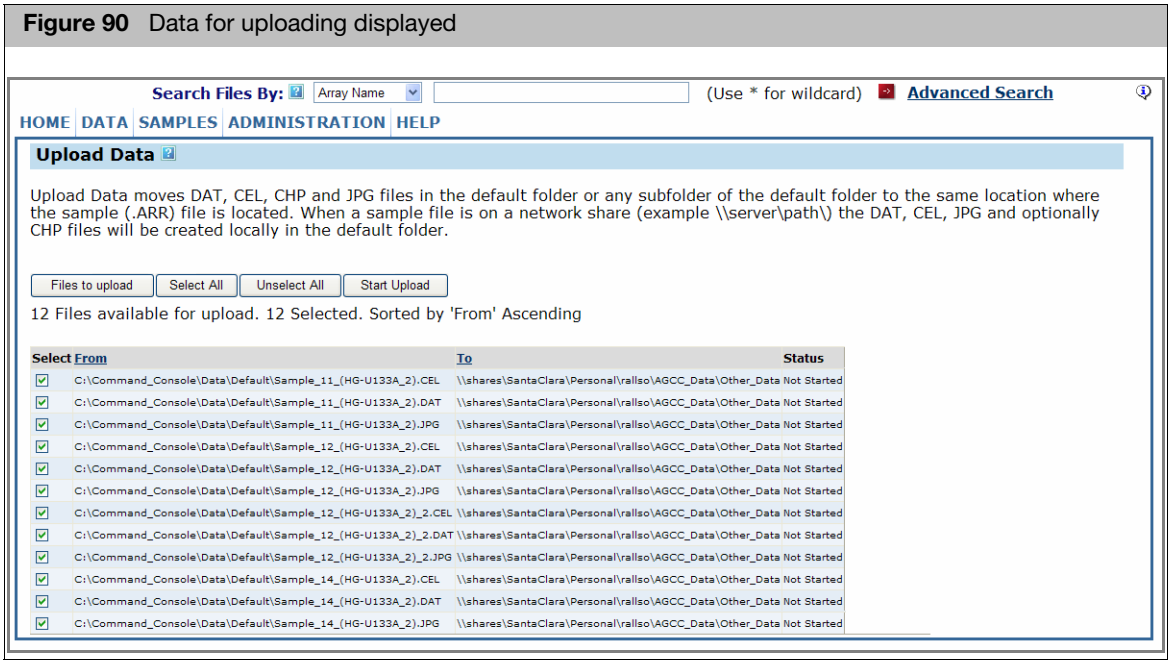
   The Upload Data page is displayed. (Figure 89)

Figure 89 Upload Data page



A new window opens with info on the files to be uploaded. (Figure 90)

Figure 90 Data for uploading displayed



The page displays a list of data files in the Default folder that are associated with a Sample (ARR) file on a network drive:

From Current location and file name.

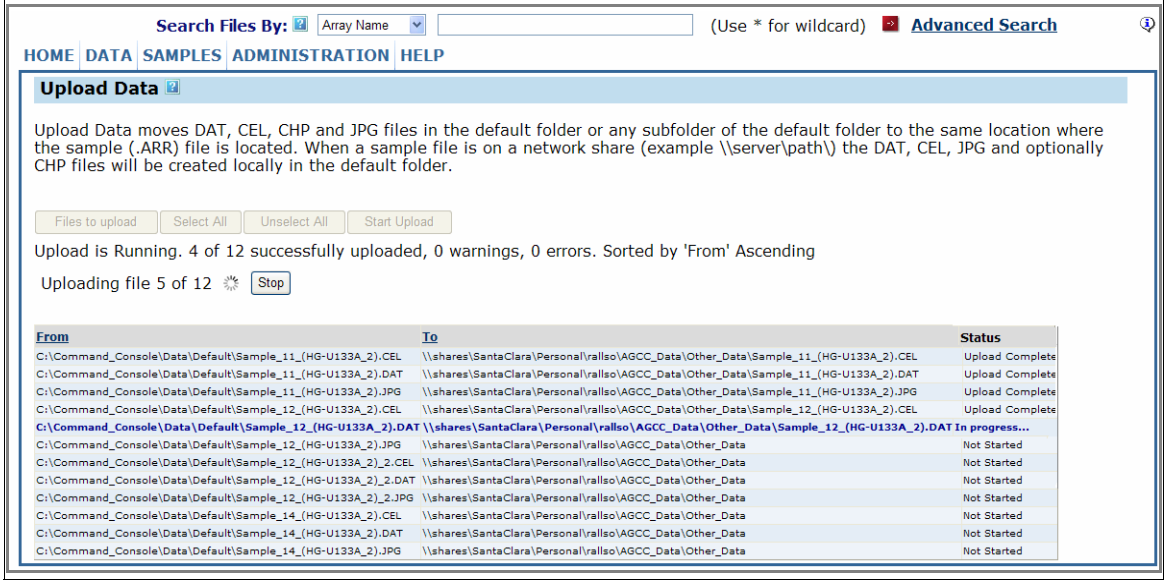
To The file destination (location of the Sample (ARR) file).

Status The current status of the move.

2. Click **Start Uploading** to upload the files to the locations.

   A notice informs you that the move is in progress. (Figure 91)

Figure 91 Move in progress

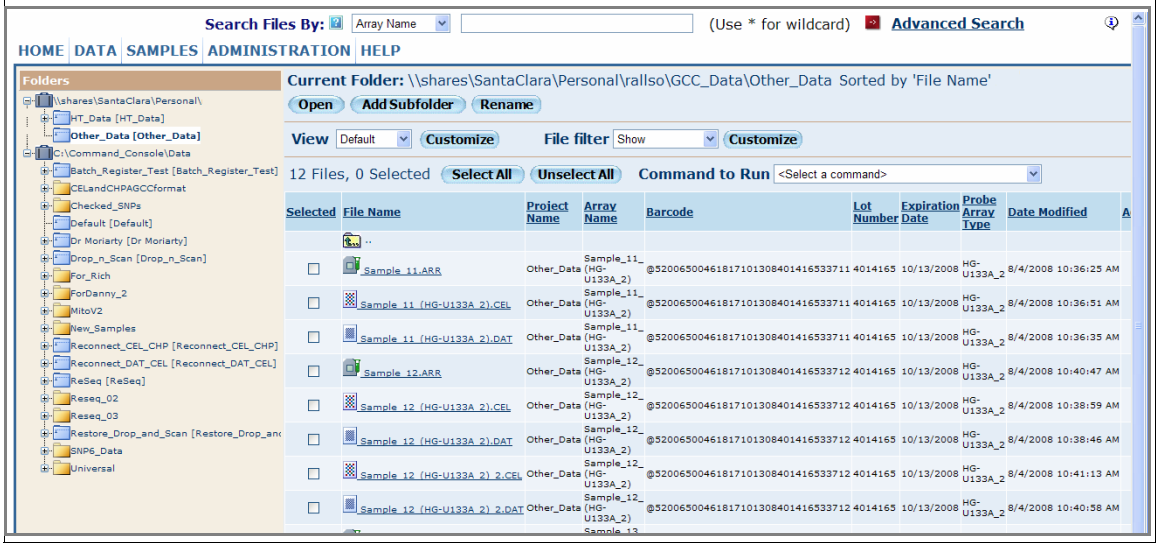


The status of the move is displayed in the lower part of the page, with a list of the files that have been transferred and their status.

When the upload is finished, the status is displayed in the page. (Figure 91)

The uploaded files can be seen in their new location. (Figure 92)

Figure 92 Data in new location



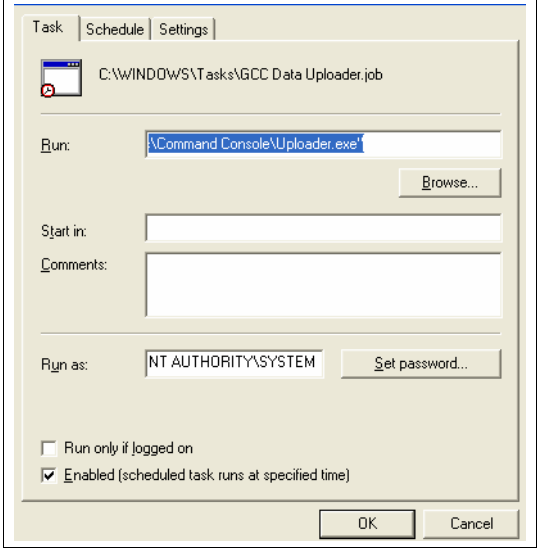
Scheduling auto-uploads

The Data Uploader Scheduler enables you to run the Data Upload automatically on a schedule you determine.

1. Click the **Data Uploader** icon in the Launcher.

   The GCC Data Uploader Scheduler window opens. (Figure 93)

Figure 93 GCC Data Uploader Scheduler, Task tab.



   The dialog box has three tabs:

   - Task
   - Schedule
   - Settings

   The Task tab enables you to set the options for the task itself.

2. In the **Run** box, enter the path to the file to be run as a scheduled task.

   Use quotation marks around the task path if the path includes spaces.

3. Enter information in the Start In box on the location of the folder with the task or other necessary files.
4. Use the Comments box for notes about the task.
5. In the Run As box, enter the user account for running the scheduled task.

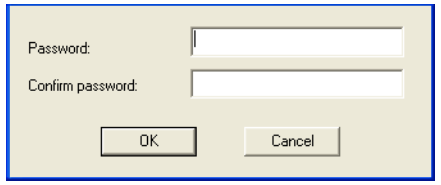
   Specify user account (must be the same account used for the GCC Services, with permissions on both the computer and the remote storage location).

6. Enter the password for the user account:

   a. Click **Set Password**.

      The Set Password dialog box opens (Figure 94).

Figure 94 Set Password dialog box

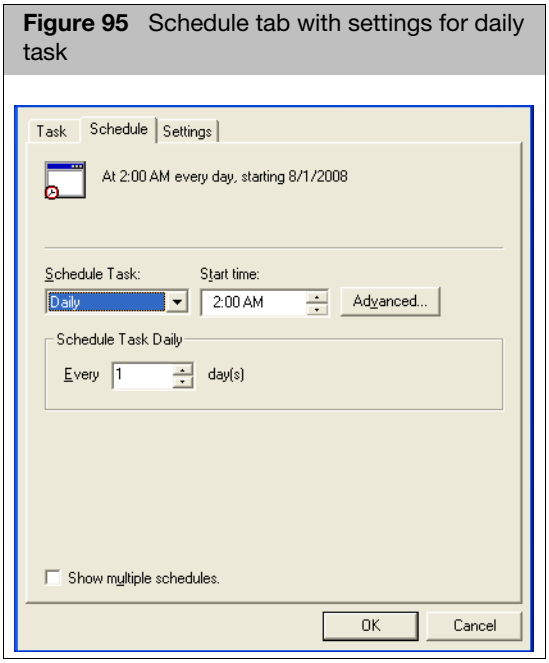


b. Enter and confirm the password for the user account and click **OK** in the Set Password dialog box.

7. Select other options:
   - Run only if logged on.
   - Enabled (scheduled task runs at specified time).
8. Click the **Schedule** tab to set up the schedule for the upload.

   The default setting is to run the upload function daily at 2 AM.

Figure 95 Schedule tab with settings for daily task



The Schedule tab (Figure 95) provides options for setting the schedule.

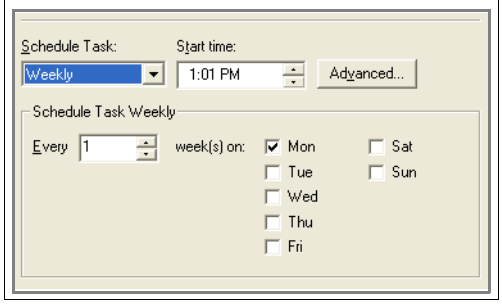
9. Select a period for performing the task from the Schedule Task drop-down.

   You can schedule the task to run:
   - Daily
   - Weekly
   - Monthly
   - Once
   - At System Startup
   - At Logon

- When idle

The options for task schedule change with the time period (Figure 96).

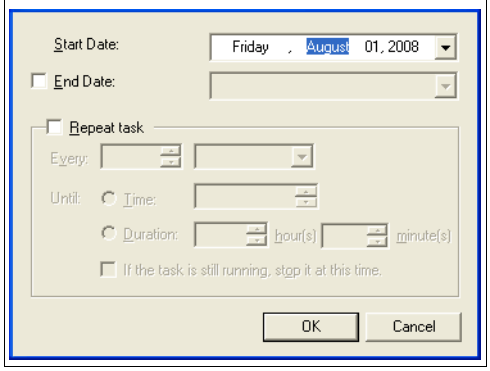
Figure 96 Settings for Weekly task



Click **Advanced Options** (Figure 97) to set Start/Stop dates and to specify how often to repeat the task.

10. Enter a time for the task to start in the Start time box.

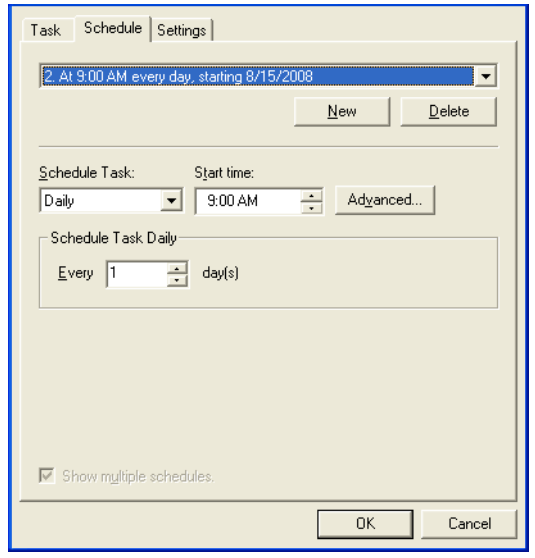
Figure 97 Advanced Schedule Options dialog box



11. You can enter multiple schedules:
    a. Select the Show Multiple Schedules check box.

       A schedule drop-down list appears at the top of the tab screen with **New** and **Delete** buttons.

Figure 98 Multiple schedules



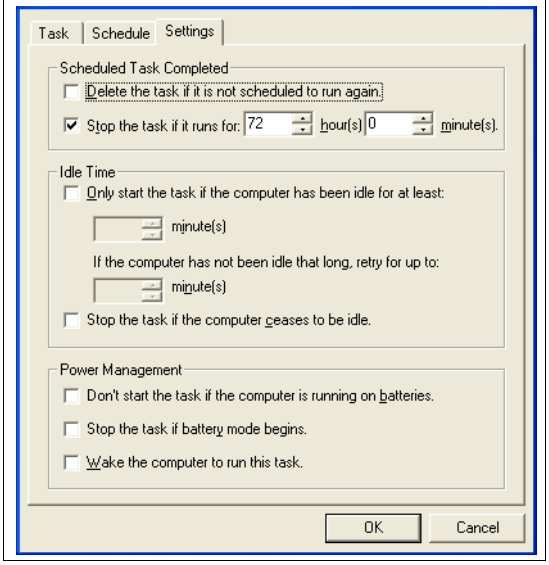
b. Click **New** to create a new schedule.

c. Set the schedule using the Schedule Task controls, as described in steps 9 and .

d. Click **Delete** to delete a scheduled task.

12. Click the **Settings** tab.

Figure 99 Settings tab



The Settings tab (Figure 99) enables you to set options for the upload:

- Scheduled Task Completed: Use these to set the options for a task that is only running once.

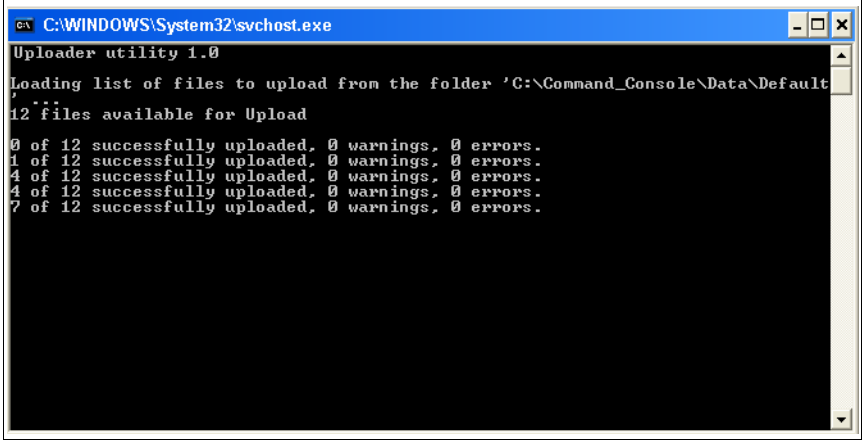
- Idle Time: Use these to start the task only if the computer has been idle for a specified period of time
- Power Management: Use these to set the options for power management if using a laptop.

13. Click **OK** when you have finished setting the task, schedule, and settings options.

    The task is scheduled and will run at the set times.

When the scheduled time comes, the Upload Utility window (Figure 100) appears on your desktop and shows the progress of the upload.

Figure 100 Upload utility running

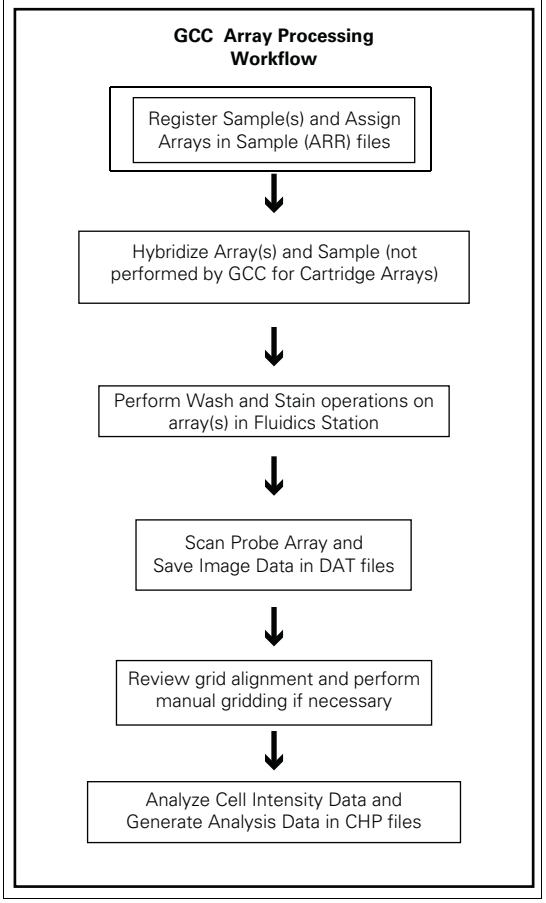


You can set up the GCC Email Configuration Editor to notify you when the Upload Utility runs or if problems arise. See Appendix E, "Notification e-mails" on page 367 for more information.

5 Creating and editing sample (ARR) files

Sample Registration is the first step in the recommended array processing workflow, as shown in Figure 101.

Figure 101 Array processing workflow



For information on scanning arrays without registering them first, see "Drop and scan" on page 206.

This chapter describes the following options for creating Sample files and registering arrays:

- "GeneTitan array plate registration" on page 135

You can also edit previously created Sample (ARR) files

- "Editing files and copying attributes" on page 110
- "Adding a barcode to a sample file" on page 142
- "Batch editing" on page 144

For information on selecting a Sample Registration method, see "Registering samples and arrays" on page 25.

See "Introduction to sample registration" for an introduction to the types of information that can be collected in a Sample file.

Introduction to sample registration

To get the most out of GCC, you need to understand the types of information that are collected in the Sample file, as described below:

- "Information in the sample file", below
- "Characters allowed in GCC" on page 104

Information in the sample file

In GCC, the samples are the beginning of the data chain for a given experiment. The sample information is stored in a Sample file with an ARR extension.

The Sample (ARR) file collects two types of information:

- Sample Attributes: information that you can use to interpret the experimental data. It can include information about the sample itself, the experimental conditions, or other information you may find useful.
- Array Information: Information about the array(s) used with the sample. More than one array can be associated with the sample. This might be useful for making sure that data from products that contain more than one array remain related or to help describe experiments that use replicates.

Sample attributes

There are two types of attributes in GCC:

- Template Attributes, which have the attribute name, data type and other information specified in a template.
- For more information on creating and managing templates, see "Working with templates" on page 328.
- User Attributes, which are created individually during registration.

Each attribute in a template is assigned one of the following data types:

- Text: Text string
- Number: Integer or floating point number
- Date: Calendar data
- SingleSelect: Presents a list of items for the user to choose

User Attributes may be Text, Number, or Date data types.

Beta Versions of GCC included other deprecated data types which are no longer available, such as:

- Integer
- Floating Point
- MultiSelect

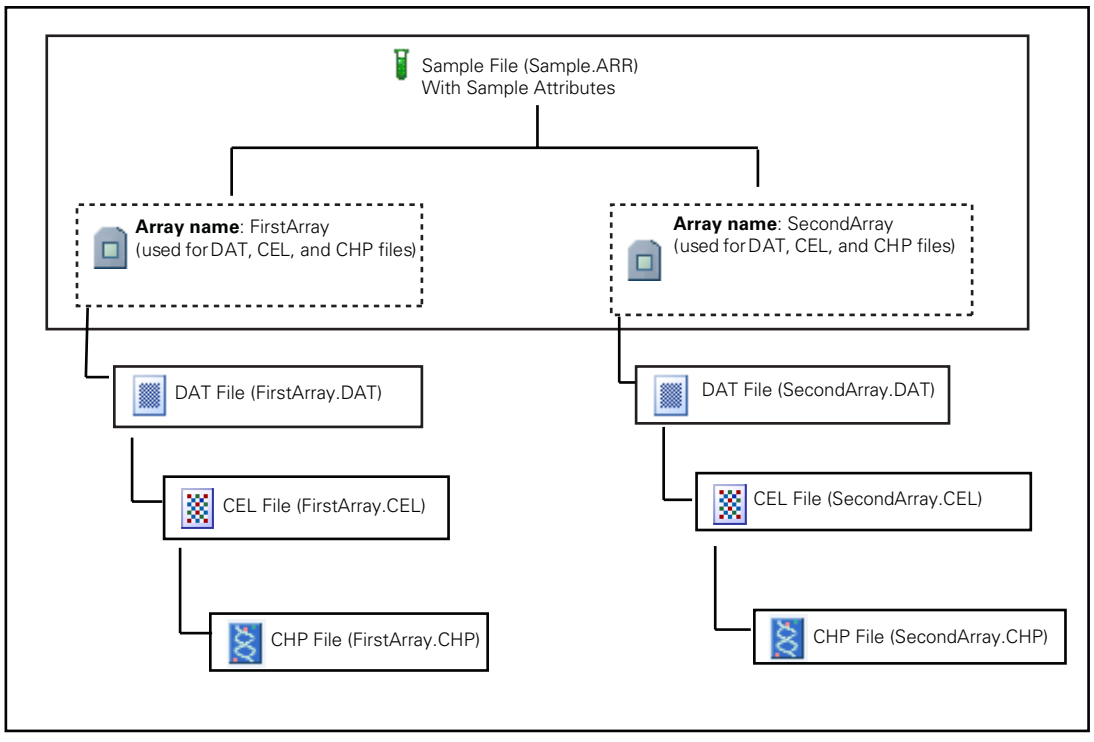
The data type determines the type of value that can be entered, and the types of comparisons that can be performed during an Advanced Search.

Array information

The Sample file also contains information about the array(s) used with the sample. More than one array can be associated with the sample. This is useful for tracking replicates; in addition, it can be used to simplify tracking data for multi-chip arrays, such as 500K arrays.

Each array is assigned an array name during registration. The array name is used to identify the DAT, CEL, and CHP data files that are generated during analysis. (Figure 102)

Figure 102 Sample File with associated arrays and data files



The array information includes:

- Array Name
- Probe Array Type
- Barcode

Characters allowed in GCC

You can only use a certain set of characters in GCC Sample File names, Folder Names, Project Names, and Array Names:

These names can contain:

- Basic Latin letters (A-Z, a-z)
- Digits (0-9)
- Spaces
- The following set of punctuation marks: ! # $ % & ' ( ) + , - . ; = @ [ ] ^ _ ` { } ~

These names cannot use the following characters: \ / : * ? " < >|

International characters are not allowed.

Sample attribute names can contain:

- Numbers
- Letters
- International characters
- The following set of punctuation marks: ! # $ % & ' ( ) + , - . ; = @ [ ] ^ _ \ / ` ~

Sample Attribute names cannot contain any of the following characters: { } : * ? " < > |

Sample attribute values of Text type can contain any characters.

Detailed sample registration

The Detailed Sample Registration page enables you to register a single sample and its associated cartridge arrays, along with any sample attribute you want to include. You can use templates to determine which attributes need to be entered for registration, and you can add user attributes that are unique to that sample.

You cannot register a GeneTitan System array plate using the Detailed Sample Registration (use "GeneTitan array plate registration", described on on page 135).You can add a cartridge array to a previously created array plate Sample file with the editing functions of the Detailed Sample Registration.

For more information see "Creating a new sample file".

The page can also be used for:

- Editing previously created Sample files
- Renaming a Sample file and/or the Array name
- Copying the attribute data over to a new file
- Adding physical arrays to an existing Sample (Arr) file

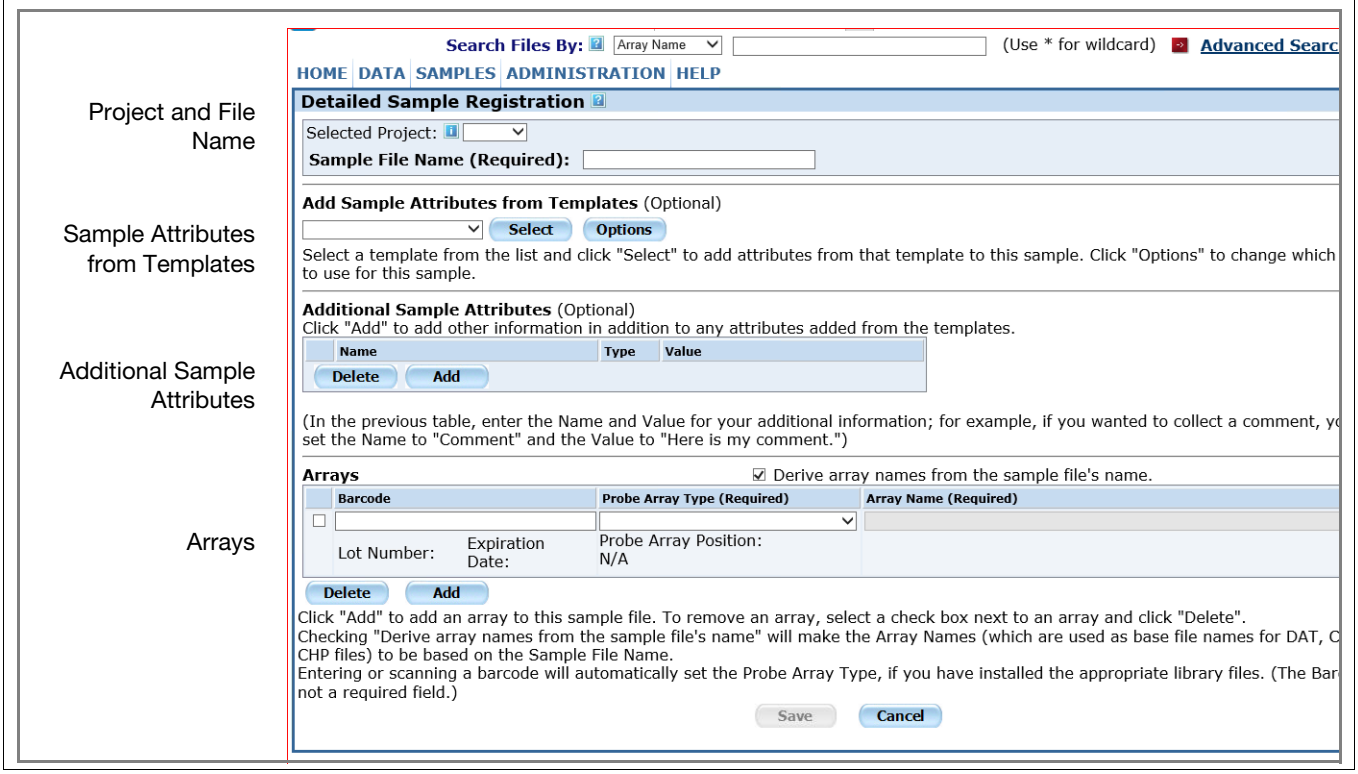
For more information, see "Editing files and copying attributes" on page 110.

If you have edited or deleted templates and attributes, you may need to change the attributes in a Sample file when you try to edit it. For more information, see "Sample attributes conversion" on page 115.

Creating a new sample file

1. From the Samples menu, select **Register**.
   The Detailed Sample Registration page opens (Figure 103).

Figure 103 Detailed Sample Registration page

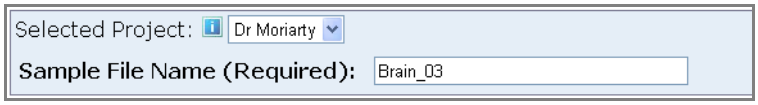


The Detailed Sample Registration page has four sections:

- Project and File Name (at the top of the page)
- Sample Attributes from Templates
- Additional Sample Attributes
- Arrays list

2. Select a Project from the drop-down list (optional) (Figure 104).
3. Enter a name in the Sample File Name box (Figure 104).

Figure 104 Entering Project and File Name

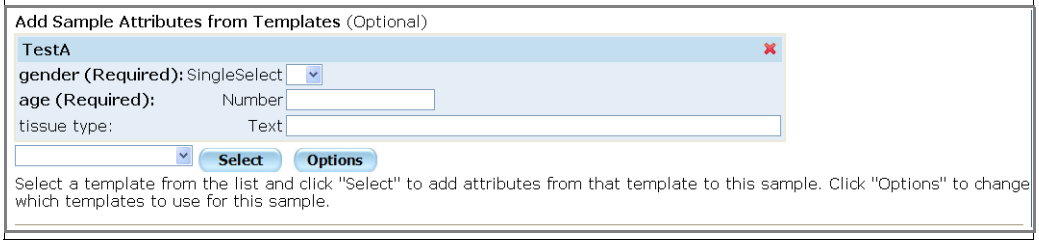


The Sample Attributes from Templates section displays a list of the attributes in the Default template when the page is first opened. See "Managing default templates" on page 335 for more information.

You can:

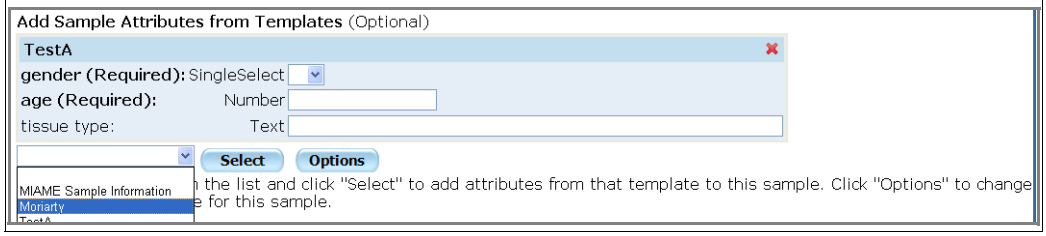
- Enter attribute values for the Default template (see Step 6 on page 107).
- Add and remove templates with additional attributes (optional—see Step 4, below).

Figure 105 Sample Attributes from Templates



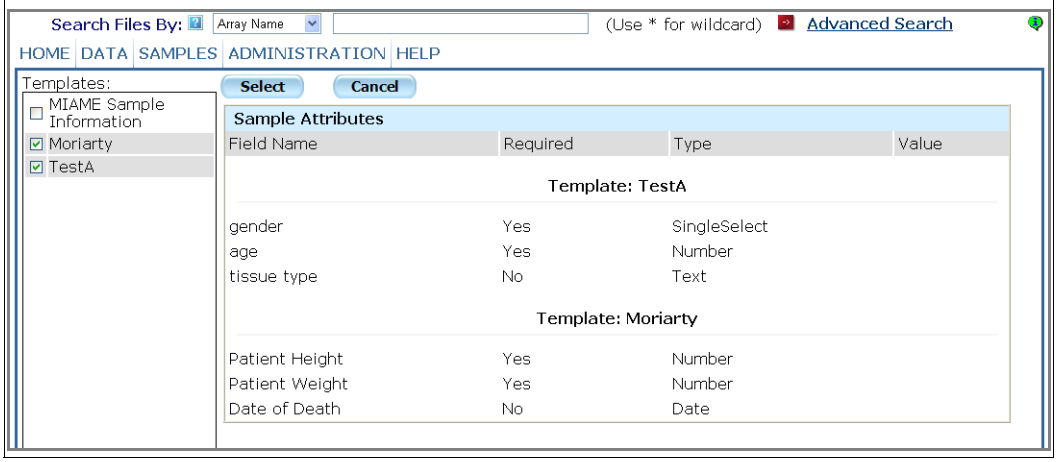
4. To add Templates, use one of the following options:
   - Select the template from the drop-down list and click **Select** (Figure 106); or

Figure 106 Template List



   - Click **Options** to open the Template Select page. (Figure 107) **Note:** You can also use the Template Select page to delete templates from the Sample (ARR) file.

Figure 107 Template Select page



The Template Select page displays a list of the available templates on the left side.

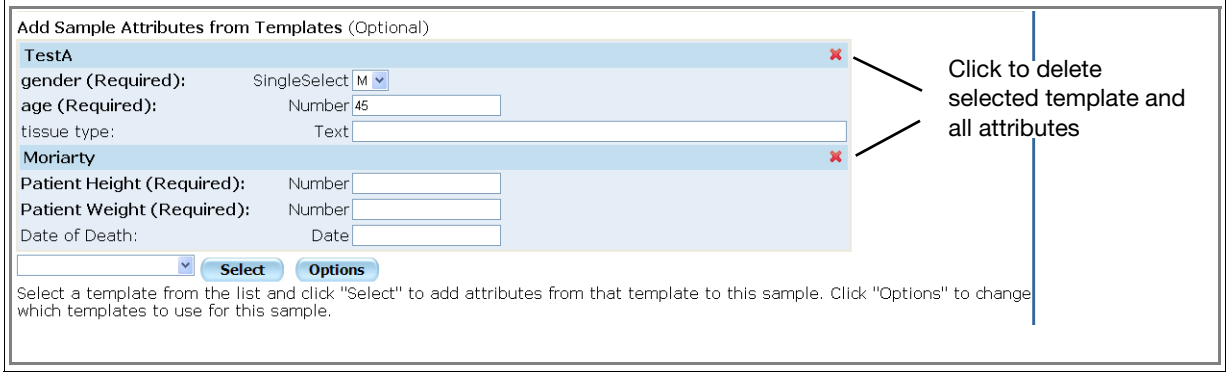
The right side displays a list of the attributes in the selected templates.

- Select the template(s) you want to use.
- Review the attributes in those templates in the Sample Attribute list.
- Click **Select** to add selected templates to the Sample (ARR) File.

The Detailed Sample Registration page returns with the attributes in the selected template(s) displayed (Figure 108).

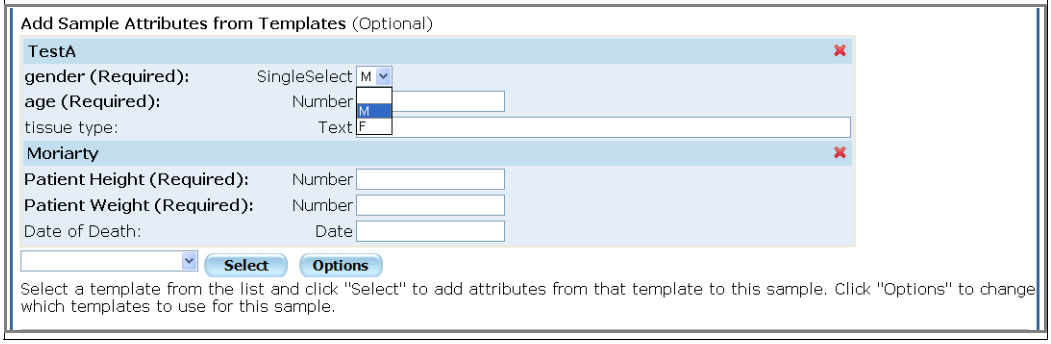
Click **Cancel** to return to the Detailed Sample Registration page without adding templates.

Figure 108 Added Templates



5. To delete a selected template and all its attributes, click the red **X** at the top of the template's attribute list (Figure 108).
6. To enter values for the Template Attributes:
   a. Enter values for the text, numerical, and date attributes.
   b. Select values from the drop down lists for the SingleSelect attributes (Figure 109).

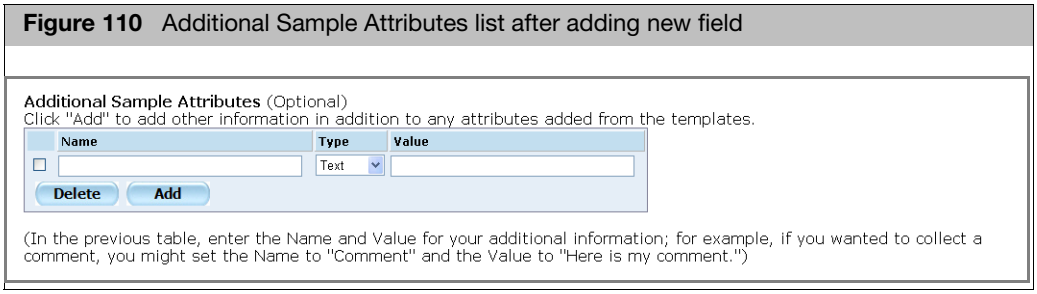
Figure 109 Entering values for the sample attributes



7. Add user-defined attributes to the Sample by using the Additional Sample Attributes list:
   a. Click **Add** under the Additional Sample Attributes list.

An empty line appears in the list. (Figure 110)

Figure 110 Additional Sample Attributes list after adding new field



b. Enter the attribute name and value.

c. Select an attribute type for the user attribute:

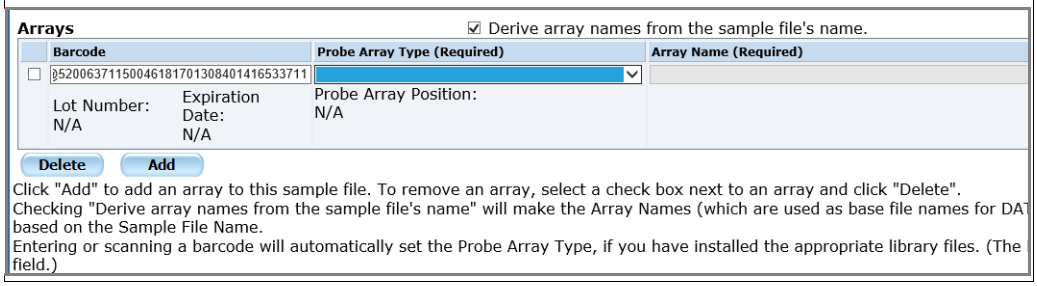
- Text: text string
- Number: Floating point or Integer
- Date: Calendar data

  The attribute type determines the sorts of comparisons you can perform during an advanced search. For more information, see "Sample attributes" on page 102 and"Advanced search" on page 67.

d. Repeat to add more attributes.

The Arrays list (Figure 111) enables you to assign an array or set of arrays to the Sample (ARR) files.

Figure 111 Arrays list



You can include the following information on the array(s):

- Barcode (optional)
- Array Type
- Array Name

To assign an array to the Sample (ARR) file:

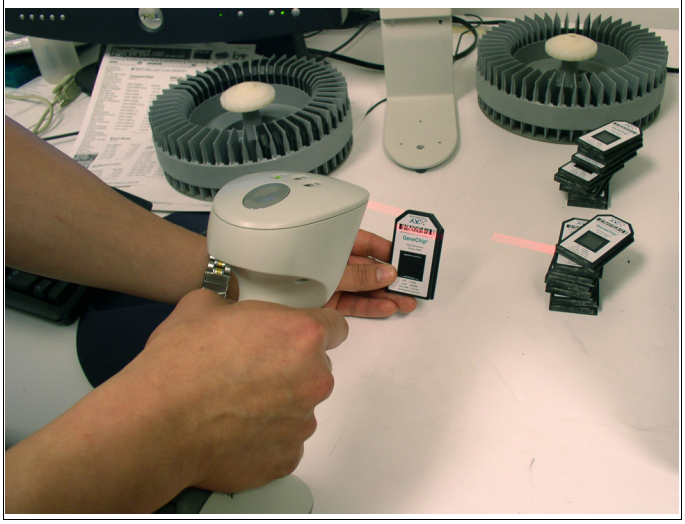
1. Enter the barcode (optional):

   Enter the barcode using the keyboard; or

   a. Click in the Barcode field.

   b. Use the barcode reader to scan in the barcode on the array. (Figure 112)

Figure 112 Reading the array barcode



The reader reads and sends the barcode to the Barcode field.

Note: You can use custom barcodes to register an array in Detailed Sample Registration.

The array's lot number and expiration date are displayed below the barcode (Applied Biosystems barcodes only).

Probe Array Position is an attribute for the GeneTitan System array plates and is not applicable to cartridge arrays.

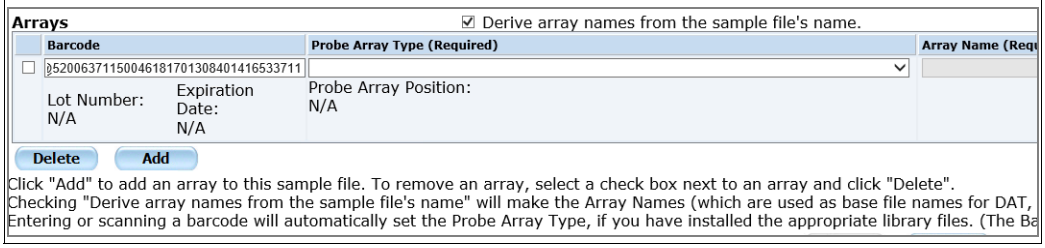
2. Select the array type.

   Note: If you are using Applied Biosystems barcodes, the array type is selected automatically after the barcode is entered. If you are using custom barcodes, you must select the array type manually.

The **Derive array names from sample names** check box is selected by default and an array name is created by linking:

- The Sample file name entered in the first set of steps
- The array type
- Incremental numbers added if necessary to distinguish arrays

Figure 113 Arrays list with array entered

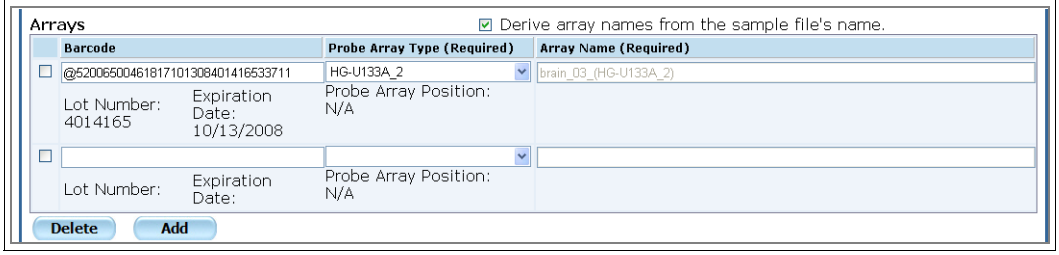


3. If you want to enter a different array name:
   a. Deselect **Derive array names from sample names** check box.
   b. Enter the name in the Array Name column.

To register additional arrays:

4. Click **Add Array**.
   An empty line appears in the list. (Figure 114)

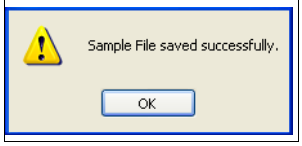
Figure 114 Array list with second array added



The line enables you to enter data on an array.

5. After you have entered arrays, click **Save**.
   A Sample file has been successfully saved message appears. (Figure 115)
6. Click **OK**.

Figure 115 Sample File Saved notice



Editing files and copying attributes

You can use the Detailed Sample Registration to:

- Edit data in the Sample (ARR) file
- Rename the Sample (ARR) file
- Change the Array name in the Sample file
- Copy attributes over to a new file

Opening the Detailed Sample Registration page for a Sample file

- Click the Sample file link in the Folder View or Search Results pages.
- While displaying information about a Sample file in the Project view, click the **Open** button.
  If there are template and attribute discrepancies, the Sample Attributes Conversion page will open.

See "Sample attributes conversion" on page 115 for more information about what you should do.

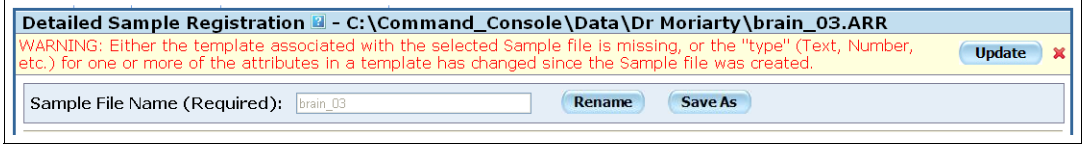
There are additional controls in the page when you have opened a previously created Sample file.

The **Rename** button enables you to change the name of the Sample file or array.

The **Save As** button copies the sample attribute and array type information over to a new Detailed Registration page which can be used to create a new file.

If you have made changes in a template used for the array file since creating the array file, you will see a notice and the **Update** button at the top of the Detailed Sample Registration page.

Figure 116 Warning message and Update button



Click the **Update** button to review the differences between the attributes and to correct the problem.

See "Sample attributes conversion" on page 115 for more information.

Editing the sample attributes in a sample file

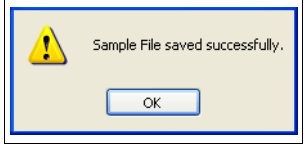
1. Open the Sample file in the Detailed Sample Registration page.
2. Edit the attributes as desired.

   Note: You cannot edit the barcode or array type information after an array has been scanned.

3. Click the **Save** button.

   A notice that the Sample file has been successfully saved appears in a dialog box. (Figure 117)

Figure 117 Sample File Saved notice



Renaming the sample file

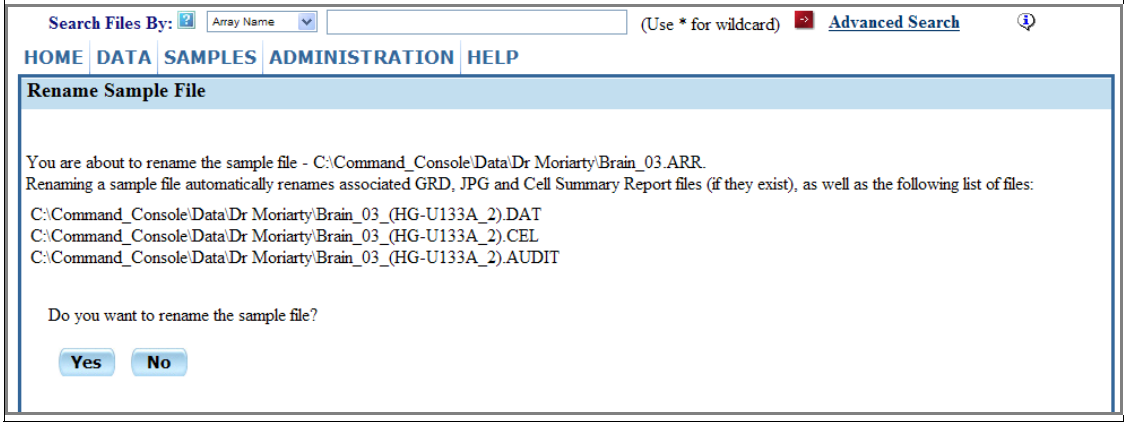
IMPORTANT! If the **Derive Array Name from Sample File** check box is selected, changing the Sample file name will require changing the names of all the data files associated with the Sample file.

Renaming a Sample (ARR) file

1. Open the file in the Detailed Sample Registration page.
2. Click the **Rename** button next to the Sample File Name at the top of the page.
3. The Sample name can now be edited, and the Save button at the bottom of the page is replaced by the Rename button.
4. Enter a new name for the Sample file.
5. Make other changes as necessary.
6. Click **Rename**.

   The Rename Sample File page opens with list of the DAT and CEL files that will be renamed. (Figure 118)

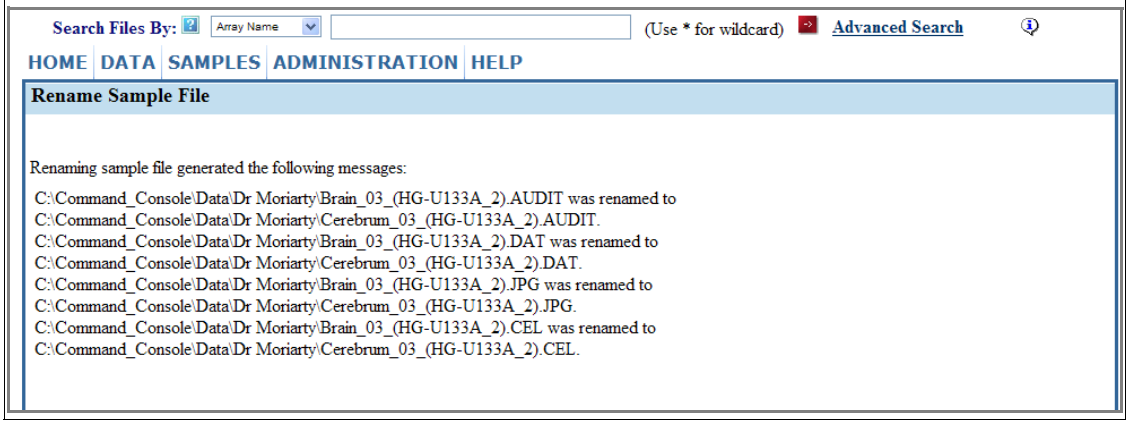
Figure 118 Rename Sample page



7. Click **Yes** to rename the sample file.

   The page displays a list of the files with the new names. (Figure 119)

Figure 119 Rename Sample File page with notice of changed data files



Changing the array name(s) for a sample file

Changing the array name for a sample file results in renaming all the data files associated with the array.

This can be done while editing or renaming a file.

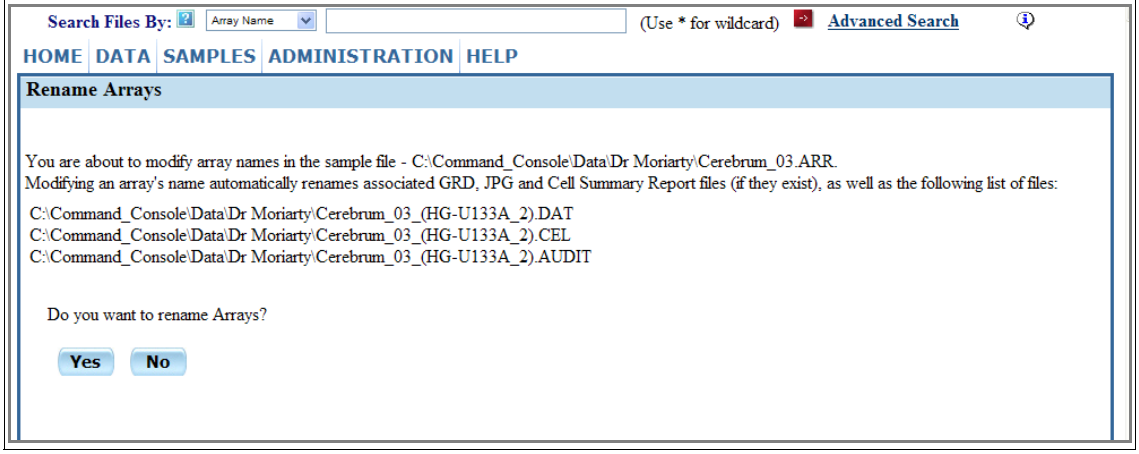
Renaming the array name(s) for a Sample file

1. Open the Sample file in the Detailed Sample Registration page.
2. Deselect the **Derive array names from sample file name** check box.
3. Click in the Array name column of the array you want to rename.
   The Rename Notice appears. (Figure 120)

Figure 120 Rename notice

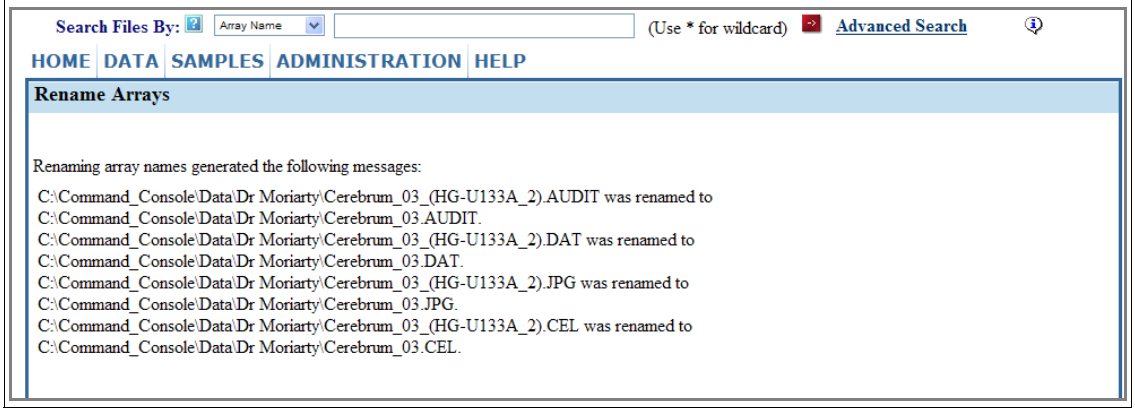
4. Click **OK** and edit the Array Name(s).
5. Click **Rename** or **Save** in the Detailed Sample Registration page.
   The Rename Arrays page opens with a list of the files that will be renamed.

Figure 121 Rename Arrays page



6. Click **Yes** to rename the arrays and the data files.
   The page displays a list of the files with the new names. (Figure 122)

Figure 122 Rename Arrays page with notice of changed data files



Copying file data over to new Sample (ARR) file

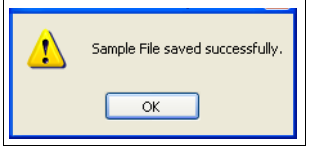
1. Open file in Detailed Sample Registration page.
2. Click the **Save As** button by the Sample File Name box.

   The Sample File Name becomes editable and the Barcode information for the arrays is erased.

   Note: The **Save As** button is not available for GeneTitan System sample files.
3. Enter a name for the new Sample file.
4. Edit the Sample Attribute information if desired.
5. Enter new Array Type and Barcode information.
6. Click the **Save** button.

   The Sample File Saved notice appears. (Figure 123)

Figure 123 Sample File Saved notice



Sample attributes conversion

You may see the Sample Attributes Conversion page when you try to open a Sample file for editing.

The Sample Attributes Conversion page appears when there is a discrepancy between the properties of an attribute in the Sample file and the properties of the attribute as defined in the current template.

Attribute conversion may be necessary if any of the following changes have been made in a template:

- The attribute has been deleted from the template.
- The entire template has been deleted from GCC.
- The data type for the attribute in the template is different from the data type in the Sample file.

The page displays the attributes with discrepancies and the conversion that will be applied to correct the discrepancy. Depending upon the type of discrepancy, the attribute will either:

- Be converted to a user attribute, with Text type.
- Have its attribute type changed to match the template.

Applying the conversions

1. Review the conversions in the Original Attribute and Converted Attribute lists.

   The details are described in:

   - "Deletion of attribute or template" on page 115
   - "Change in attribute type" on page 117
2. Click **Yes** in the Sample Attributes Conversion page.

   The Detailed Sample Registration page opens with the Sample file displayed.

   The converted attributes will be displayed in the Detailed Sample Registration page, but the conversions will not be applied to the Sample file until you:
3. Click **Save** in the Detailed Sample Registration file.

   The changes will be applied to the Sample file.

The attribute conversion may affect how you search for Sample files using that particular attribute in the Advanced search page. The sections below describe this in more detail.

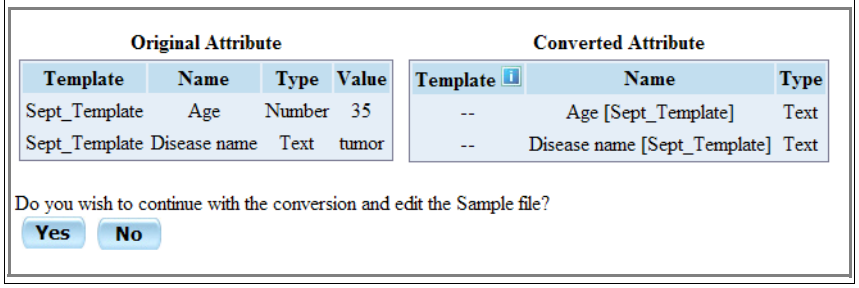
For more information about templates and data types, see:

- "Sample attributes" on page 102
- "Working with templates" on page 328

Deletion of attribute or template

If the attribute has been removed from the template, or if the entire template has been deleted, the attribute in the Sample file will be converted to a user-defined Sample attribute. (Figure 124)

Figure 124 Attribute deleted from template (converted to user attribute)



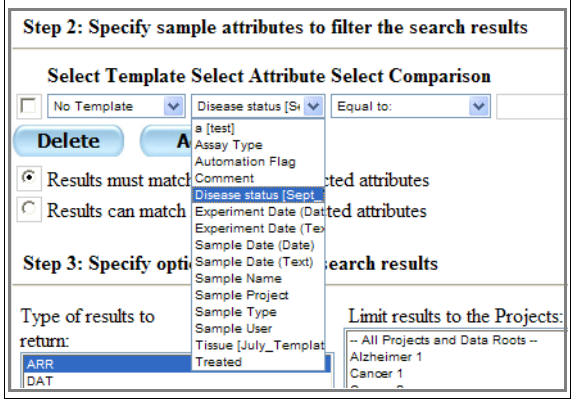
This is indicated by the blank cell in the Template column for the converted attribute. The new user attribute name will use the original attribute name with the original template name in square brackets to indicate the source, as in the example `Disease Status [Sept_Template]`.

In case of a name conflict, the new user attribute will have an underscore-number (_1) added to the attribute name:

`Disease Status_1 [Sept_Template]`

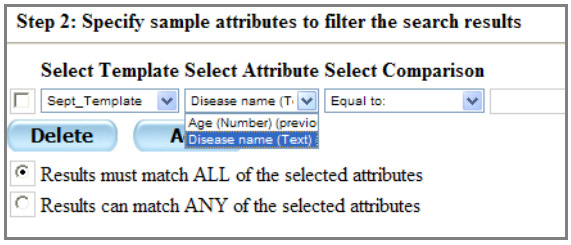
The user attribute will be listed in the No_Template attribute list in the Select Template drop-down list of the Advanced Search page. (Figure 125)

Figure 125 Advanced Search: selecting a user attribute from the No Template list



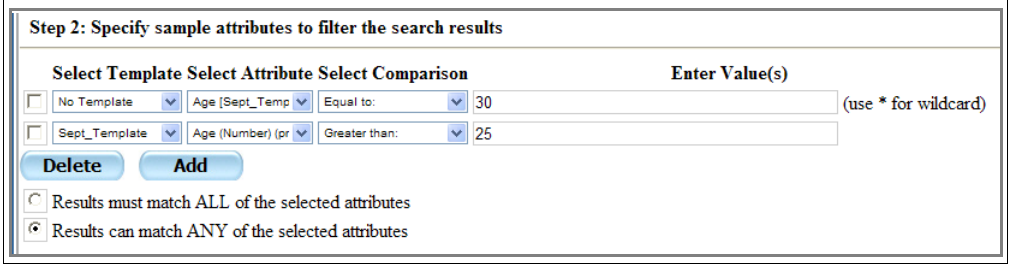
If other Sample files still have the original template attribute, the template will be listed in the Select Templates list. (Figure 126)

Figure 126 Advanced Search, Unconverted attributes in template attribute list



When doing an advanced search, if you want to find Sample files having the previous attribute type and the current attribute type, you will need to select both attributes in the Select attributes section. (Figure 127)

Figure 127 Advanced Search, specifying converted and unconverted attributes



For more information about performing searches, see "Advanced search" on page 67.

Change in attribute type

Each attribute in a template is assigned to one of the following data types:

- Text: Text string
- Number: Integer or floating point number
- Date: Calendar data
- SingleSelect: Presents a list of items for the user to choose

Beta Versions of GCC included other data types which are no longer available, such as:

- Integer
- Floating Point
- MultiSelect

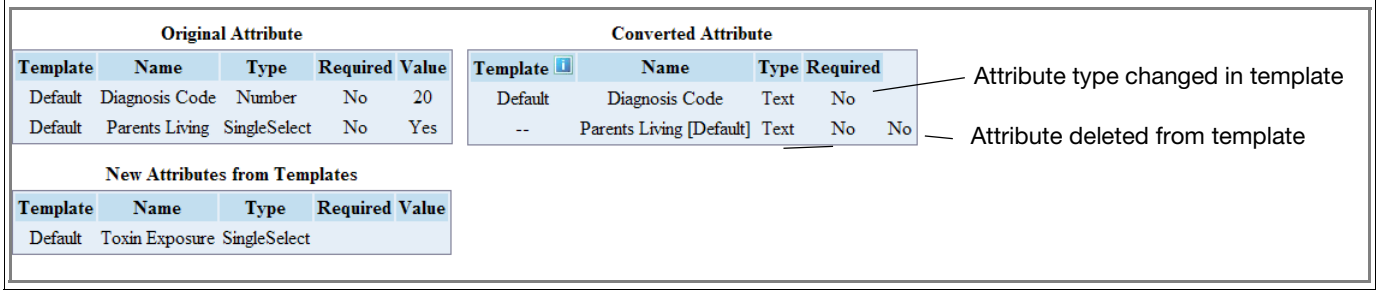
The data type determines the type of value that can be entered, and the types of comparisons that can be performed during an Advanced Search.

In this case, the results of the Attribute conversion depends upon the original attribute data type and the new attribute data type in the template.

- If the data types are compatible, the sample attribute will be converted to the new data type.

The Sample Attributes Conversion page shows the old and new attribute data types. (Figure 128)

Figure 128 Conversion details



If the data types are not compatible, the existing sample attribute will be added as a user attribute with the text data type.

This gives you the option of manually transferring the attribute value to the new template attribute and deleting the added user attribute.

The attributes are converted according to the rules in the table below.

Table 1 Conversion rules

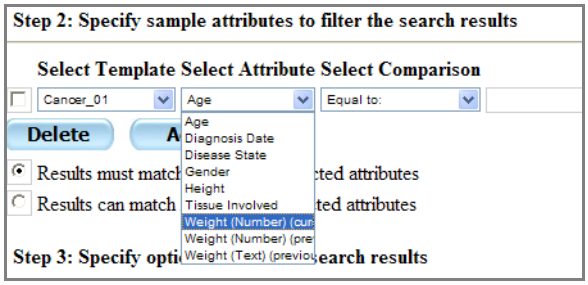
Old Sample File Data Type	New Template Attribute data type	Results
Text	Number	The attribute is converted to user attribute.
	Date	The attribute is converted to user attribute
	SingleSelect	Attribute type converted if it matches to one of the items in the Selection list; otherwise the attribute is converted to user attribute.
Number	Text	Attribute type converted.
	Date	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.
Integer and Float (no longer supported)	Number	Attribute type converted.
	Text	Attribute type converted.
	Date	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.
Date	Text	Attribute type converted.
	Number	Attribute is converted to user attribute.
	SingleSelect	Attribute is converted to user attribute.

Table 1 Conversion rules

Old Sample File Data Type	New Template Attribute data type	Results
SingleSelect	Text	Attribute type converted.
	Number	Attribute is converted to user attribute
	Date	Attribute is converted to user attribute
MultiSelect (no longer supported)	Text	Attribute type converted.
	Number	Attribute is converted to user attribute
	Date	Attribute is converted to user attribute
	SingleSelect	Attribute is converted to user attribute

If the sample attribute has the data type changed, you will be able to find the attribute listed for the template in the Advanced Search screen. (Figure 129)

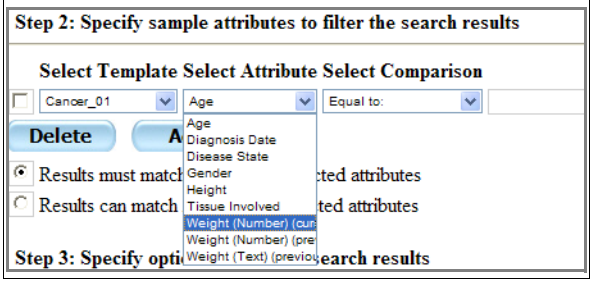
Figure 129 Advanced search, selecting new attribute type



If the attribute type is changed, but it remains in the template, the type of comparisons you can perform when searching for the attribute may change.

If converted to a user attribute, you will need to select the attribute from the No Template list in the Specify Sample Attributes section of the Advanced search (Figure 130).

Figure 130 Advanced Search: selecting converted attributes from a template

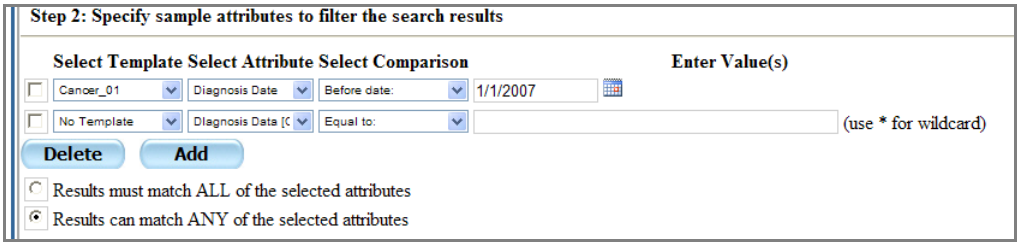


If other Sample files still have the original attribute type, the attribute will be listed with both the old and new attribute types.

- The current attribute type in the template will have (current type) appended to the attribute name
- The previous attribute type will have (previous type) appended to the attribute name.

When doing an advanced search, if you want to find Sample files with the previous attribute type and with the current attribute type, you will need to select both attributes in the Select attributes section. (Figure 131)

Figure 131 Advanced Search, specifying converted and unconverted attributes



For more information about performing searches, see "Advanced search" on page 67.

Quick sample registration

The Quick Sample Registration enables you to create a set of Sample (ARR) files quickly with the following basic information for the Sample and Array:

- Probe Array Type
- Sample File Name and Array Name
- Project
- Barcode (optional)

Barcodes and sample attributes can be added later on using various editing options. For more information, see "Adding a barcode to a sample file" on page 142 and "Batch editing" on page 144.

Both the Sample (ARR) file and the array name will have the same value when using Quick Sample Registration. As an example, Sample1ARR will have a physical array entry called Sample1.

You can create up to 48 Sample (ARR) files (one AutoLoader carousel's worth) at a time.

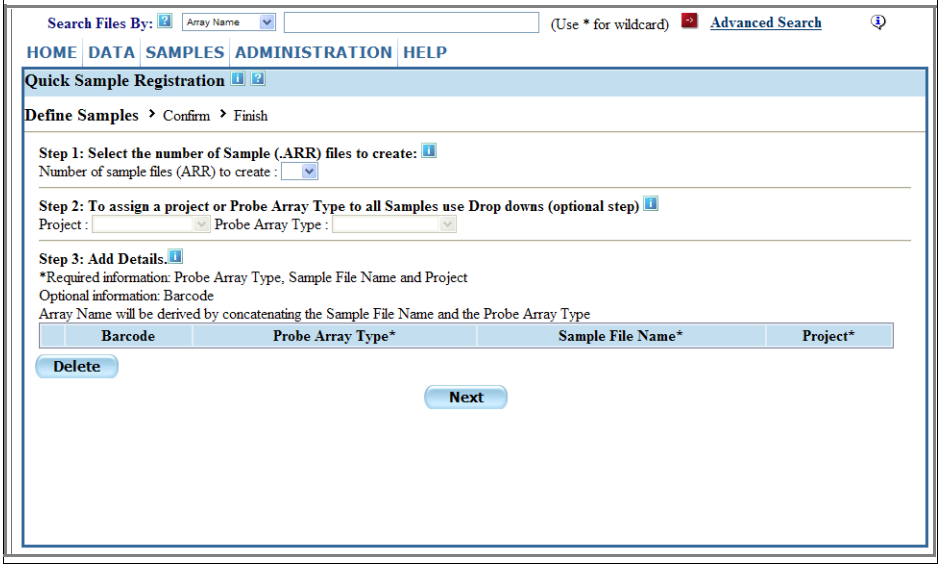
Note: This function works best for registering arrays that are not part of a set. If your array set contains an A and B array then use Register or Batch Register to create sample files (ARR). In addition, you cannot use Quick Sample Registration to register arrays for GeneTitan MC instrument.

Creating a set of Sample files with basic information

1. From the Samples menu, select **Quick Register**.

   The Quick Sample Registration page opens. (Figure 132)

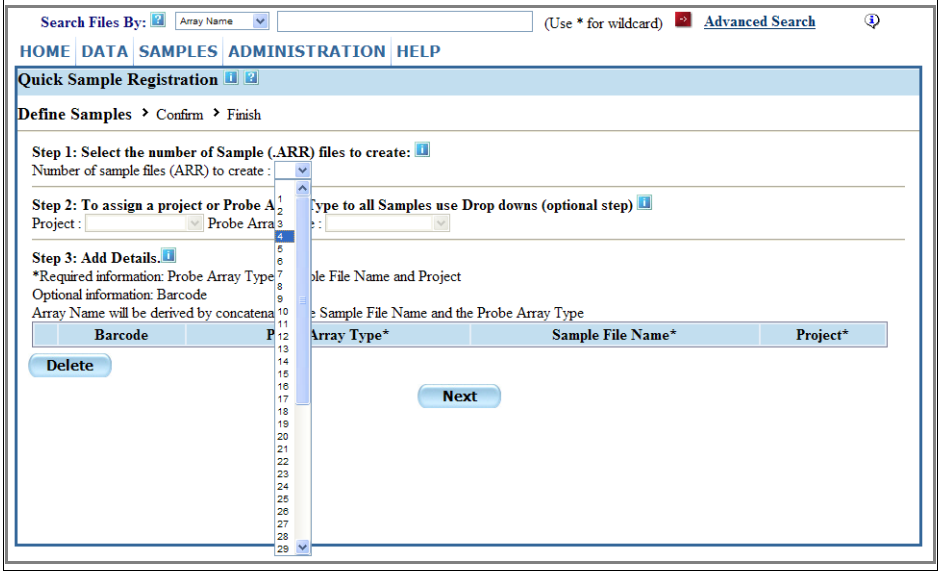
Figure 132 Quick Sample Registration page



2. Select the number of Sample (ARR) files to create. (Figure 133)

   You can add up to 48 arrays (an AutoLoader Carousel's worth) during one quick registration operation.

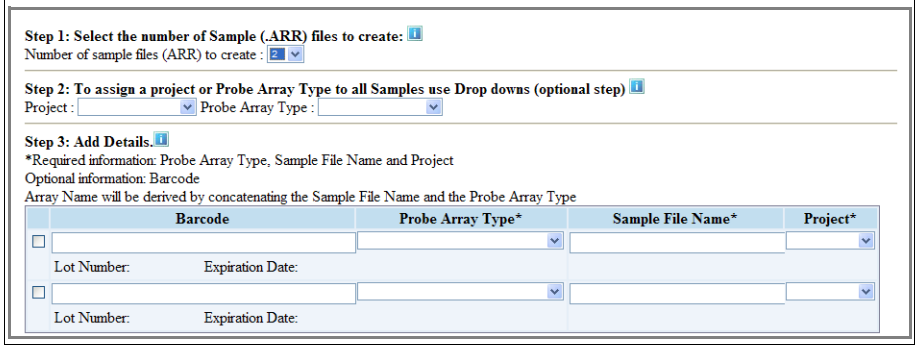
Figure 133 Drop-down list



- Select a number from the drop-down list.

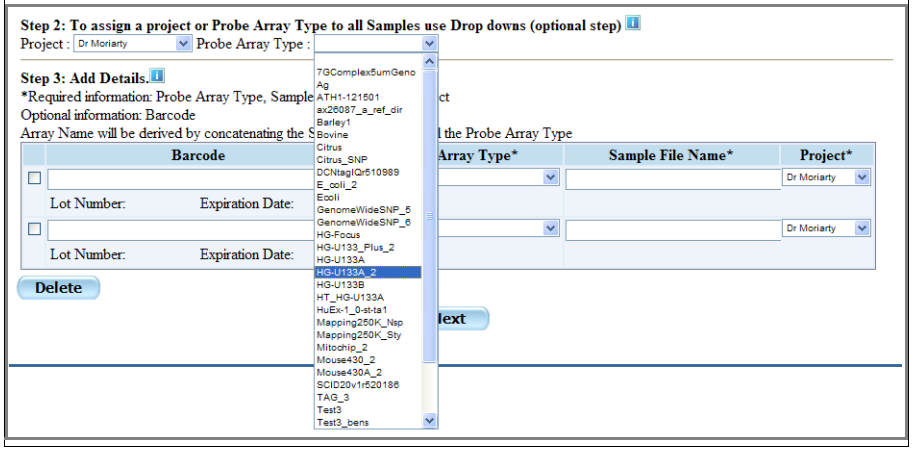
  Blank array information lines appear in the Array list. (Figure 134)

Figure 134 Add Details section with added rows



3. Set default values for all projects and/or probe array types (optional):

Figure 135 Set Defaults

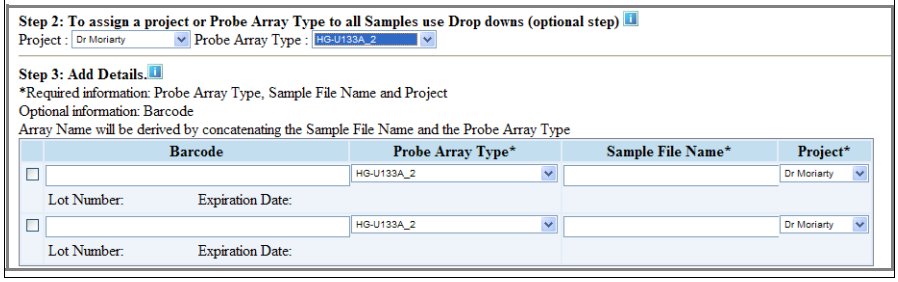


a. Select a project for the Project drop-down list.
b. Select a probe array type from the Probe Array Type drop-down list.

   The selected projects and probe arrays appear in the Array list. (Figure 136)

You can change the values for any sample file later on. Selecting these options will not erase your previously entered values for probe array type and project.

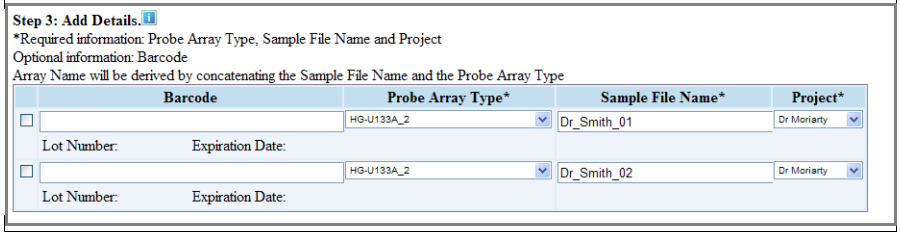
Figure 136 Add Details section with default probe array and project selected



4. (Optional) Enter the barcode using the keyboard; or
   a. Click in the Barcode box.
   b. Hold a GeneChip probe array in front of the barcode reader and squeeze the trigger for approximately four seconds until you hear a beep.

      Note: You can use custom barcodes to register an array in Quick Sample Registration. Also, the array's lot number and expiration date are displayed below the barcode (Thermo Fisher Scientific barcodes only).
5. Enter a name for the Sample (ARR) file and the Array name (used for the DAT, CEL, and CHP files).
6. Change the project or probe array type using the individual drop-down lists in the list.

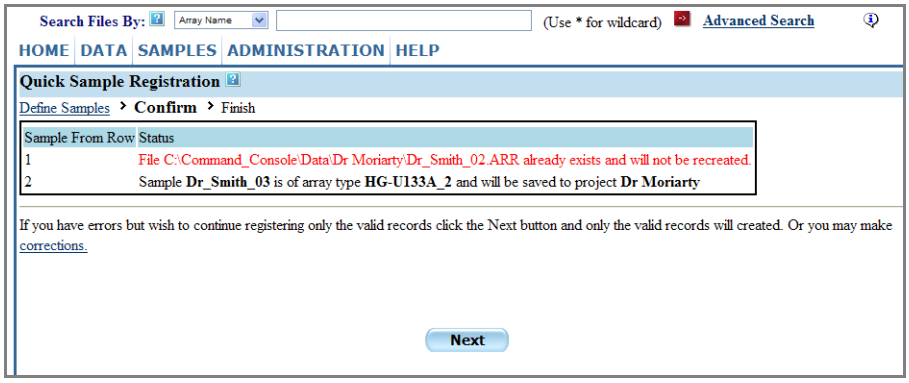
Figure 137 Sample names entered



7. To delete Sample (ARR) files you do not want:
   a. Select the check box in the row.
   b. Click **Delete**.
8. Click **Next**.

   The Confirm page opens. (Figure 138)

Figure 138 Confirm page



The page displays the status of the sample files, indicating any errors that would prevent the registration.

These errors can include

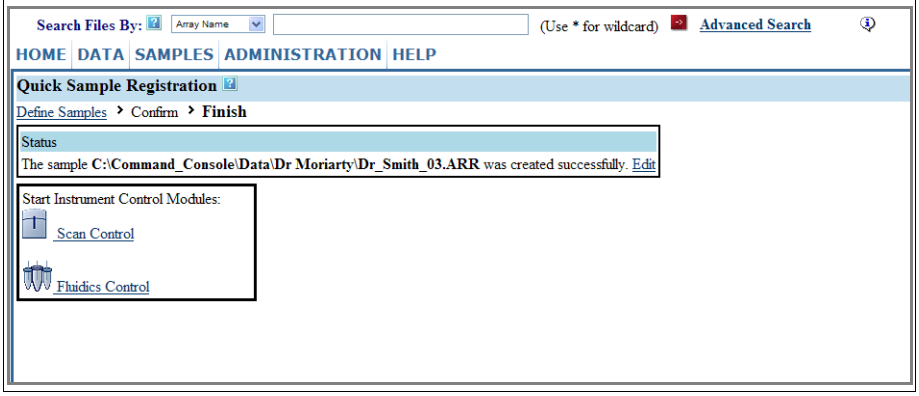
- Same Sample (ARR) file name
- Missing file name
- Other conflicts with previously registered arrays

  If errors appear for certain sample files, but other sample files are correct, you can click the **Corrections** link to return to the Quick Sample Registration page and correct the errors.

9. Click **Next** to register the valid sample (ARR) files.

   The Finish page appears. (Figure 139)

Figure 139 Quick Sample Registration Finish page



Click the **Edit** link to open the Sample file in the Detailed Sample Registration page (see "Detailed sample registration" on page 104)

You can use the links in the lower left corner of the screen to open the GCC Scan Control or GCC Fluidics Control software for further processing of the arrays.

Batch registration

The batch registration features enable you to create multiple Sample (ARR) files with different information, entering data using a specially formatted batch registration file.

Custom barcodes can be used in batch registration.

Batch registration involves three different sets of steps:

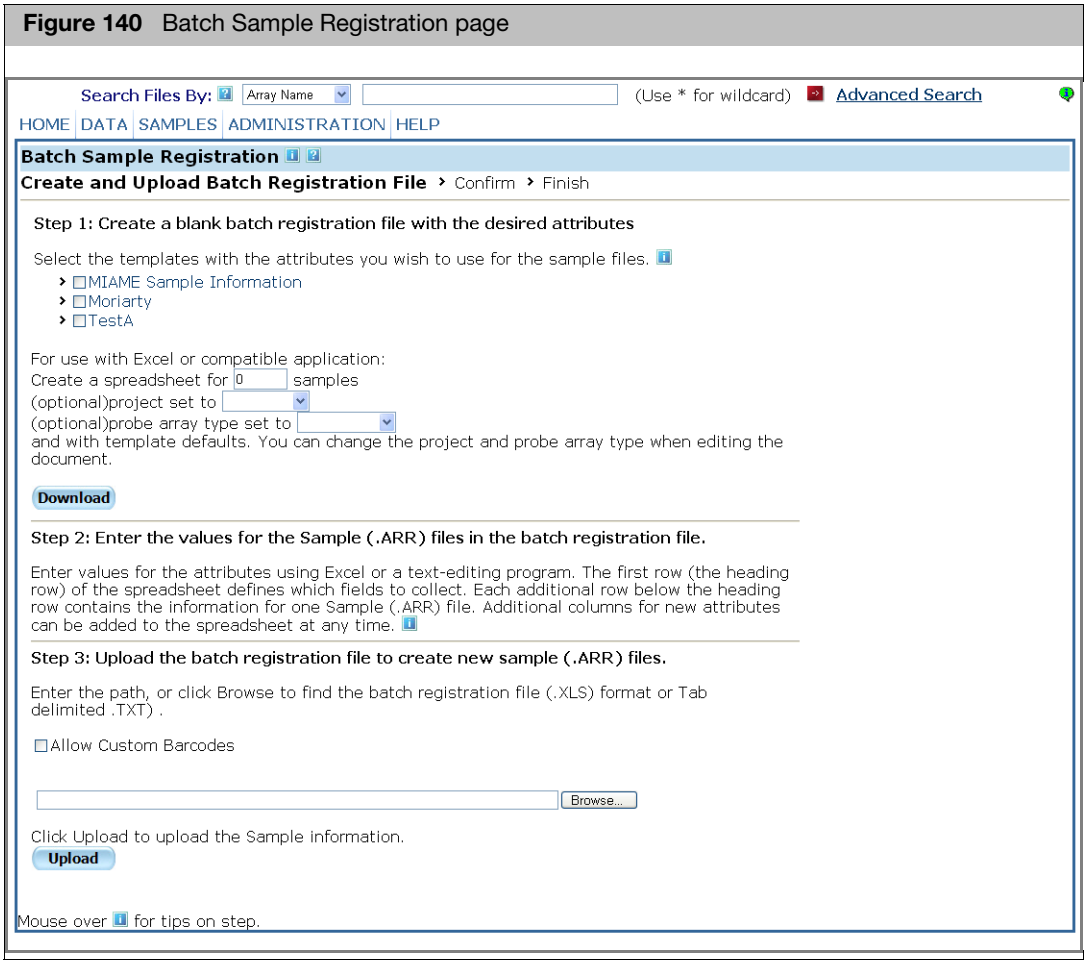
1. "Downloading an empty batch registration file"
2. Entering values for the arrays into the batch registration file.
   See "Entering values in the batch registration file" on page 126.
3. Uploading the data in the batch registration file to create the Sample (ARR) files.
   See "Uploading the batch registration file" on page 130.

Downloading an empty batch registration file

The batch registration file is downloaded as an Excel workbook.

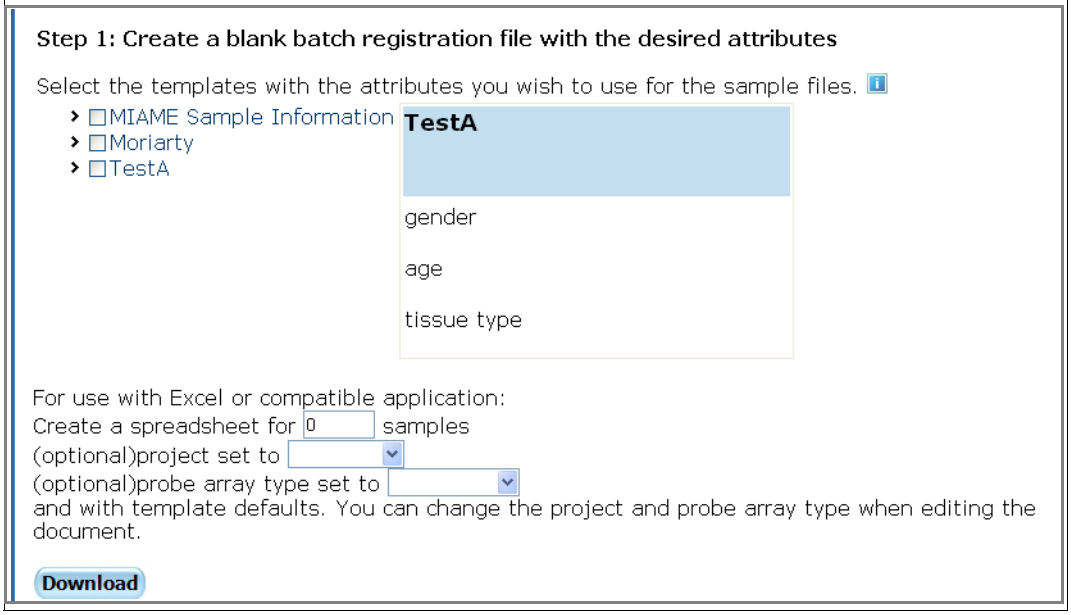
1. From the Samples menu, select **Batch Registration**.
   The Batch Sample Registration page opens. (Figure 140)

Figure 140 Batch Sample Registration page



2. Select the templates you want to use by placing a check in the box next to their names. (Figure 141)

Figure 141 Select Templates (with attributes displayed for template)



You can display the attributes in the template by clicking on the template name.

3. Specify the number of samples. The maximum number of samples for which the downloaded worksheet works well is 1000.
4. Specify project and array type for the Sample files.
5. Click **Download** to download the Excel workbook.

   When using GCC Portal, the Excel program displays the created workbook, which you can edit and save on your computer.

Entering values in the batch registration file

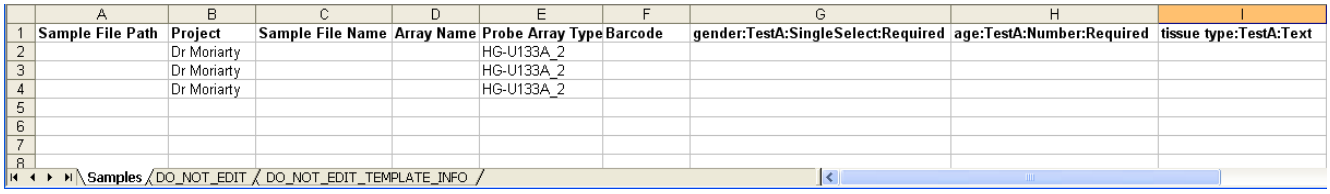
The Batch Registration file can be used to enter data for several different Sample (ARR) files at once.

The downloaded batch registration file is an Excel workbook with three worksheets:

- Samples worksheet, where you enter the data
- General info worksheet (do not edit), where GCC Portal stores information about Array types, projects, and file format
- Template Info worksheet (do not edit), where GCC Portal stores information about the template attributes.

  Note: You cannot create TSV files in GCC 4.3, but you can use TSV files. created in previous versions of GCC to perform batch registration. For more in formation, see Appendix G, "TSV files" on page 372.

Figure 142 Batch Registration Workbook, Samples Worksheet



	A	B	C	D	E	F	G	H	I
1	Sample File Path	Project	Sample File Name	Array Name	Probe Array Type	Barcode	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Text
2		Dr Moriarty			HG-U133A_2				
3		Dr Moriarty			HG-U133A_2				
4		Dr Moriarty			HG-U133A_2				
5									
6									
7									
8									

Samples / DO_NOT_EDIT / DO_NOT_EDIT_TEMPLATE_INFO /

The columns in the Samples worksheet have column headers that define the information on the Sample files, the physical array, and the attributes:

Sample File Path The path to where the Sample file will be created. Can be used to place Sample files in project folders.

Project The project that the Sample (ARR) file will be assigned to.

Note: You must specify either the **Path** or **Project** for your files. Specifying both will produce an error message.

Sample File Name Unique identifier for the Sample file.

Array Name Name assigned to the array during registration.

Probe Array Type Part number for the array(s).

Barcode Barcode on the array(s).

Attributes Additional information about the sample and experiment that you can use to interpret your results.

Path

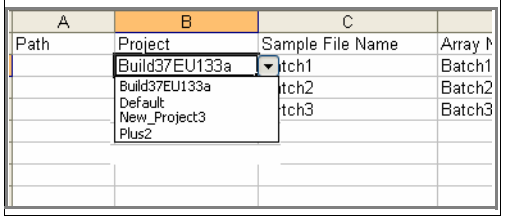
The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

You can select the project from a drop-down list. (Figure 143)

Figure 143 List of projects



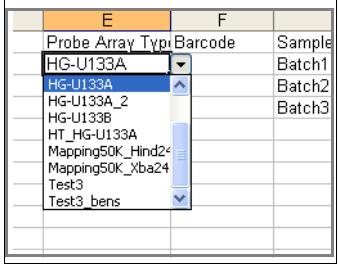
Sample file name

Enter the name assigned to the Sample file that will be created.

Array name, array type, and barcode

If you are using Excel, you can select the probe array type from a drop-down list. (Figure 144)

Figure 144 List of probe arrays



You can also enter multiple array information for a single sample file.

Entering multiple arrays

1. Enter the sample file information (File path, project, and file name) on a separate line of the worksheet for each array you want to use.
2. Enter a different array name for each array for the sample.
3. Select the array type from the Probe Array Type list.
4. Enter the array barcodes in the appropriate lines.
5. Make sure that the attributes are the same for all sample entries.

Figure 145 Worksheet with multiple arrays entered for samples

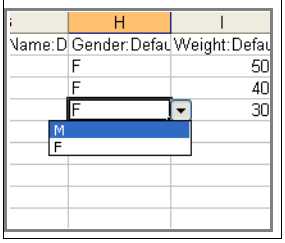
	A	B	C	D	E	F	G	H	I
1	**Sample File Path**	**Project**	**Sample File Name**	**Array Name**	**Probe Array Type**	**Barcode**	**gender:TestA:SingleSele**	**age:TestA:Number:Req**	**tissue type:TestA:Text**
2		asdf	X_Sample_01	X_Sample_01_A	HG-U133A		M	34	Brain
3		asdf	X_Sample_01	X_Sample_01_B	HG-U133B		M	34	Brain
4		asdf	X_Sample_02	X_Sample_02_A	HG-U133A		M	35	Liver
5		asdf	X_Sample_02	X_Sample_02_B	HG-U133B		M	35	Liver
6		asdf	X_Sample_03	X_Sample_03_A	HG-U133A		F	44	Kidney
7		asdf	X_Sample_03	X_Sample_03_B	HG-U133B		F	44	Kidney
8									

Attributes

Enter the values for the attributes in the appropriate columns.

You can select the value for a SingleSelect attribute from a drop-down list. (Figure 146)

Figure 146 Selecting the value for a SingleSelect attribute

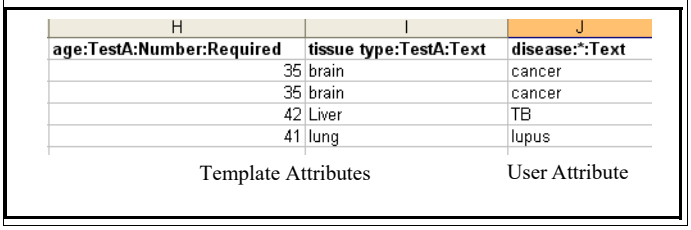


GCC uses two types of attributes for Batch Registration:

- Template Attributes: Attributes that have been defined in a template. When you select templates for the downloaded batch registration file, the array attributes in those templates will be included as headings in the batch registration file.
- User Attributes: Attributes that you add in the Batch Register file.You create a user attribute by entering the attribute name and other characteristics in the column header, and then entering attribute values in the appropriate cells.

Attributes need to have the following characteristics defined:

Figure 147 Template and user attributes in the Batch Edit file



- AttributeName
- TemplateName (if any; not used for User Attributes)
- DataType
- Required status, if any

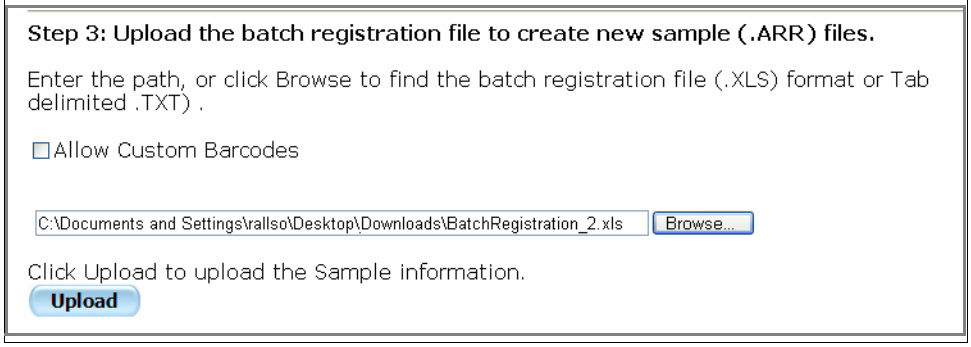
The column headings are in the format:

- Header format for Template Attribute: `AttributeName:TemplateName:AttributeType:RequiredStatus`
- Header format for User Attribute: `AttributeName:*:AttributeType`

Uploading the batch registration file

1. Enter the file path and name in the text box (Figure 148) or click **Browse**.

Figure 148 Upload file



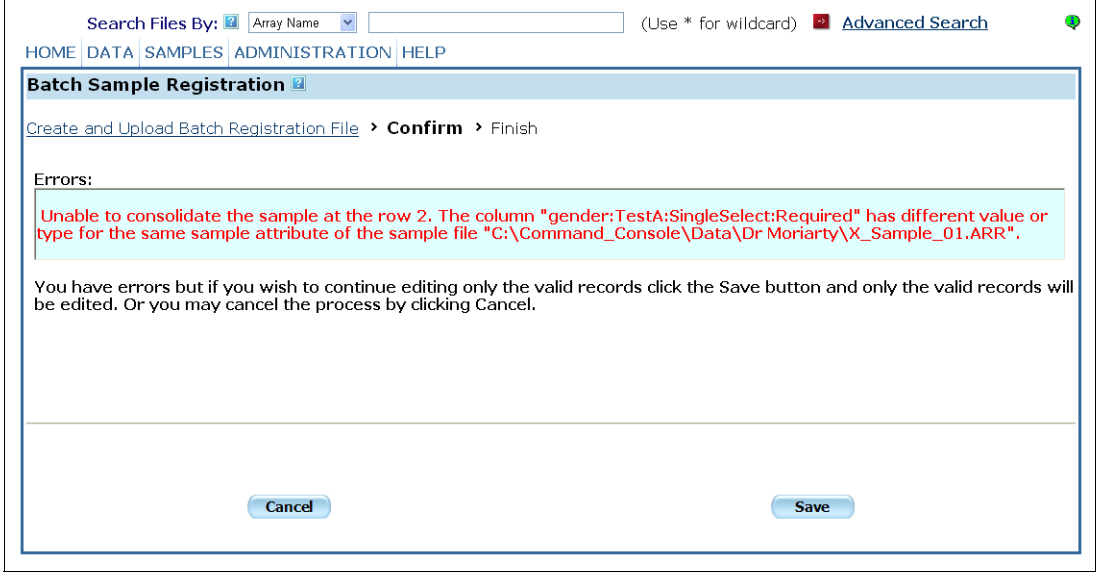
   - Clicking **Browse** opens a Choose File window.
   - Select the Batch Registration file and click **Open**.

     The file and its path is displayed in the box.

2. Click the **Allow Custom Barcodes** check box to use barcodes that are not provided by Applied Biosystems.
3. Click **Upload**.

   If there are problems with the workbook, an error notification page appears. (Figure 149)

Figure 149 Error notification



   The error messages indicate problems such as bad barcodes, problems with registering multiple arrays on a sample, etc.

   - Click **Cancel** to cancel the registration and fix the problems; or

Click **Save** to register the valid records.

If the upload doesn't have a problem the Folders View page appears with the newly created folders.

Sample prep plate registration

Sample Prep Plate Registration provides a convenient way to register samples and cartridge arrays for up to two 96-well plates by using an Excel workbook.

To perform Sample Prep Plate Registration for a target prep plate:

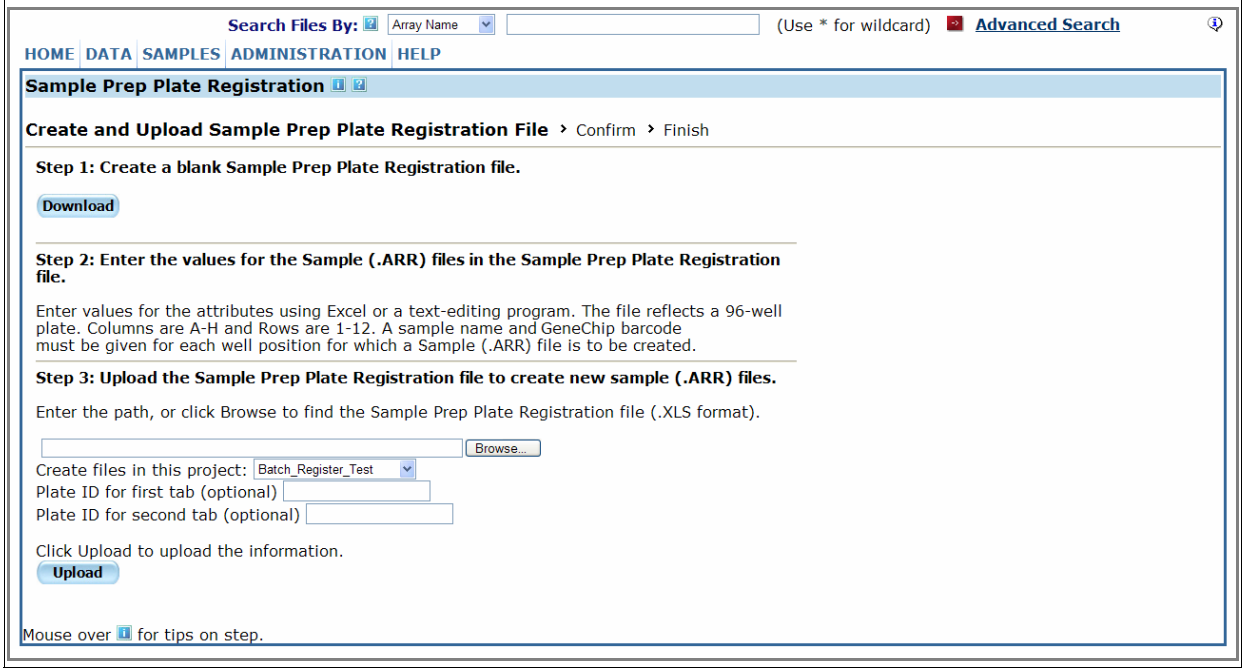
1. "Downloading the sample prep plate registration file", below
2. "Entering data in the workbook" on page 132
3. "Uploading the data for the files" on page 132

Downloading the sample prep plate registration file

1. From the **Samples** menu, select **Sample Prep Plate Registration**.

   The Sample Prep Plate Registration page appears (Figure 150).

Figure 150 Sample Prep Plate Registration page



2. Click **Download** to create a blank Sample Prep Plate Registration file.

   The Excel program displays the created workbook, which you can edit and save on your computer.

Entering data in the workbook

Entering data for the Sample Prep Plate Registration file

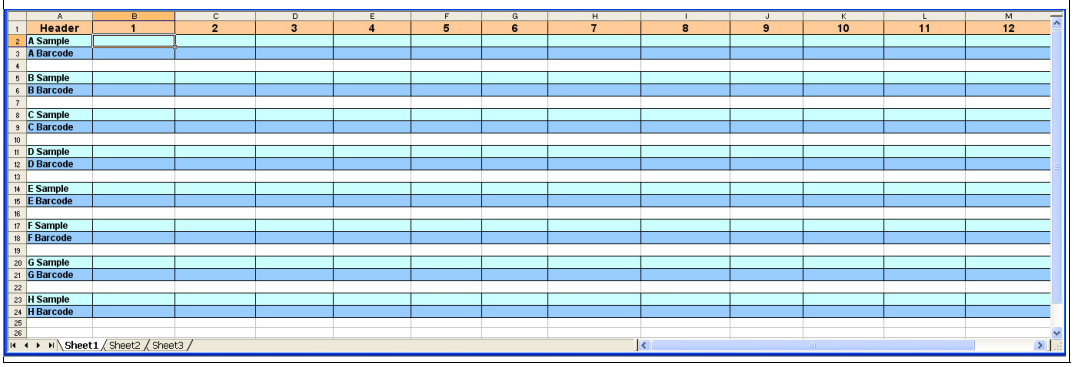
- Enter a sample (ARR) file name and GeneChip barcode for each well position you are analyzing using Excel or text-editing software.

  The blank Sample Prep Plate Registration file (Figure 151) is an Excel workbook with two tabs, to enable use with arrays that require two prep plates.

  The worksheet rows are marked A through H, corresponding to the plate rows.

  The worksheet columns are marked 1 through 12, corresponding to the plate columns.

Figure 151 Excel File for the target prep plate



For each well position, enter the Sample name for the Sample (ARR) and the barcode for the probe array.

Uploading the data for the files

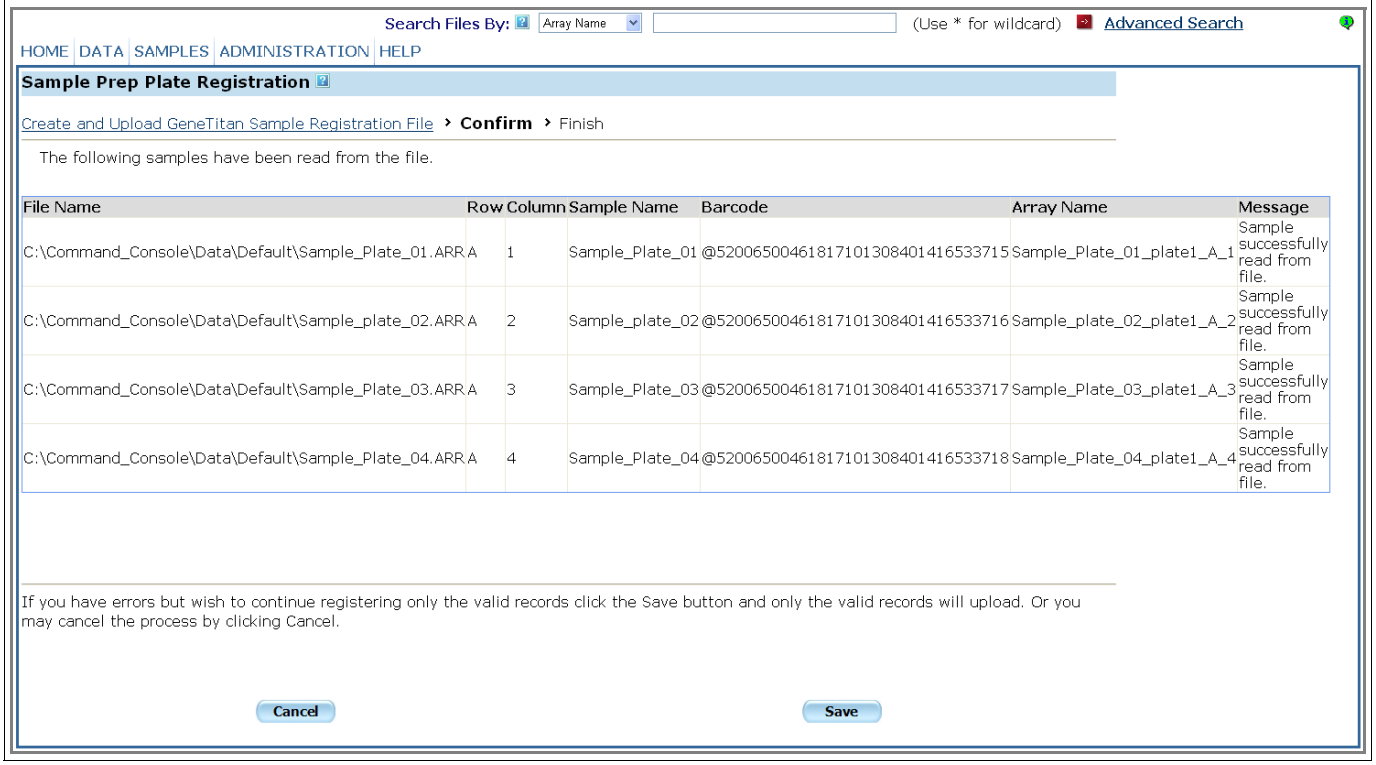
1. From the **Samples** menu, select **Sample Prep Plate Registration**.

   The Sample Prep Plate Registration page appears.
2. Enter the path or click **Browse** to select the plate registration file.
3. Select a project for the Sample (ARR) files (optional).
4. Enter plate IDs if registering samples for two plates.

   The Array names will be based on the Sample Name entered in the worksheet, concatenated with the plate ID, if any, and the Well position as indicated by their position in the worksheet.
5. Click **Upload**.

   The Confirm page appears. (Figure 152)

Figure 152 Confirm page



The page displays a list of the Sample (ARR) files created for the plate, along with Sample name, barcodes, and array names.

Error messages are displayed if there is a problem. These errors must be corrected before finishing the registration.

If there are any errors:

a. Click **Cancel**

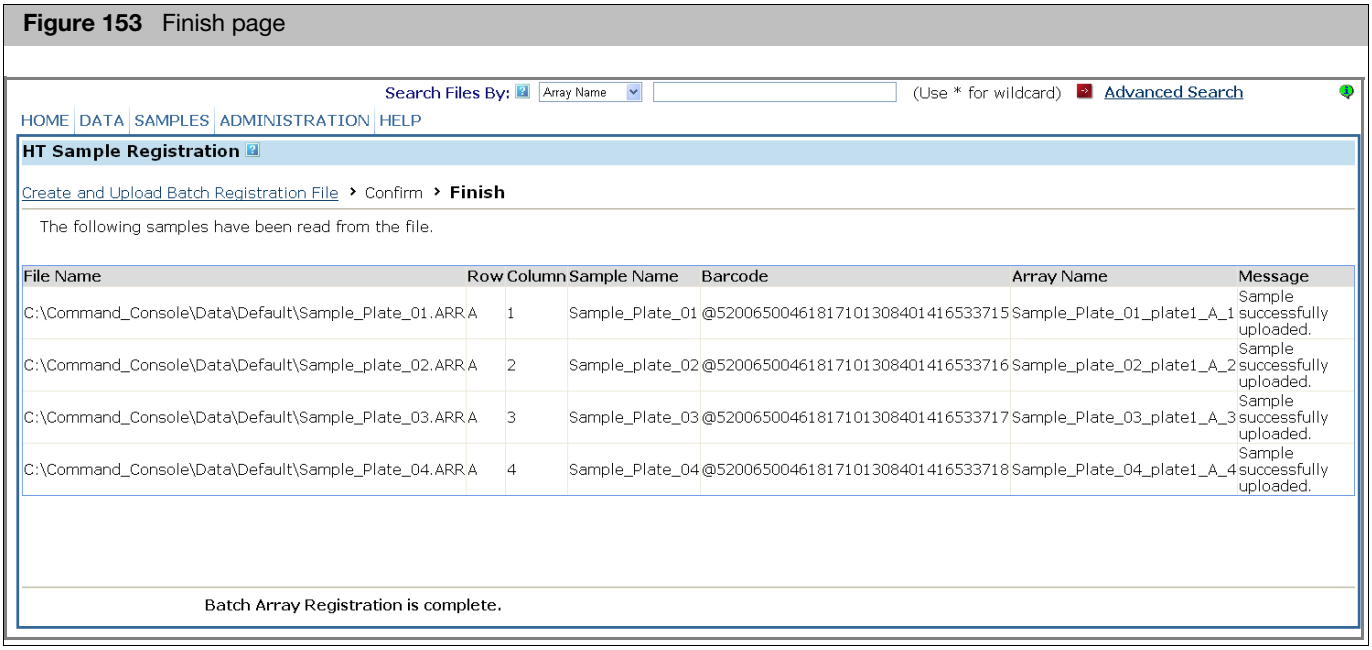
b. Check the plate worksheet.

c. Proceed with the upload again.

6. Click **Next**.

The Finish page opens. (Figure 153)

Figure 153 Finish page



Click **Create Summary Spreadsheet for Batch Edit** to open the Summary page and create a workbook summary of the Sample files that can be used for batch editing the Sample (ARR) files.

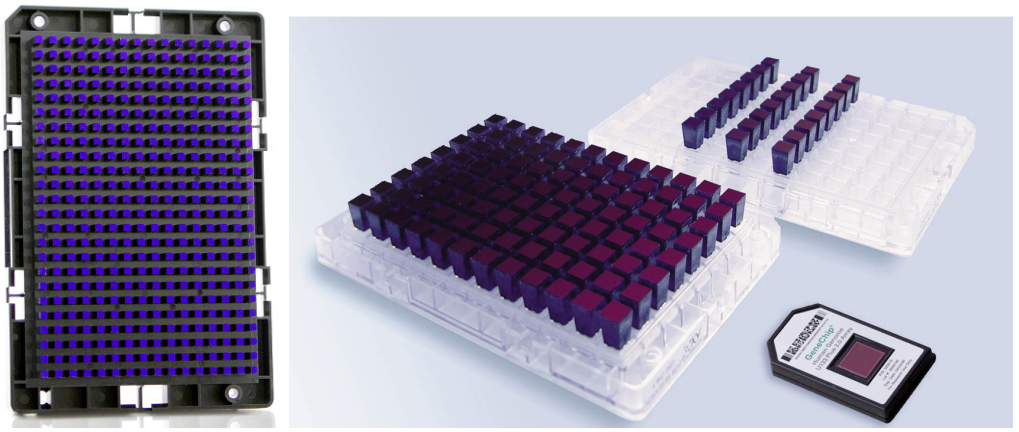
GeneTitan array plate registration

GeneTitan Array Plate Registration provides a convenient way to register samples and plate arrays for an Array Plate by using an Excel workbook.

A 384 or Mini 96 array plate can be used. A 96 array plate (Figure 154) may contain 16, 24, or 96 arrays. A Mini 96-array plate contains 96 arrays on a 384 format.

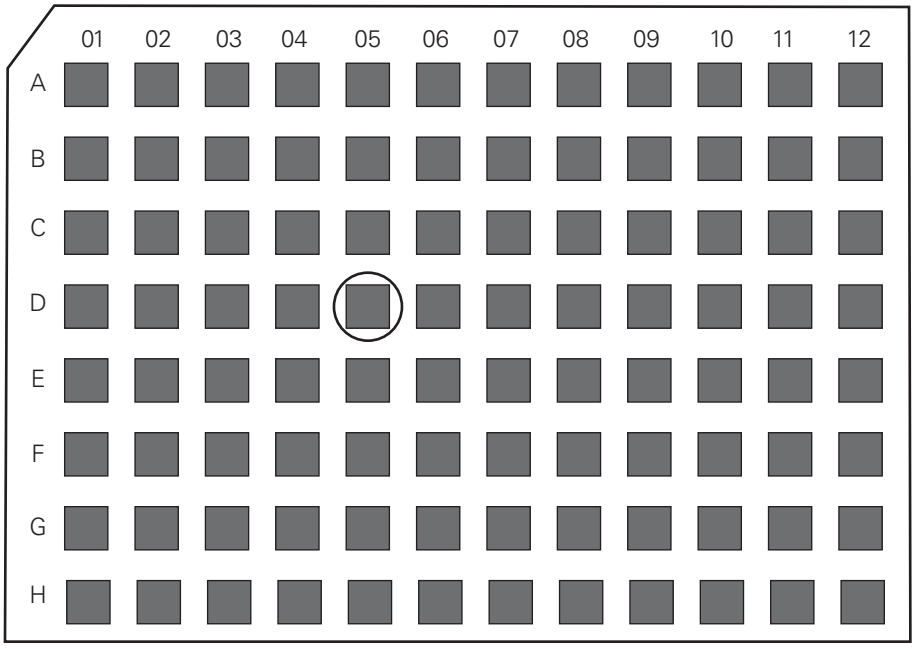
These formats allow for increased automation and processing times for large array counts.

Figure 154 384-,96-, and 24-Array Plates and Cartridge Array



The array plate has a barcode for tracking. Each individual array on the plate is identified by its row and column. For example, the circled array in the figure below is array D05.

Figure 155 Arrangement of Arrays on Array Plate



There are three sets of steps:

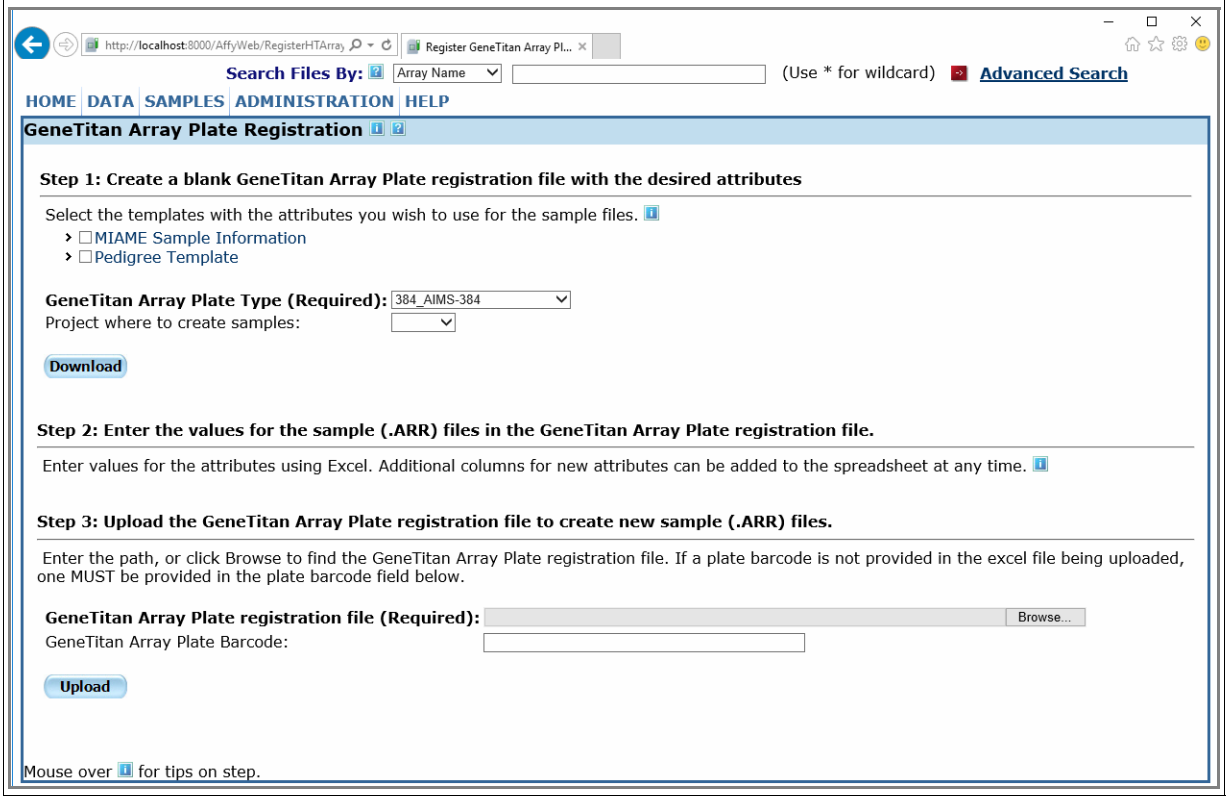
- "Downloading the GeneTitan array plate workbook", below.
- "Completing the workbook" on page 138.
- "Uploading the workbook" on page 139.

Downloading the GeneTitan array plate workbook

Downloading the Excel Workbook

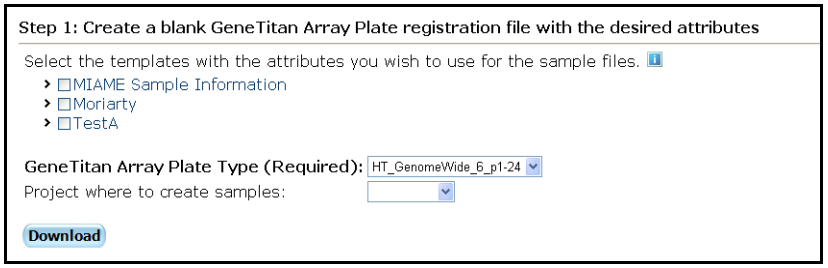
1. From the **Samples** menu, select **GeneTitan Array Plate Sample Registration**.
   The GeneTitan Array Plate Sample Registration page appears (Figure 156).

Figure 156 GeneTitan Array Plate Registration page



2. Select the templates you want to use by placing a check in the box next to their names (Figure 157).

Figure 157 Select Templates



You can display the attributes in the template by clicking on the template name.

3. Specify the GeneTitan Array Plate type and the project for the Sample files (required).
4. Click **Download** to download the file.

   The Excel program displays the created workbook, which you can edit and save on your computer.

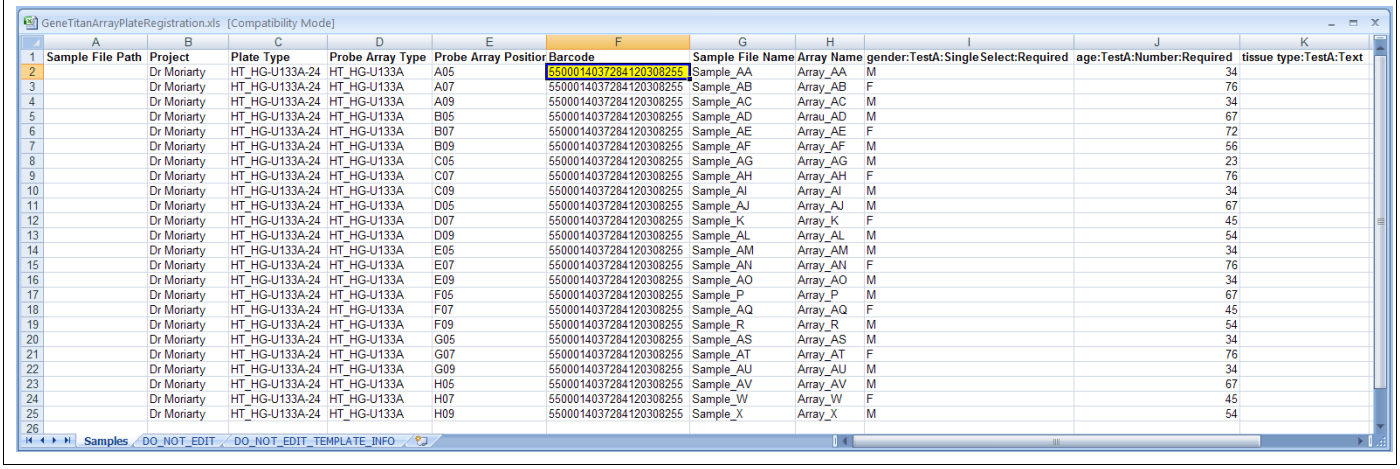
Completing the workbook

The Batch Registration file can be used to enter data for all of the plate arrays on an array plate in one operation.

The downloaded workbook has three worksheets:

- Samples worksheet, where you enter the data
- General info worksheet (do not edit), where GCC Portal stores information about Array types, projects, and file format
- Template Info worksheet (do not edit), where GCC Portal stores information about the template attributes

Figure 158 Excel file for Batch GeneTitan Array Plate Registration



GeneTitanArrayPlateRegistration.xls [Compatibility Mode]

	A	B	C	D	E	F	G	H	I	J	K
1	Sample File Path	Project	Plate Type	Probe Array Type	Probe Array Position	Barcode	Sample File Name	Array Name	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Text
2		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A05	55000140372841203082555	Sample_AA	Array_AA	M	34	
3		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A07	55000140372841203082555	Sample_AB	Array_AB	F	76	
4		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	A09	55000140372841203082555	Sample_AC	Array_AC	M	34	
5		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B05	55000140372841203082555	Sample_AD	Arrau_AD	M	67	
6		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B07	55000140372841203082555	Sample_AE	Array_AE	F	72	
7		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	B09	55000140372841203082555	Sample_AF	Array_AF	M	56	
8		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C05	55000140372841203082555	Sample_AG	Array_AG	M	23	
9		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C07	55000140372841203082555	Sample_AH	Array_AH	F	76	
10		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	C09	55000140372841203082555	Sample_AI	Array_AI	M	34	
11		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D05	55000140372841203082555	Sample_AJ	Array_AJ	M	67	
12		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D07	55000140372841203082555	Sample_K	Array_K	F	45	
13		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	D09	55000140372841203082555	Sample_AL	Array_AL	M	54	
14		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E05	55000140372841203082555	Sample_AM	Array_AM	M	34	
15		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E07	55000140372841203082555	Sample_AN	Array_AN	F	76	
16		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	E09	55000140372841203082555	Sample_AO	Array_AO	M	34	
17		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F05	55000140372841203082555	Sample_P	Array_P	M	67	
18		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F07	55000140372841203082555	Sample_AQ	Array_AQ	F	45	
19		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	F09	55000140372841203082555	Sample_R	Array_R	M	54	
20		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G05	55000140372841203082555	Sample_AS	Array_AS	M	34	
21		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G07	55000140372841203082555	Sample_AT	Array_AT	F	76	
22		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	G09	55000140372841203082555	Sample_AU	Array_AU	M	34	
23		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H05	55000140372841203082555	Sample_AV	Array_AV	M	67	
24		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H07	55000140372841203082555	Sample_W	Array_W	F	45	
25		Dr Moriarty	HT_HG-U133A-24	HT_HG-U133A	H09	55000140372841203082555	Sample_X	Array_X	M	54	
26											

Samples | DO_NOT_EDIT | DO_NOT_EDIT_TEMPLATE_INFO

The Sample worksheet has columns with headers that define the property being entered.

Some properties define the sample and data files file and the physical array:

Sample File Path	The path to where the Sample file will be created. Can be used to place Sample files in project folders.
Project	The project that the Sample (ARR) file will be assigned to.
Plate Type	Model of array plate.
Probe Array Type	The array type on the plate.
Probe Array Position	Column and row position for the plate array.
Barcode	Plate barcode: can be entered when you upload the batch registration file.
Sample File Name	Name to be used for the Sample (ARR) file.
Array Name	Name to be used for the array plate and for all the data files (DAT, CEL, and CHP)
Attributes	Additional information about the sample and experiment that you can use to interpret your results.

Path

The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

If you are using Excel, you can select the project from a drop-down list. (Figure 143)

Figure 159 List of projects in Excel workbook

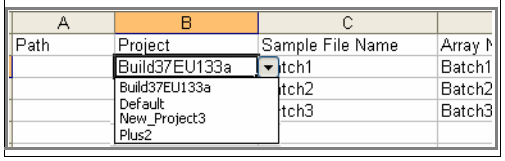


Plate type, probe array type, probe array position

These items specify the array plate type, the plate array type, and the array plate position.

They are automatically filled out when you create the plate batch workbook file.

File names

Enter the name assigned to the Sample file that will be created.

Barcode

This is the array plate barcode; if you enter a barcode into the A05 probe array position barcode cell, the same barcode is copied automatically into all of the other rows.

Sample file and array name

Enter the names to be used for:

- The Sample (ARR) file.
- The Array plate and for all the data files (DAT, CEL, and CHP) for the array on the Array Plate.

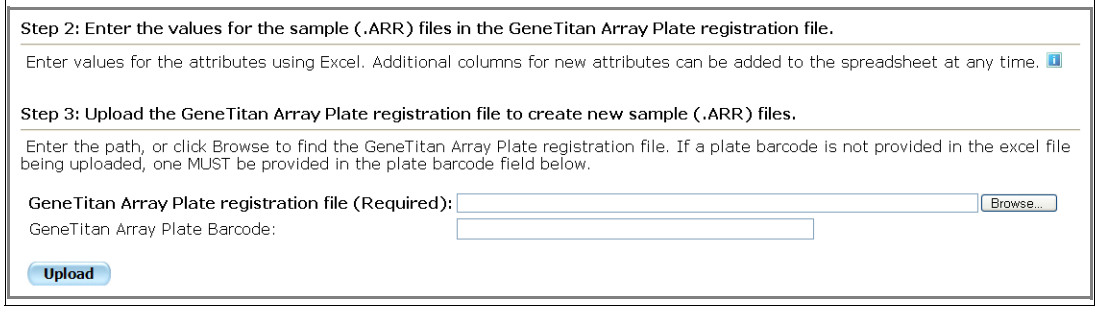
Attributes

Enter the values for the attributes in the appropriate columns. See "Attributes" on page 129 for more information.

Uploading the workbook

1. From the **Samples** menu, select **GeneTitan Array Plate Registration**.
   The GeneTitan Array Plate Sample Registration page appears (Figure 156).
2. Enter the file path and name in the Registration file box (Figure 160); or

Figure 160 Upload file



3. Click **Browse**.

   The Choose File window appears.

4. Click to select the array plate registration file, then click **Open**.

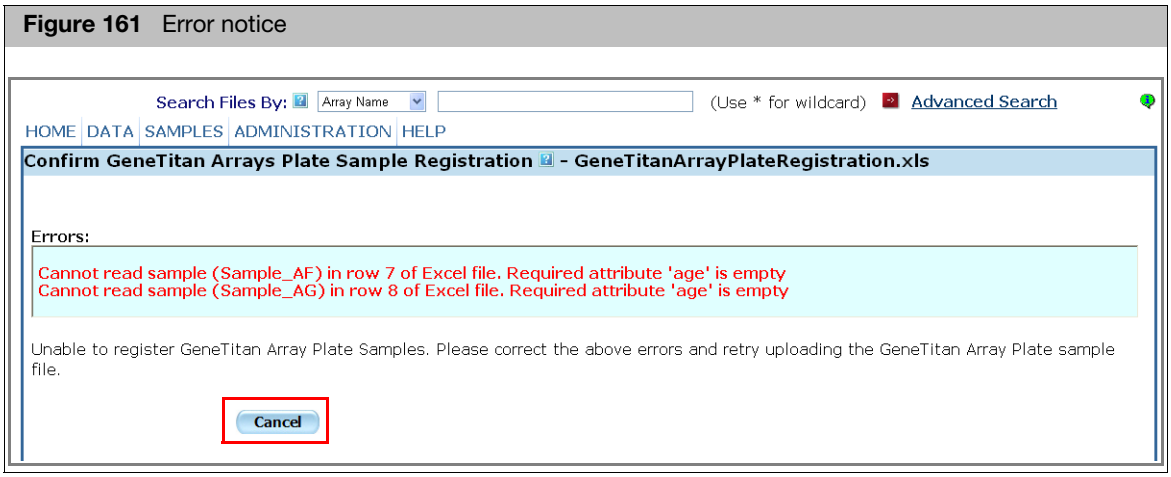
   The file and its path is displayed in the Registration file box.

   Note: If the plate barcode did not auto-populate, enter it now.

5. Click **Upload**.

   If there are problems, the Errors page appears. (Figure 161)

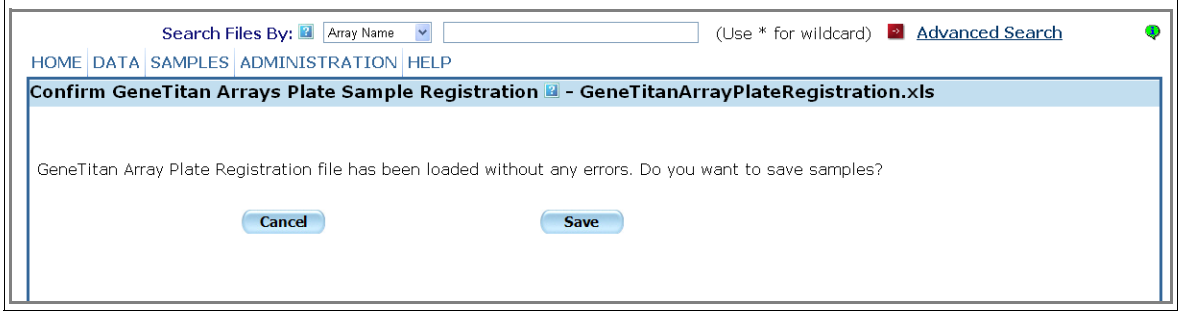
Figure 161 Error notice



- Click **Cancel in order** to correct problem(s) before uploading.

IF there are no problems, the Confirm Batch Sample Registration page opens. (Figure 162)

Figure 162 Confirm Batch Sample Registration



6. Click **Save** to register the valid records.

   The page displays a message that the Batch Sample Registration is complete. (Figure 163)

Figure 163 Confirmation page, upload successful

Adding a barcode to a sample file

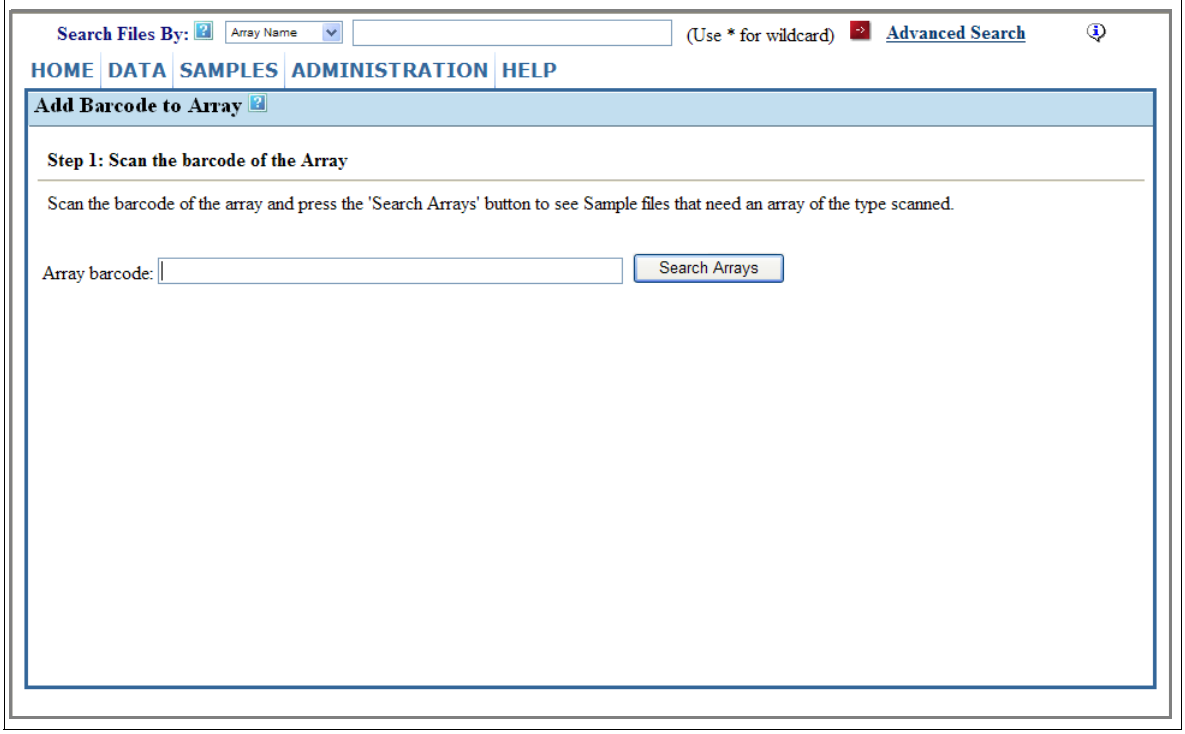
You may not have the barcode available when the Sample file is first created; if so, you can add it later using the Add Barcode page.

Note: The Add Barcode page can only be used to add one barcode at a time. The Batch Edit workbooks can be used to add barcodes to multiple sample files or multiple barcodes to one sample file in a single operation (see "Batch editing" on page 144). The Add Barcode page cannot be used to add a barcode for a Array Plate. Array Plate barcodes must be provided at the time of registration

1. From the Samples menu, click **Add Barcode**.

   The Add Barcode window opens. (Figure 164)

Figure 164 Add Barcodes page



2. Enter the barcode:

   Enter the barcode using the keyboard; or

   a. Click in the Barcode field.

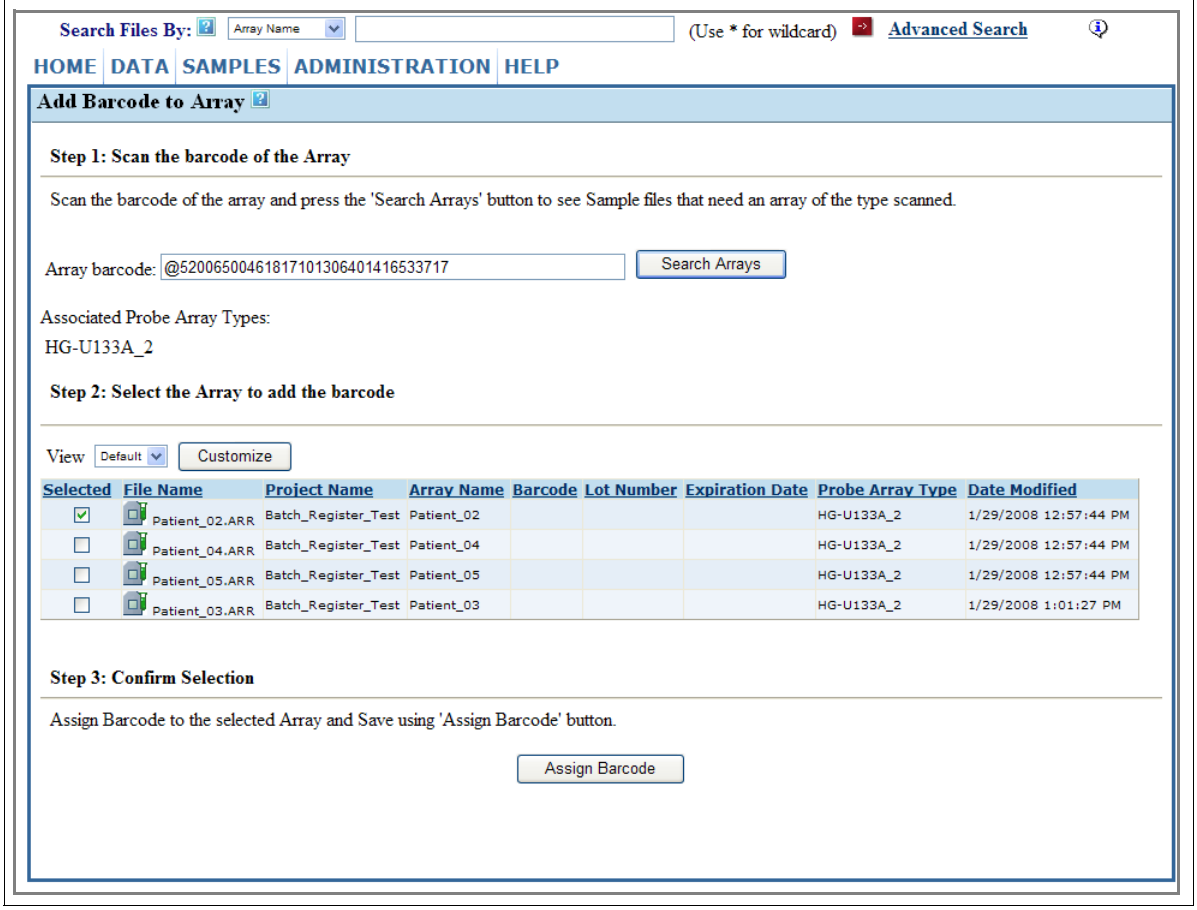
   b. Use the barcode reader to scan in the barcode on the array.

      The reader reads and sends the barcode to the Barcode field.

3. Click **Search Arrays**.

   A list of Array names for that type of array that need a barcode appears in the Array list. (Figure 165)

Figure 165 Sample files displayed



4. Select the check box for the array that corresponds to the array barcode.

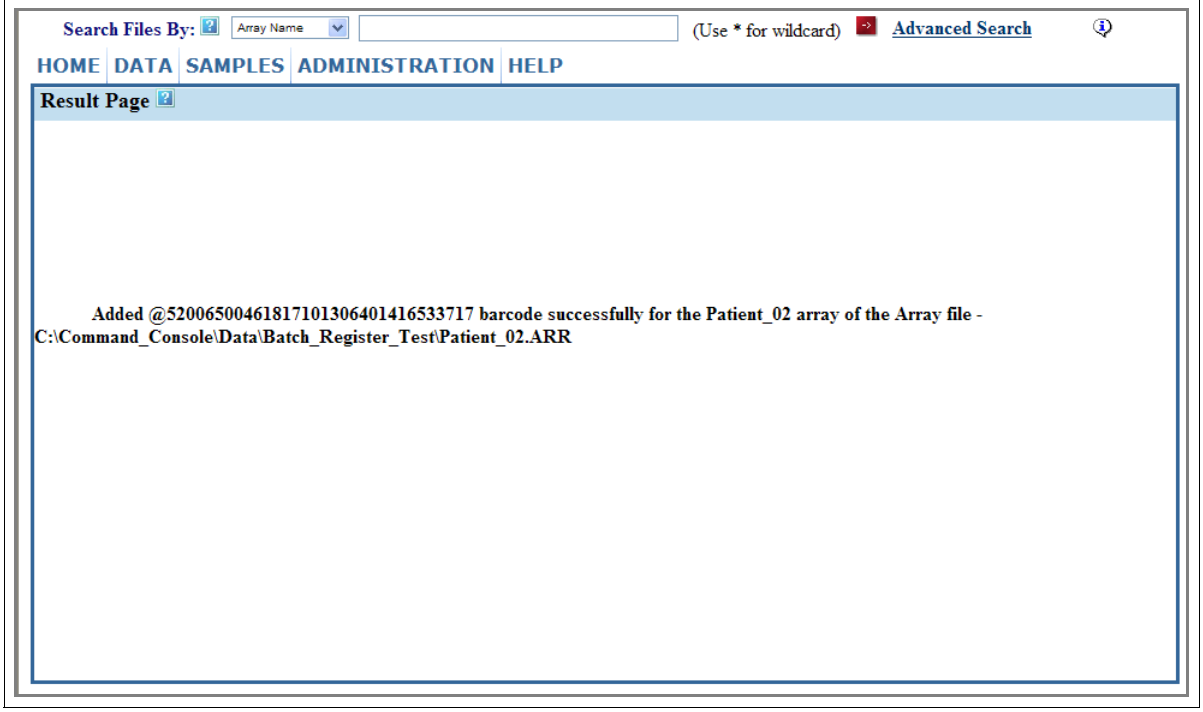
   Note: You can use the View drop-down box and Customize button to add or delete attributes for display in the Array list. For more information, see "Selecting attributes for the file list" on page 57.

5. Click **Assign Barcode**.

   If it is successful, the result page is displayed. (Figure 166)

   If the assignment was unsuccessful, the Add Barcode page is displayed with an error message.

Figure 166 Results page



Batch editing

Batch Edit enables you to make edits to a set of previously created Sample (ARR) files.

Note: Batch edit cannot be used to create new Sample (ARR) files. Use the various Sample Registration functions described in this chapter to create new files. Also, Batch edit cannot be used to change file or array names. Use the editing functions of the Detailed Sample Registration page to do this. See "Editing files and copying attributes" on page 110 for more information.

Using Batch Edit involves three sets of steps:

1. Create a batch edit file listing the files you want to edit, using the Project view, Folder, Search Results view, or use a previously created batch registration Excel file.
2. Edit the batch edit file, adding and changing attributes as needed.
3. Upload the batch edit file using the **Batch Edit Upload** function.

Creating the batch edit file

You can create a batch edit file for:

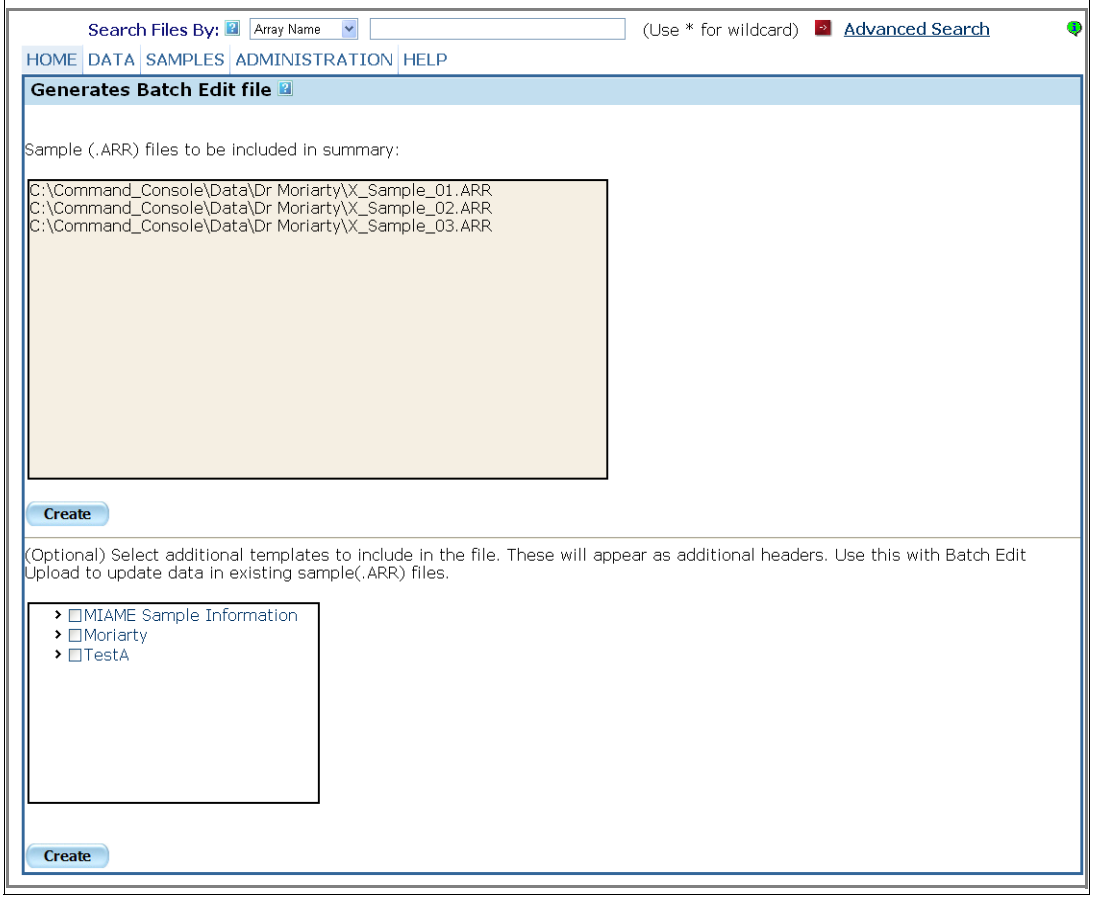
- The Sample (ARR) files in a project or folder (see "Generating a project summary" on page 86).
- Selected Sample (ARR) files (see below)

To generate a Batch Edit File for selected Sample files:

1. Select the Sample files from the:
   - Folder view page
   - Project view page
   - Search Results page
2. From the Command to Select drop-down, select the **Create Batch Edit Files from Selected Arr files** link.

   The Summary page opens (Figure 167).

Figure 167 Summary page



   A list of Sample (ARR) files that will be in the summary appears.
3. Select a template to be used in editing (optional).
4. Click **Create**.

The Excel program displays the created workbook (Figure 168), which you can edit and save on your computer.

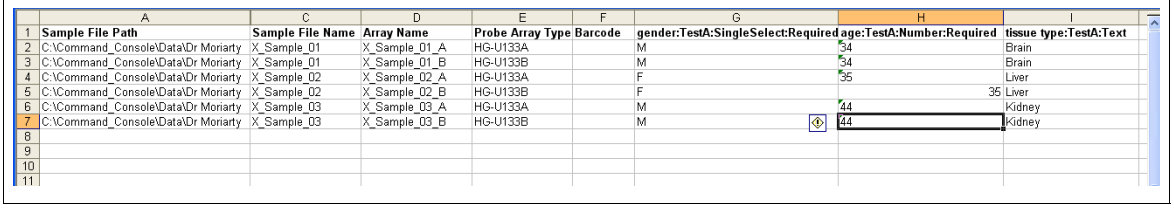
You can also edit a previously created Batch Registration file, adding attributes as needed. See "Entering values in the batch registration file" on page 126 for more information about editing Batch Registration files.

Editing the batch edit file

The downloaded Excel workbook has three worksheets:

- Samples worksheet
- General info worksheet (do not edit)
- Template Info worksheet (do not edit)

Figure 168 Batch Edit Excel Workbook, Samples worksheet



	A	C	D	E	F	G	H	I
1	Sample File Path	Sample File Name	Array Name	Probe Array Type	Barcode	gender:TestA:SingleSelect:Required	age:TestA:Number:Required	tissue type:TestA:Text
2	C:\Command_Console\Data\Dr Moriarty	X_Sample_01	X_Sample_01_A	HG-U133A		M	34	Brain
3	C:\Command_Console\Data\Dr Moriarty	X_Sample_01	X_Sample_01_B	HG-U133B		M	34	Brain
4	C:\Command_Console\Data\Dr Moriarty	X_Sample_02	X_Sample_02_A	HG-U133A		F	35	Liver
5	C:\Command_Console\Data\Dr Moriarty	X_Sample_02	X_Sample_02_B	HG-U133B		F	35	Liver
6	C:\Command_Console\Data\Dr Moriarty	X_Sample_03	X_Sample_03_A	HG-U133A		M	44	Kidney
7	C:\Command_Console\Data\Dr Moriarty	X_Sample_03	X_Sample_03_B	HG-U133B		M	44	Kidney
8								
9								
10								
11								

The header row of the Samples worksheet includes special properties that define the file and the physical array:

Sample File Path	The path to where the Sample file is located.
Sample File Name	Unique identifier for the Sample file.
Array Name	Name assigned to the array during registration.
Probe Array Type	Part number for the array(s).
Barcode	Barcode on the array(s)
Attributes	Additional information about the sample and experiment that you can use to interpret your results.

The General Information Worksheet and the Template Info Worksheet (both marked **Do Not Edit**) contain information used by GCC in processing the data in the workbook.

Make the changes in the summary file to edit the files. You can:

- Enter attribute values
- Add user attributes with values
- Delete attributes from the Sample (ARR) file

  Note: You can not make changes to file names or array names using this feature. Do not make changes to file names in the downloaded file.

The following items in the workbook must not be edited.

Sample File Path	The Path and Sample (ARR) file name.
Array Name	Array name assigned to the files.

Note: If you delete a the entire column for a template attribute, including the header, then an error will be generated. In order to remove attribute values from a sample file, users need to leave the header intact and remove the attribute values from the column

The first row of the workbook defines the data to be edited. Each additional row contains the information for one Sample (ARR) file.

Multiple arrays for a single sample (ARR) file

If you have multiple arrays assigned to a single sample file, each array is on a separate line of the worksheet.

Figure 169 Multiple arrays

Sample File Path	Sample File Name	Array Name	Probe Array Type
C:\Command_Console\Data\Dr Moriarty	Dr_Smith_01	Dr_Smith_01_(HG-U133A_2)	HG-U133A_2
C:\Command_Console\Data\Dr Moriarty	Dr_Smith_01	Dr_Smith_01_(HG-U133A)	HG-U133A

You cannot enter different attributes values for the same attributes for arrays associated with the same Sample (ARR) file.

Editing the barcode

You can only add a barcode to a Sample (ARR) file that does not already have one. You cannot edit a barcode that is already assigned to the Sample (ARR) file.

- If you assign a barcode to a Sample file, a warning message appears if the probe array type specified in the barcode does not match the probe array type previously assigned to the array.
- You can assign a custom barcode to a Sample file.

Editing attributes

Enter the values for the attributes in the appropriate columns. See "Attributes" on page 129 for more information.

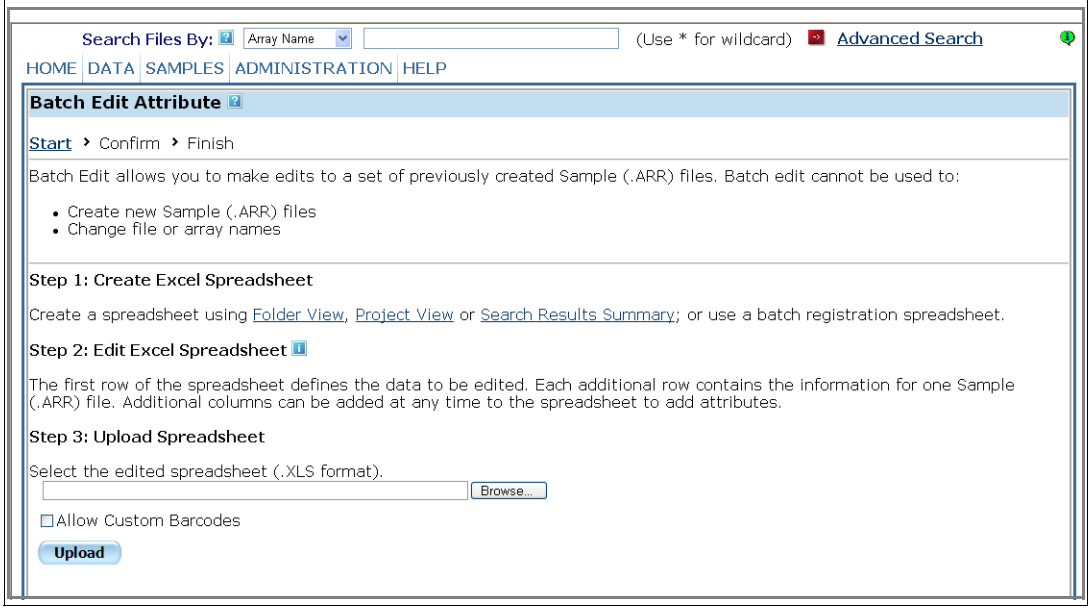
Uploading the edited file

After editing the batch edit file, you need to upload the data into GCC.

1. From the Samples menu, select **Batch Edit Upload**.

   The Batch Edit Attribute page opens. (Figure 170)

Figure 170 Batch Edit Attribute page

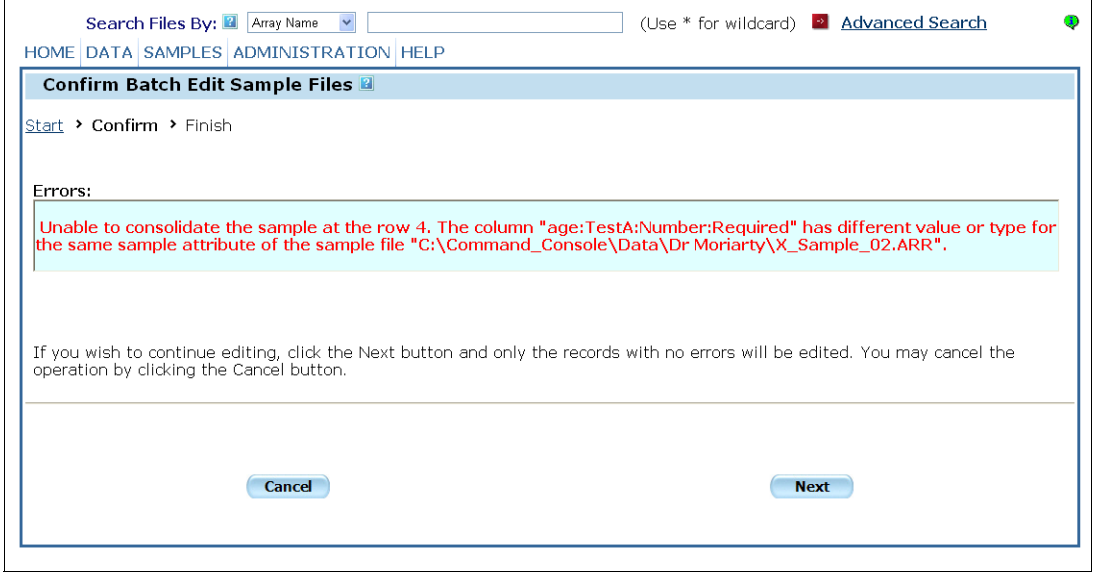


2. Enter the file path and name in the box; or
   a. Click **Browse** to open the Choose File window.
   b. Select the Batch Registration or Batch Edit file and click **Open**.

      The file and its path is displayed in the box.
3. In the Upload Spreadsheet section, click on **Upload**.

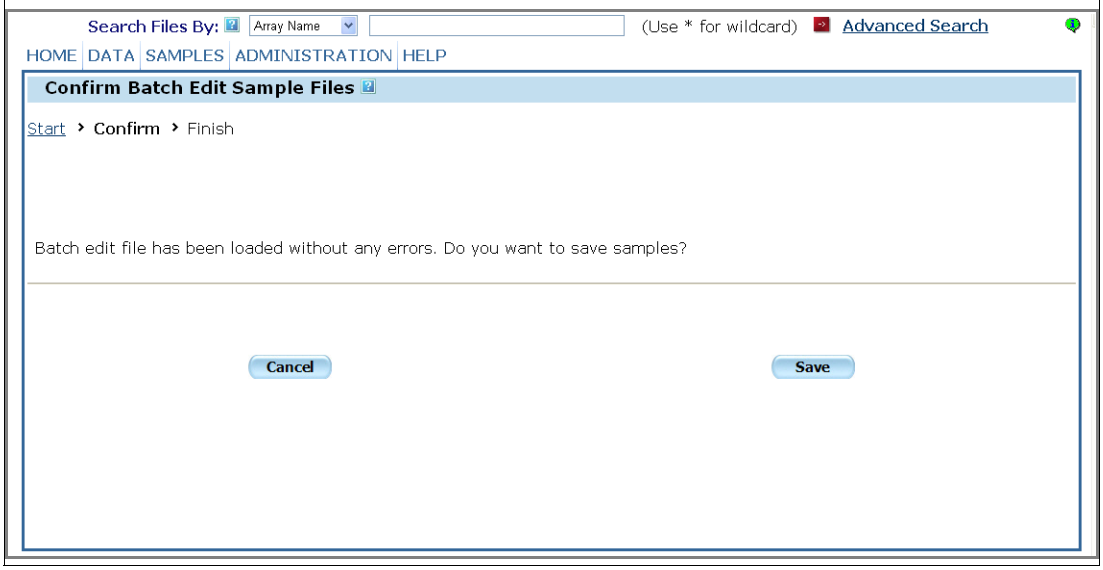
   If there is a problem with the workbook, the Confirm Batch Edit Sample Files produces a warning, as shown in Figure 171.

Figure 171 Error notice



If there are no issues, the Confirm Batch Edit page opens. (Figure 172)

Figure 172 Confirm Batch Edit



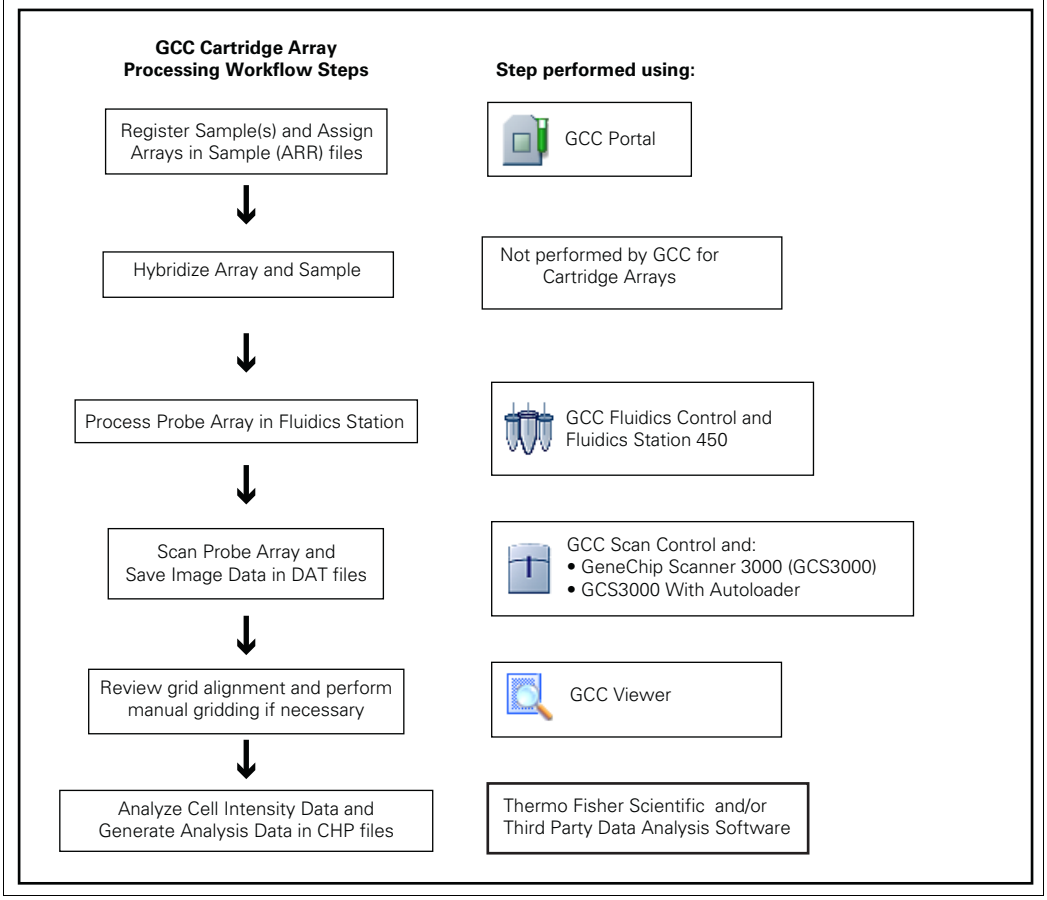
4. Click **Save** to edit the valid records.

   A batch edit is complete message appears.

6 Controlling the fluidics station

Hybridizing and processing the array is the next step after sample registration in the recommended array processing workflow. (Figure 173)

Figure 173 Recommended Cartridge Array Processing Workflow



The Fluidics Station 450 is used to hybridize, wash, and stain the GeneChip probe arrays (called arrays in this manual). The FS450 can independently process an array using a different fluidics protocol in each of four different modules.

Instrument care

- Disconnect the power cord of Fluidics Station before replacing fuses.
- Use a surge protector on the power line to the fluidics station.
- The fluidics station should be positioned on a sturdy, level bench away from extremes in temperature and away from moving air.

  Note: You must have the required fluidics protocols installed before using the FS450. For more information, see "Installing and updating protocols" on page 172.

The GCC Fluidics Control software is used to control the FS450 Fluidics Station. A workstation with GCC Fluidics Control software and a Sealevel card installed can control up to eight different fluidics stations.

Note: Before you use the fluidics station, check the fluidics station configuration and prime the fluidics station with appropriate buffer. For more information, read this chapter.

This chapter describes how to use the GCC Fluidics Control software in the following sections:

- "GCC fluidics control software"
- "Running protocols" on page 155
- "Filtering the sample file list" on page 166
- "Adding a label to a station and modules" on page 171
- "Installing and updating protocols" on page 172
- "Editing protocols" on page 175

Refer to the *GeneChip Fluidics Station User's Guide* for a description of the instrument itself.

You can set things up to provide email notification when protocols are complete or problems develop. See Appendix E, "Notification e-mails" on page 367 for more information.

GCC fluidics control software

The GCC Fluidics Control software is used to control the FS450 Fluidics Station. The software is introduced in the following sections:

- "Starting", below
- "Master controls" on page 153
- "Station controls" on page 153
- "Status window" on page 155

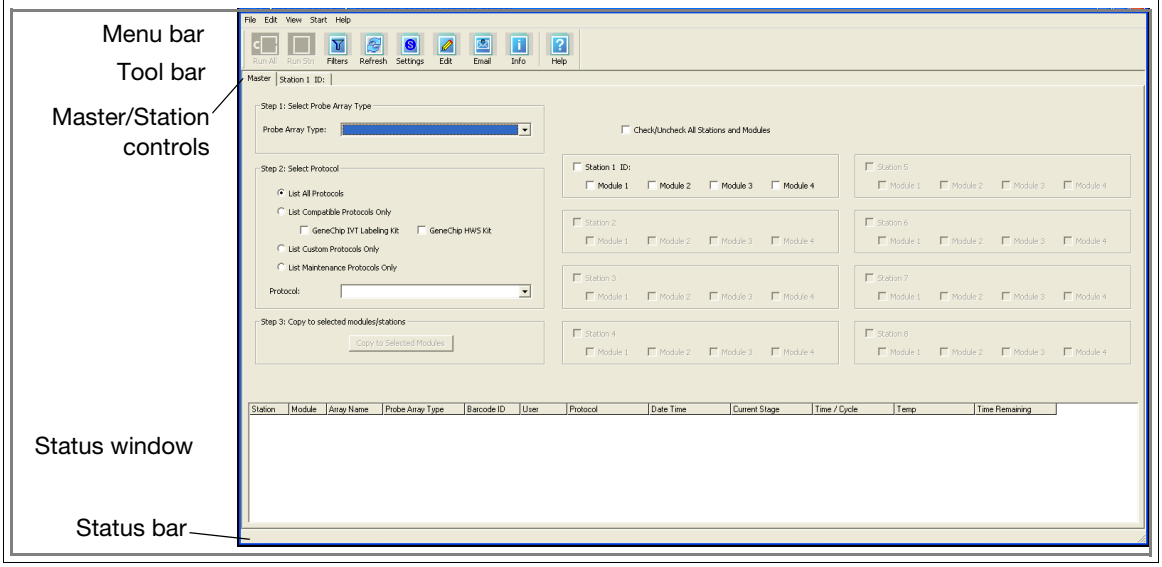
Starting

1. In the GCC Launcher, click the GCC Fluidics Control Icon; or

   Click **Start** → **Thermo Fisher Scientific** → **GCC Fluidics Control**...

   The GCC Fluidics Control window opens (Figure 174).

Figure 174 GCC Fluidics Control window, Master controls



Components of the GCC Fluidics Control window:

- **Menu bar**: Provides access to Fluidics Control functions.
- **Tool bar**: Provides quick access to frequently used functions.
- **Master/Station controls**: Click the tabs to switch between:
  - "Master controls" (see below): Use to select a single protocol to run on multiple stations and/or modules.
  - "Station controls": Use to select different protocols to run on different modules in a station.
- **Status window**: Displays list of arrays in process with information on their status. See "Status window" on page 155.
- **Status bar**: Displays information about the status of the Fluidics station and the fluidics run in progress.

Hiding or displaying the tool bar

1. From the View menu, select **Toolbar** → **Standard Toolbar**.

Adding text labels to the toolbar buttons

1. From the View menu, select **Toolbar** → **Text Labels**.

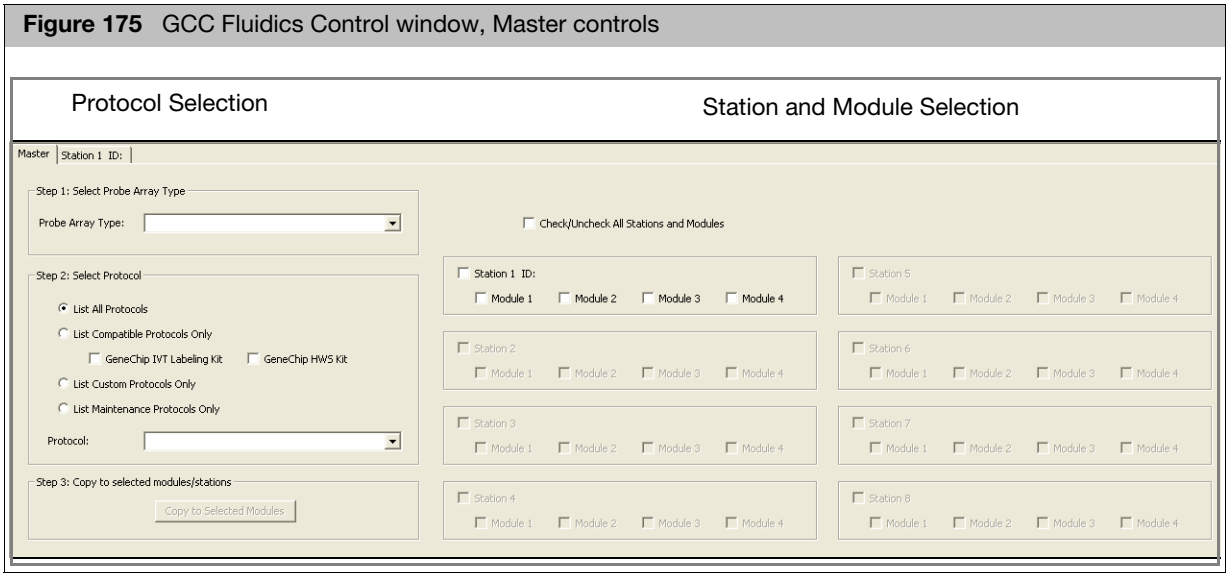
Hiding or displaying the status bar

1. From the View menu, select **Status Bar**.

Master controls

The Master controls (Figure 175) enable you to select a single protocol to run on any or all stations and modules attached controlled by the workstation.

Figure 175 GCC Fluidics Control window, Master controls



The Master controls are used for:

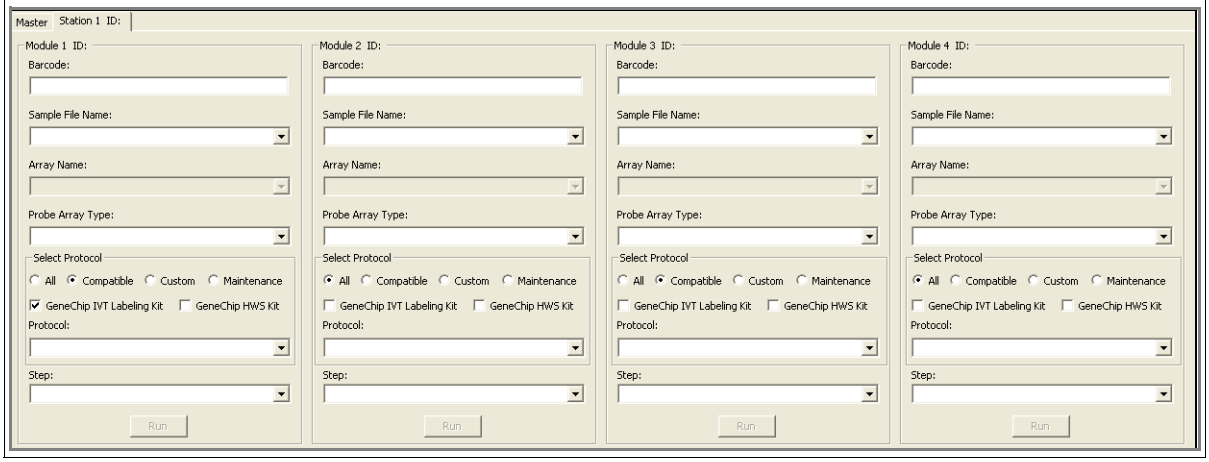
- "Running a priming or maintenance protocol on multiple stations and modules" on page 156.
- "Running a fluidics protocol on multiple stations" on page 157

Station controls

The Station controls enable you to select arrays and protocols for each module of a selected station (Figure 176). The controls enable you to:

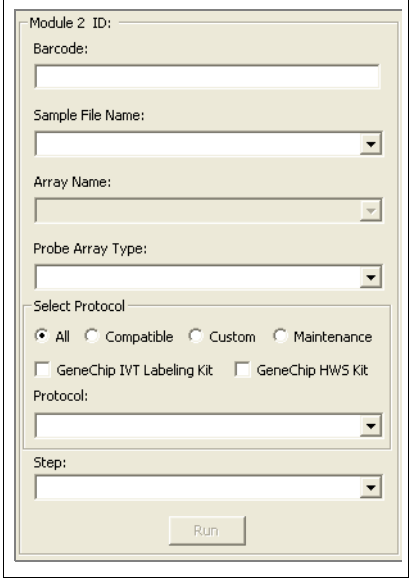
- Select a particular array for processing using the following parameters:
  - Sample File Name
  - Array Name
  - Probe Array type
- Select a specific protocol for the array.

Figure 176 GCC Fluidics Control window, Station controls



Each module has its own set of controls. (Figure 177)

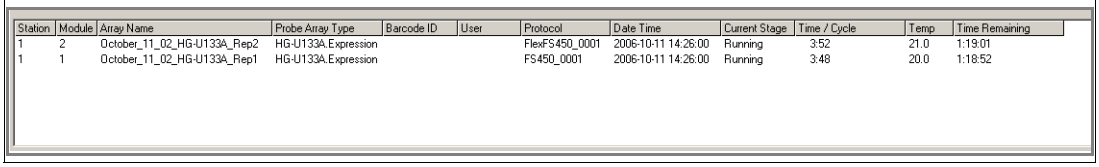
Figure 177 Module controls



The use of the module controls is described in "Running fluidics on individual stations" on page 160.

Status window

Figure 178 Status window



Station	Module	Array Name	Probe Array Type	Barcode ID	User	Protocol	Date Time	Current Stage	Time / Cycle	Temp	Time Remaining
1	2	October_11_02_HG-U133A_Rep2	HG-U133A.Expression			FlexFS450_0001	2006-10-11 14:26:00	Running	3:52	21.0	1:19:01
1	1	October_11_02_HG-U133A_Rep1	HG-U133A.Expression			FS450_0001	2006-10-11 14:26:00	Running	3:48	20.0	1:18:52

The Status Window (Figure 178) displays:

- **Station:** Fluidics station in operation.
- **Module**: Module in operation.
- **Array Name**: Name assigned to the array.
- **Probe Array Type**
  - **Barcode ID**: The last five digits of the probe array barcode.
  - **User**: Person who created the Sample file.
  - **Protocol**: Protocol used for the fluidics run.
  - **Date Time**: Current data and time when a protocol is running, or data and time when it was complete.
  - **Current Stage**: Fluidics protocol stage currently running.
  - **Time/Cycle**: Amount of time left for current stage or wash cycle number (e.g. 2 of 4).
  - **Temp**: Temperature used for current stage.
  - **Time Remaining**: Total time remaining for protocol.

Running protocols

You have several different options for selecting and running protocols with GCC Fluidics Control, depending upon:

- The type of protocol you want to run.
- Whether you want to run it on multiple stations.
- Whether you want to select different protocols for different modules in a station.

This section describes how to select and run protocols using GCC Fluidics Control:

- "Running a priming or maintenance protocol on multiple stations and modules" on page 156
- "Running a fluidics protocol on multiple stations" on page 157
- "Running fluidics on individual stations" on page 160
- "Resuming a fluidics protocol" on page 164
- "Bypassing steps in a fluidics protocol" on page 165

Running a priming or maintenance protocol on multiple stations and modules

Priming fills the fluidics station lines with wash buffers and deionized water. The GeneChip Fluidics Station must be primed before it can be used to run assay protocols. Prime the fluidics station when:

- The fluidics station is first turned on.
- A wash solution is changed.
- The fluidics station is to be used again after a shutdown has been performed.
- A module LCD window informs you that the module is not primed.

This section explains how to run priming or maintenance protocols on multiple stations and modules.

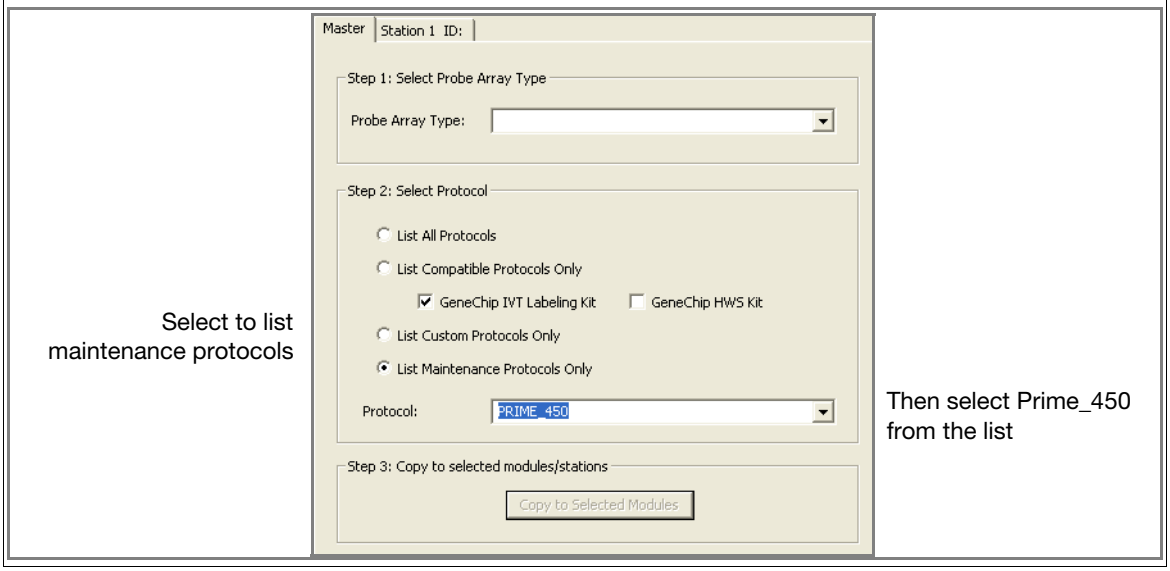
Priming the fludics station

1. Start the GCC Fluidics Control Software.

   See "GCC fluidics control software" on page 151.

   The software opens with the Master controls displayed.
2. In the Select Protocols section of the Master controls, select **List Maintenance Protocols Only**.

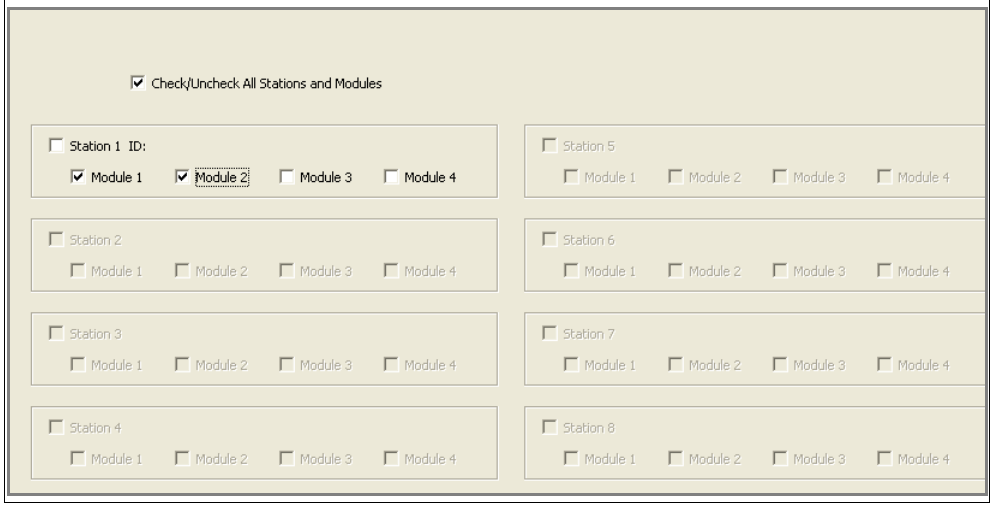
Figure 179 Selecting the Prime protocol



3. Select *Prime_450* from the **Protocol** drop-down list; or

   Select the maintenance protocol you want to run.
4. Select the modules to be primed (Figure 180).

Figure 180 Selecting the stations and modules for priming



You can:

- Select individual check boxes for each module.
- Click the Station ID check box to select all modules for a particular station.
- Click **Check/Uncheck all Stations and Modules** to select/deselect every station and module.

5. Click **Copy to Selected Modules**.
6. The selected protocol (Prime_450) is applied to the selected stations and modules.
7. Fill the intake buffer reservoirs A and B with the appropriate priming buffer. (Refer to the appropriate GeneChip probe array package insert).
8. Empty the waste bottle and fill the water reservoir with deionized water.
9. Load an empty, standard 1.5 mL microcentrifuge tube in the sample holder of each module to be primed.
10. Click the **Run All** button  ; or

    Select **Start** → **Run All Modules Selected on Master Page**.
11. Follow the prompts in the **Status window** (also shown in the module LCD window).

    The Status window and the module LCD window display the status of the procedure. The fluidics station is ready to use when priming is completed and **Priming done, Ready** appears in the module LCD window.

Running a fluidics protocol on multiple stations

You can run a selected protocol on any or all modules in the Fluidics stations attached to the workstation using the Master controls.

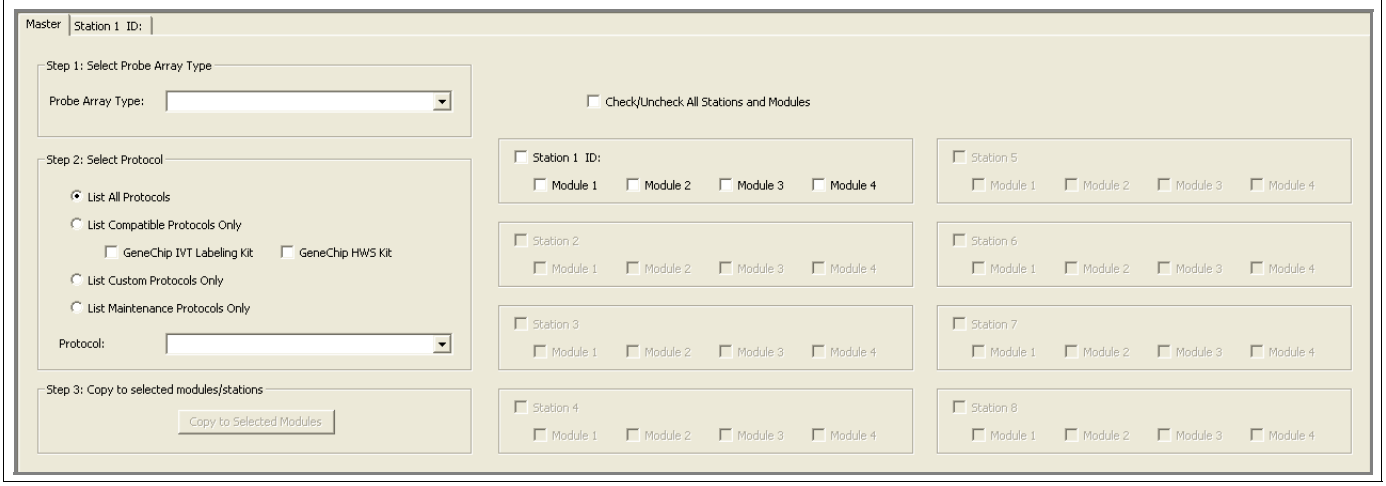
Selecting and running a fluidics protocol for a set of probe arrays

1. Start the GCC Fluidics Control Software.

   See "GCC fluidics control software" on page 151.

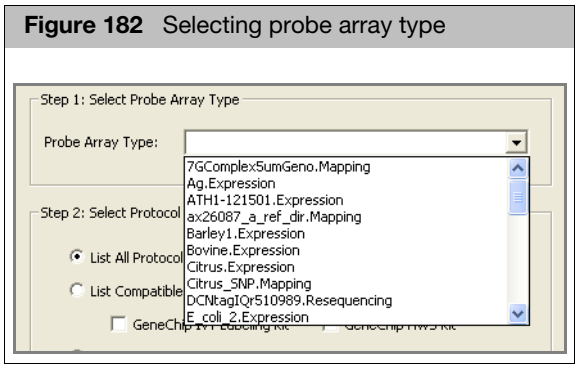
The software opens with the Master controls displayed (Figure 181).

Figure 181 Master controls



2. Select the array type from the **Probe Array Type** list. (Figure 182)

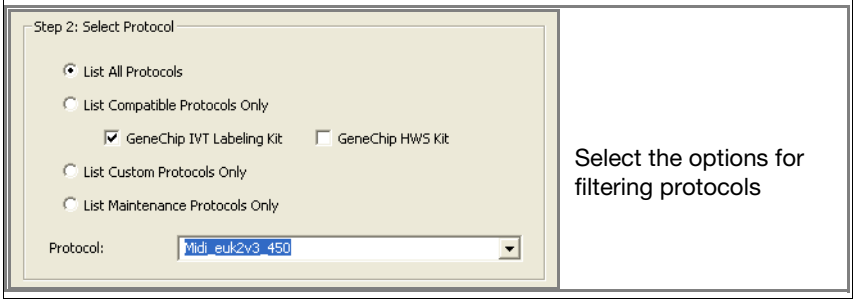
Figure 182 Selecting probe array type



IMPORTANT! The protocol that is displayed in the Protocol drop-down box after selecting the probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, follow the steps below.

3. Limit the protocols listed by selecting from the different options (Figure 183).

Figure 183 Selecting options to filter the list of protocols



To limit the protocols listed:

c. Select one of the following buttons:

- List All Protocols
- List Compatible Protocols Only (displays only protocols that can be used with the selected labeling kit):

  Select the appropriate check box:

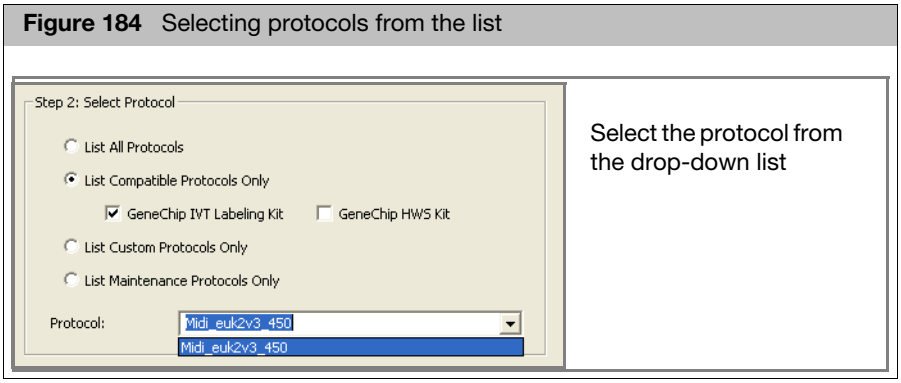
  –GeneChip IVT Labeling Kit

  –GeneChip HWS Labeling Kit
- List Custom Protocols Only (displays only protocols that have been edited or provided by the user)
- List Maintenance Protocols Only (displays only maintenance protocols)

Only the protocols that meet the selected requirements are displayed in the Protocol drop-down list.

4. Select the protocol from the **Protocol** drop-down list (Figure 184).

Figure 184 Selecting protocols from the list



IMPORTANT! The protocol that is displayed in the Protocol drop-down box after selecting the probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, select the correct options for filtering the protocol list as described above.

5. Select the modules to be run by:

- Selecting individual check boxes for each module.

- Clicking the Station ID check box to select all modules for a particular station.
- Clicking **Check/Uncheck all Stations and Modules** to select/deselect every station and module.

Figure 185 Selecting stations and Modules

6. Click **Copy to Selected Modules**.

   The selected protocol is applied to the selected stations and modules.
7. Fill the intake buffer reservoirs A and B with the appropriate solutions (Refer to the appropriate GeneChip probe array package insert).
8. Empty the waste bottle and fill the water reservoir with deionized water.
9. Click the **Run All** button ; or

   Select **Start** → **Run All Modules Selected on Master Page**.

   The Status window and the module LCD window display the status of the procedure.
10. After the protocol is finished, remove the probe array and inspect the probe array window for air bubbles.

    If air bubbles are present, reinsert the probe array into the fluidics station to automatically drain and refill the probe array with the last wash buffer used. (Refer to the appropriate GeneChip probe array package insert.) If no bubbles are present, the probe array is ready to be scanned.

Running fluidics on individual stations

You can also select a particular fluidics protocol on an individual station and module.

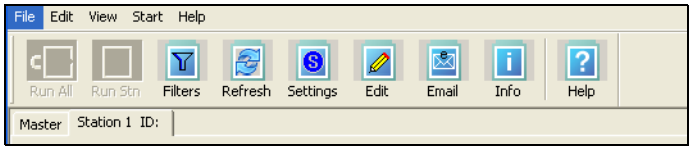
Selecting and running a fluidics protocol on an individual station and module

1. Start the GCC Fluidics Control Software.

   See "GCC fluidics control software" on page 151.

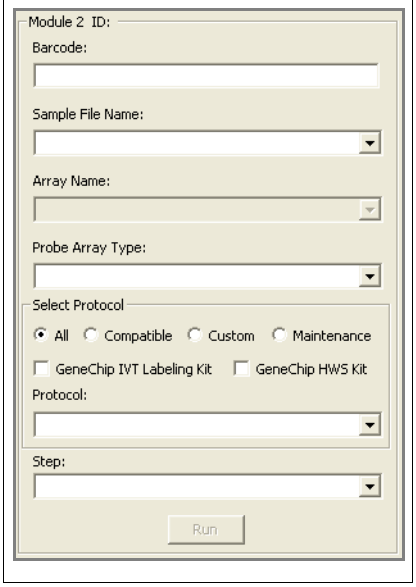
   The software opens with the Master controls displayed.
2. Click the tab for the station you want to use (Figure 186).

Figure 186 Tabs for Master and Station controls



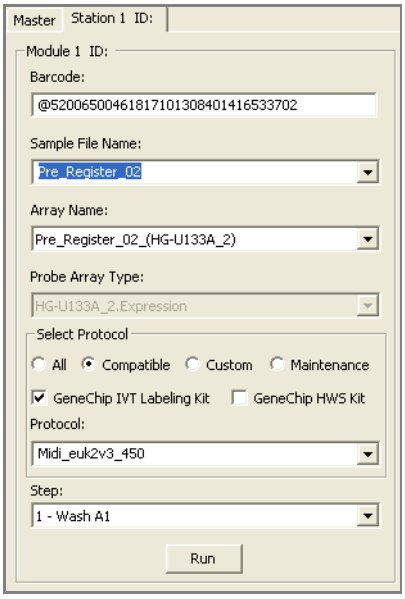
The Station controls displays the module controls for the selected station. Each module control has the same functions (Figure 187).

Figure 187 Module control



3. Click the **Refresh** button to refresh the list of Sample files.
4. Click in the Barcode box and enter the barcode using the keyboard; or
   Scan the barcode with an external barcode reader.
5. Press the **Tab** key.
   The following items are selected automatically if the barcode is valid:
   - **Sample File name**: Sample File with which the barcode is associated.
   - **Array Name**: Array name with which the barcode is associated.
   - **Probe Array Type**: Probe array type with which the barcode is associated.

Figure 188 Barcode entered, Sample File name, Array Name, and Probe Array type automatically selected



If you enter a valid barcode or specify the array name by other means, the fluidics protocol information is kept with the Audit file for the array.

You can also:

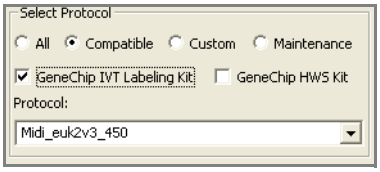
- Select a Sample file without entering the barcode. In this case, if the Sample file has more than one array associated with it, you will need to select the proper array from the Array Name list.
- Specify a protocol without specifying a Sample file or array. In this case, the fluidics protocol information is kept in an audit file that does not link to a particular Sample file.

Note: You can use the Filter dialog box to limit the Sample (ARR) files displayed by various properties. See"Filtering the sample file list" on page 166.

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after entering a barcode or selecting a sample name or probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, follow the steps below.

6. Set the options to filter the fluidics protocol selections.

Figure 189 Selecting options for protocol selection



Select the options for filtering protocols

To limit the protocols listed select one of the following buttons:

- All (lists all protocols available on your computer)
- Compatible (displays only protocols that can be used with the selected labeling kit):

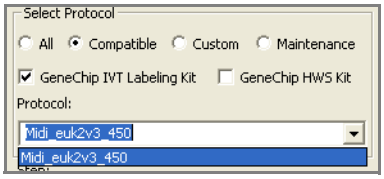
  Select the appropriate check box:

  - GeneChip IVT Labeling Kit
  - GeneChip HWS Labeling Kit
- Custom (displays only protocols that have been edited or provided by the user)
- Maintenance (displays only maintenance protocols)

  Only the protocols that meet the selected requirements are displayed.

7. Select the fluidics protocol from the Protocol list.

Figure 190 Selecting the protocol



Select the protocol from the list

IMPORTANT! The protocol that is displayed in the Protocol drop-down box after entering a barcode or selecting a sample name or probe array type may or may not be the correct protocol for the array, depending upon the type of analysis being performed. To make sure the correct protocol is selected, select the correct options for filtering the protocol list as described above.

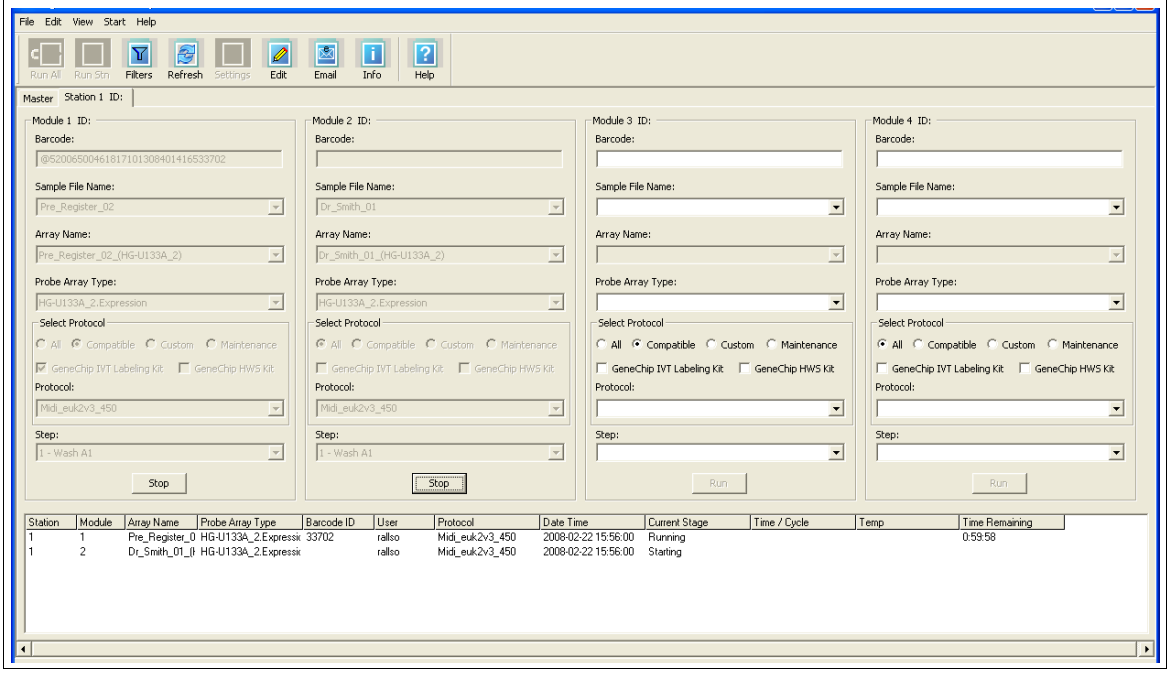
8. Click **Run** to start the protocol on the selected module; or

   From the Start menu, select **Run All Modules on Current Station**; or

   Click the **Run All Modules on Current Station** button  .
9. Load the probe array and sample vial holder containing the appropriate solution in each active module.

Sensors in the fluidics station detect when the probe array and sample vial holder have been loaded. The process will proceed automatically from this point, although some protocols may require removal and substitution of the sample vial and solution. The Fluidics Status window displays the status of the procedure (see "Status window" on page 155).

Figure 191 Fluidics Control window, protocol running



10. Repeat as necessary for other modules in the fluidics station(s).
11. After the protocol is finished, remove the probe array and inspect the probe array window for air bubbles.

    If air bubbles are present, reinsert the probe array into the fluidics station to automatically drain and refill the probe array with the last wash buffer used. (Refer to the appropriate GeneChip probe array package insert.) If no bubbles are present, the probe array is ready to be scanned.

Resuming a fluidics protocol

GCC tracks the progress of a fluidics protocol run. If the protocol stops before completion, it can be resumed at the point where it was interrupted.

Note: The resume feature is only available for fluidics protocols that display multiple steps in the **Step** drop-down list of the Fluidics Station dialog box and that have failed. If you exit GCC Fluidics Control while a fluidics protocol is running, the resume feature will be unavailable upon startup of the software.

1. Click **Resume** in the Modules controls.

   The selected protocol is started in modules one through four of the fluidics station.

Bypassing steps in a fluidics protocol

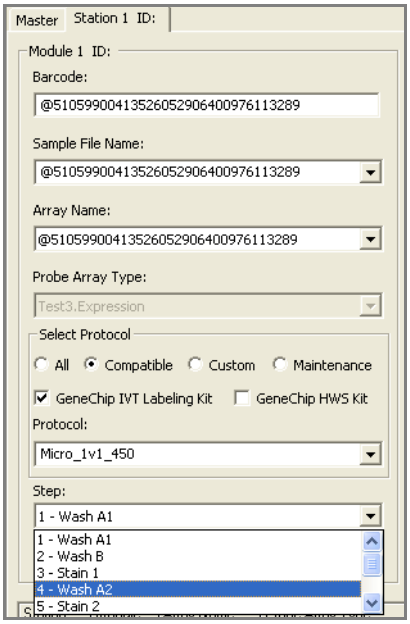
Some multi-step fluidics protocols can be started at any step, so that part of a protocol can be bypassed.

Note: The bypass function is only available for fluidics protocols that display multiple steps in the **Step** drop-down list of the Fluidics Station dialog box.

Bypassing steps

1. Select an array and protocol as described in "Running a fluidics protocol on multiple stations" on page 157.
2. Select the desired beginning step from the **Step** drop-down list (Figure 192).

Figure 192 Bypassing protocol steps 1, 2, and 3

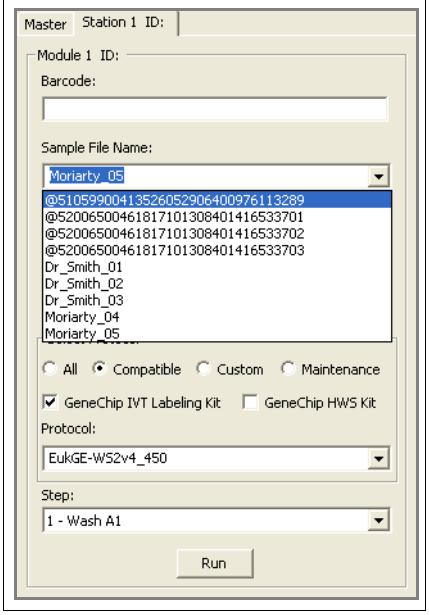


3. Click **Run** to start the fluidics protocol at the selected step.

Filtering the sample file list

When first opened, the Sample file list in the module control displays all the Sample files available in GCC. (Figure 193)

Figure 193 Station controls with unfiltered Sample File list



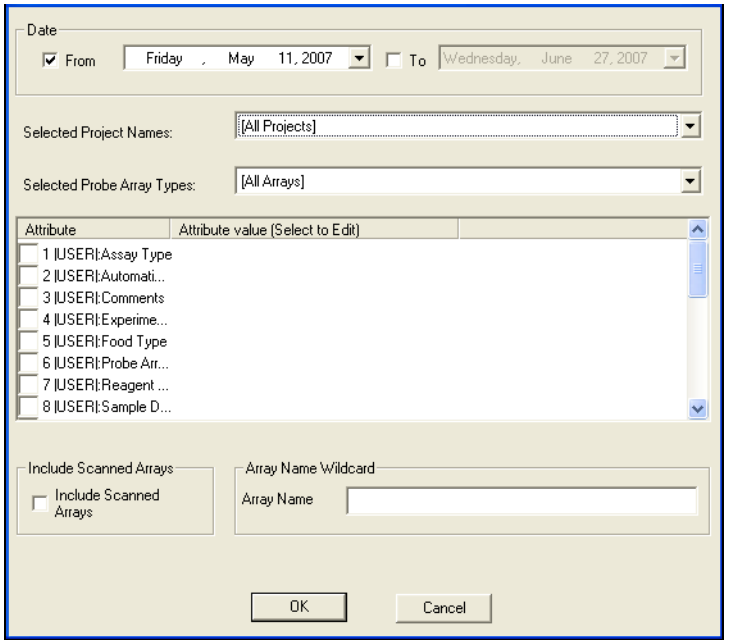
You can use the Filter dialog box to limit the types of files displayed in the Sample File list.

Note: The Filter dialog box can also be used in the GCC Scan Control in Manual mode.

Using the Filter dialog box

1. Click the **Filters** button  ; or
   From the Edit menu, select **Filters...**.
   The Filters dialog box opens. (Figure 194)

Figure 194 Filters dialog box

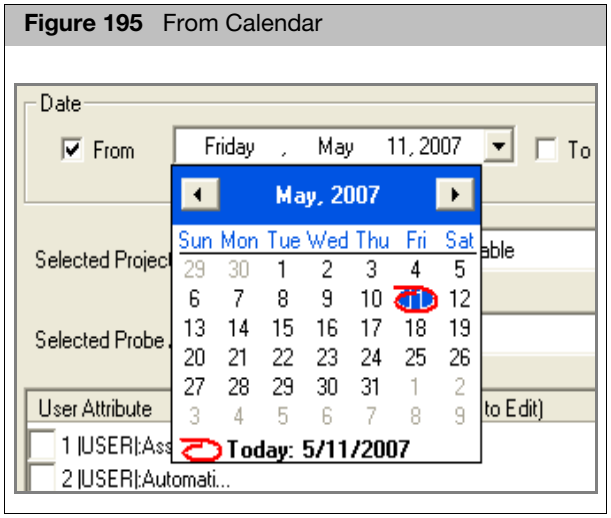


The Filters dialog box enables you to filter the displayed Sample files by:

- **Date**: Files created on a date or range of dates.
- **Selected Project Names**: Files associated with a particular project.
- **Selected Probe Array Types**: Files for a specific probe array model.
- **Template attributes and values**: Files associated with a particular attribute value.
- **Array Scan status**: Files for arrays that have already been scanned.
- **Array Name wildcard**: Array names with a specified text string in their file name.

2. Select a date or range of dates for file creation:
   a. Select the **From** check box.
   b. Click the arrow at the date (displays the current date).
      A calendar for the current month appears. (Figure 195)

Figure 195 From Calendar



c. Select a date for the start of the range. You can move from month to month by clicking the < and > buttons.

   If you only select one date, the filter will display only the files created on that date.

To select a range of dates:

d. Select the **To** check box.

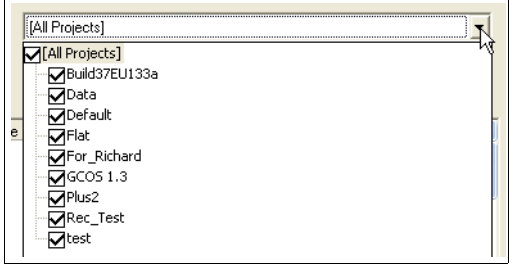
e. Select a date for the end of the range.

3. Select projects from the Project Name drop-down list:

   a. Click the down button in the Project Name list.

      A list of the projects available in GCC on this computer is displayed. (Figure 196)

Figure 196 Displaying Project List



   b. Select the check boxes next to the projects you want displayed in the filtered list.

      Note: For more information about creating and using projects, see "Projects" on page 34.

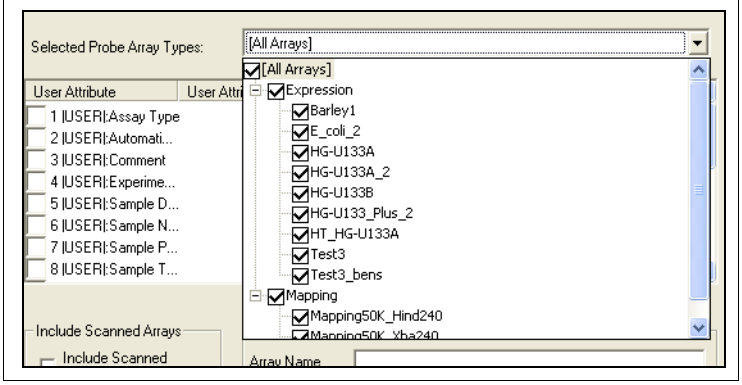
4. Select Probe Array Types:

   a. Click on the down arrow in the Selected Probe Array Types list.

      A list of the available probe array types is displayed. (Figure 197)

In some cases there may be multiple array models under the same header. in these cases you can click the + button to display the additional probe arrays.

Figure 197 Displaying array types



b. Select the check boxes next to the probe array types you want displayed in the filtered list.

5. Select template attributes and enter values:

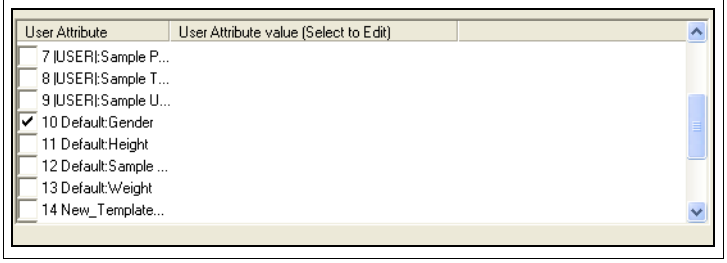
a. Locate the attribute you want to filter by.

Attributes are listed in the format: |Template Name|: Attribute Name.

User attributes are listed as: |USER|: Attribute Name. See "User attributes" on page 25 for more information about user attributes.

b. Click in the check box next to the attribute name. (Figure 198)

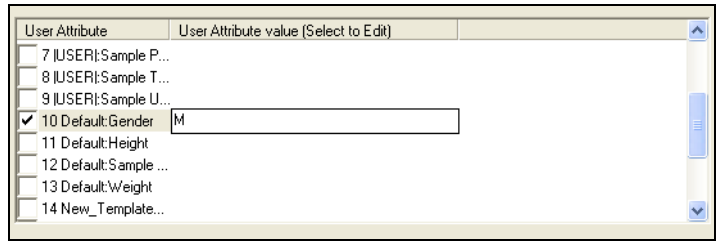
Figure 198 Selecting an attribute



c. Click in the User Value column next to the attribute and enter a value (Figure 199).

You can use the * symbol as a wildcard in the User Value column.

Figure 199 Entering an attribute value



Note: The Sample Attribute Conversion function may impact your selection of templates and attributes. For more information, see ""Sample attributes conversion" on page 115.

6. Deselect the **Include Scanned arrays** check box to exclude arrays that have already been scanned; or

   Select the check box to display all arrays, including scanned arrays.

7. Enter a text string (used in different array names) in the Array Name wildcard text box, using the * symbol as a wild card.

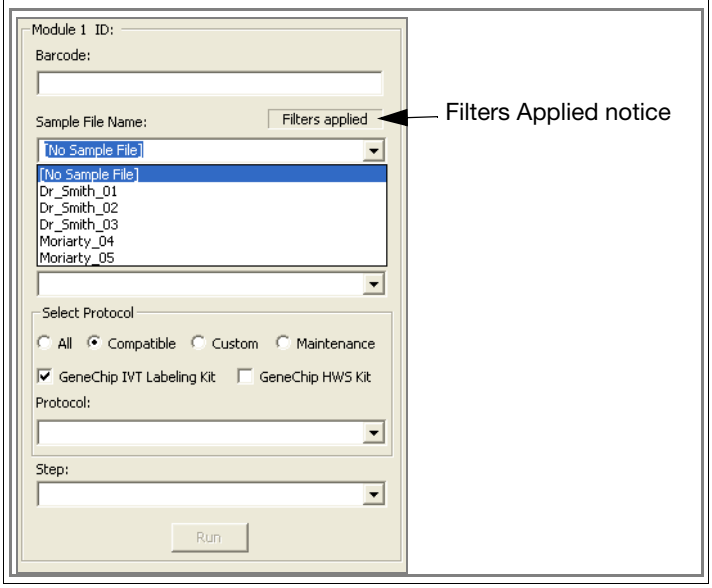
   For example, if you have used the barcode as an array name, entering "@*" will display all array with filenames using a barcode.

8. Click **OK**.

   The filtered Sample file list is displayed in the module controls. (Figure 200)

   A Filters Applied notice appears above the list.

Figure 200 Filtered Sample file list

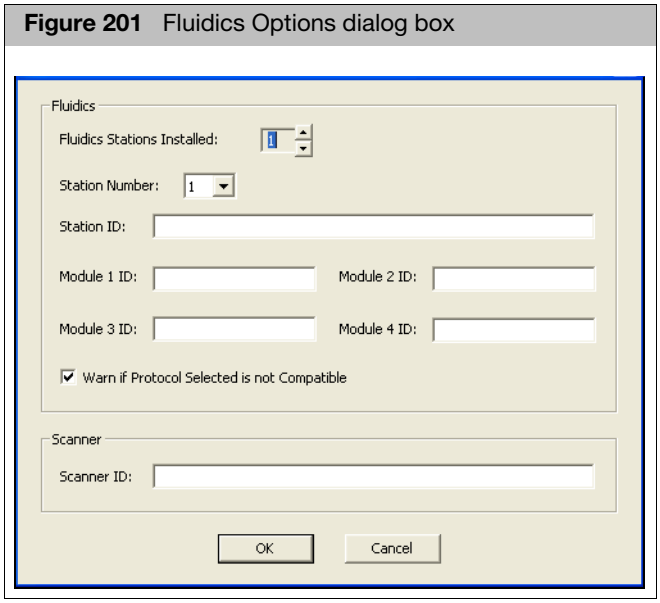


Adding a label to a station and modules

You can add a label to a station or module in the GCC Fluidics Control software. The labels can be useful when you are using more than one Fluidics station. The labels appear in the Fluidics Control software and will be used in status e-mails and in the Audit file (see Appendix E, "Notification e-mails" on page 367).

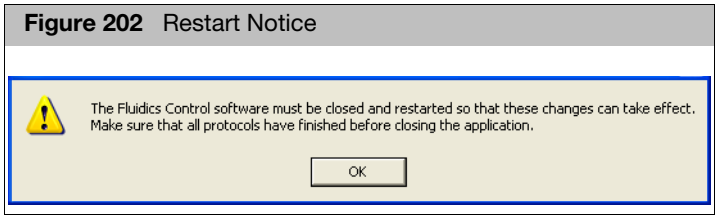
1. Click the Settings button ; or
   From the Edit menu, select **Station Settings...**
   The Fluidics Options dialog box opens (Figure 201).

Figure 201 Fluidics Options dialog box



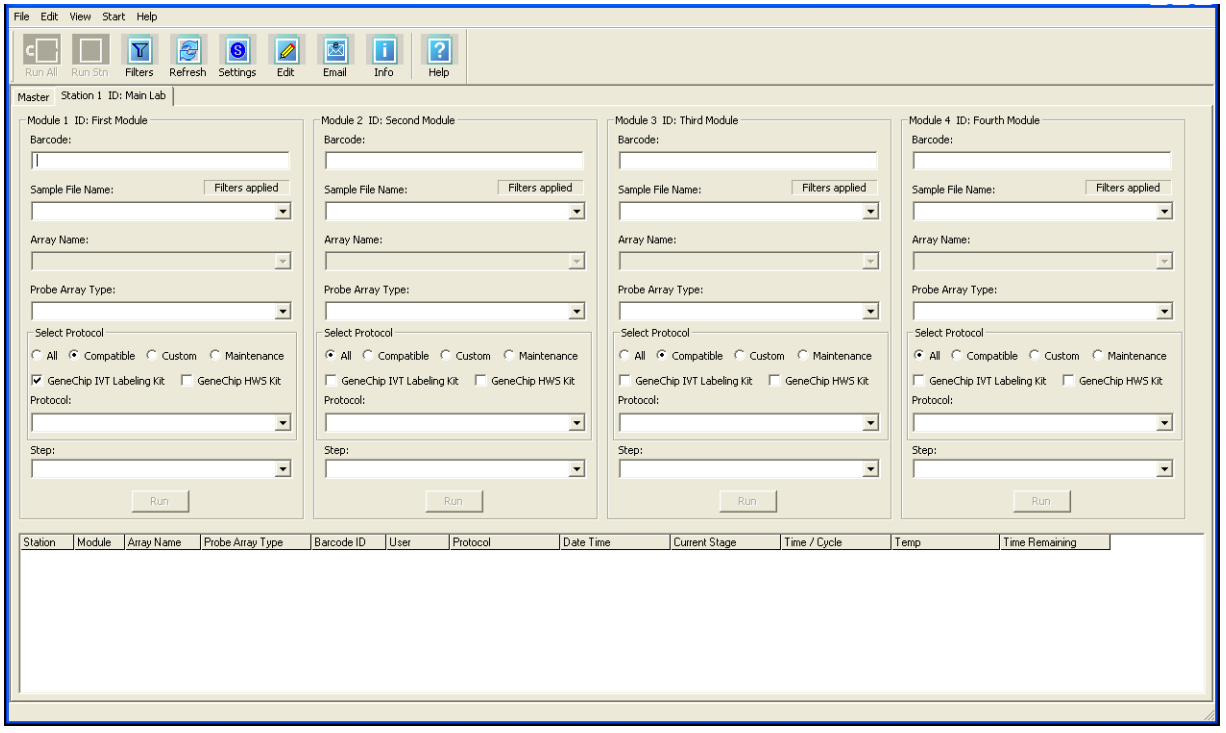
2. Set the number of Fluidics stations installed in the Fluidics Stations Installed box.
3. Select the number of the station you want to label from the Station Number list.
4. Enter a label for the station in the Station ID box.
5. Enter labels for the modules in the Module ID boxes.
6. Click **OK**.
7. The Restart Notice appears (Figure 202).

Figure 202 Restart Notice



8. Click **OK** to close the Restart Notice.
9. Shut down and restart GCC Fluidics Control.
   The labels are used in the station controls. (Figure 203)

Figure 203 Station Controls with labels



Installing and updating protocols

The fluidics protocols are files that list the steps used to process different types of probe arrays. After installing the GCC Fluidics Control software, you must install the fluidics protocols.

Installing protocols

1. From the Files menu, select **Install Protocols...**

   The Fluidics Scripts Installer opens.

2. Click **Next**.

   The Select Software screen appears.

3. Select the software you want to install scripts for and click **Next**.

   The Select Source screen appears.

   The screen enables you to:

   - Install the protocols from a directory on the file system.
   - Install the protocols from the thermofisher.com web site. **Note:** You must be a registered user before using this feature.

   To install from a directory:

   a. Select the option.

b. Enter the path to the directory or click **Browse** and use the Select Directory dialog box to locate the directory with the scripts.

To install from thermofisher.com:

a. Select the option.

b. Enter user name and password.

4. Click **Next**.

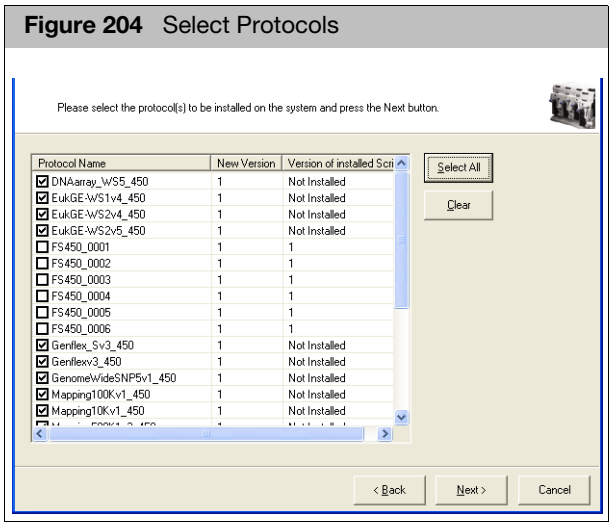
   The Select Package screen appears.

   The screen displays a list of the fluidics scripts packages available from the selected source.

5. Select the package you want to install and click **Next**.

   The Select Protocols screen appears. (Figure 204)

Figure 204 Select Protocols



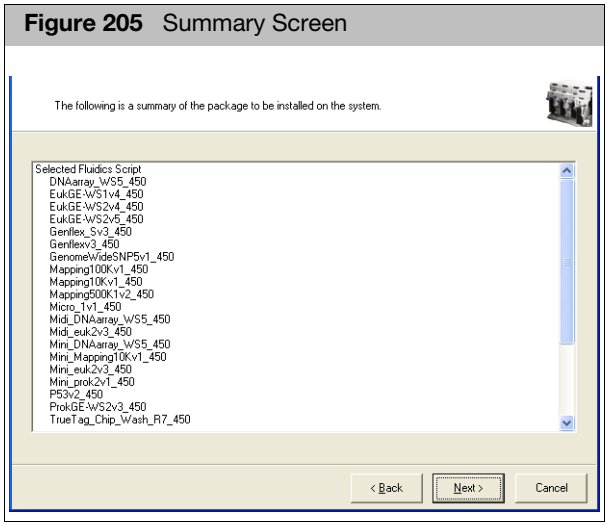
The screen displays a list of the protocols in the selected package with the following information:

- **Protocol Name**: With check box to select protocol for installation.
- **New Version**: Version of protocol in selected installation package.
- **Version of installed Script**: Version of protocol installed on your computer.

6. Select the check boxes for the protocols you want to install and click **Next**.

   The Summary Screen appears. (Figure 205)

Figure 205 Summary Screen



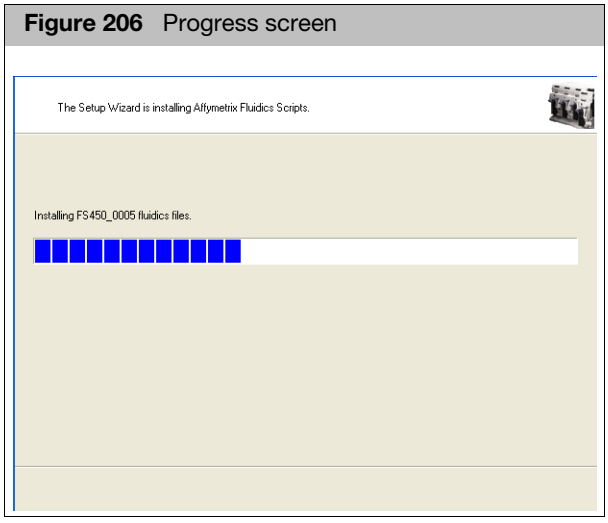
The Summary screen displays information about:

- Selected fluidics scripts
- Source Path
- GCC Target Directory
- GCC Log Path: Location of the log file for this installation.

7. Review the information and click **Next**.

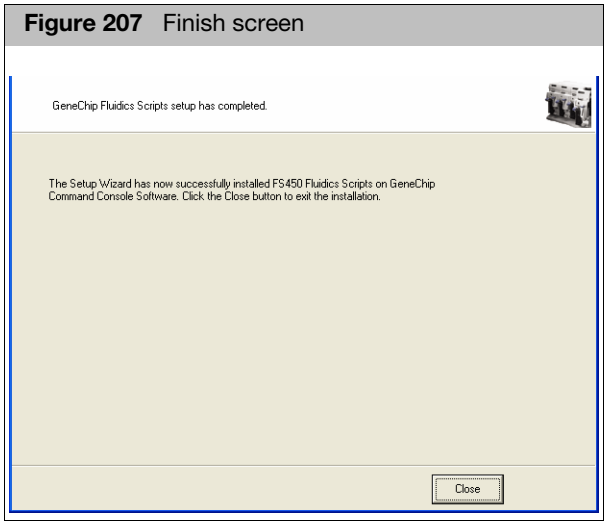
   A progress bar displays the progress of the install. (Figure 206)

Figure 206 Progress screen



When the install is completed, the Finish screen appears. (Figure 207)

Figure 207 Finish screen



8. Click **Close**.

Editing protocols

You can edit some hybridization and wash (Hybwash) protocols.

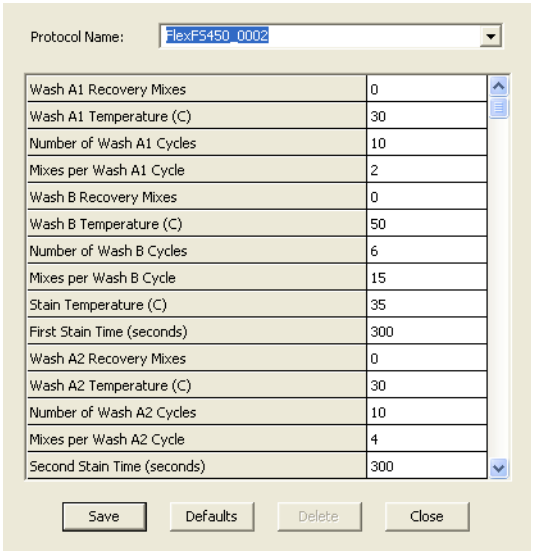
Note: Modifications to a Hybwash protocol must be completed before it is run. Protocol changes made during a run do not affect the run in progress.

1. From the Edit menu, select **Edit Protocol**; or

   Click the **Edit** button  .

   The Fluidics Protocol Editor dialog box appears. (Figure 208)

Figure 208 Fluidics Protocol Editor



2. Choose the fluidics protocol you want to edit from the Protocol Name drop-down list. The listed protocols are the same ones displayed when you select **Custom in the Master and Station controls**.

   Note: Only the protocols in this list may be edited. All others are defined for specific applications and cannot be customized.

3. Highlight the parameter value you want to change and enter the new value (Parameters values must be within the ranges shown in Table 2 on page 177). Enter a Hybridization Time of zero if only a wash is desired. To omit Wash A or B, enter zero for the Number of Wash A or Wash B cycles.

The FS450 instrument specifications

Fluidics Station Dimensions

(height, depth, width)
40.2 x 41.0 x 71.1 cm or 15 13/16 x 16 1/8 x 28 inches

Product Weight

Approximately 80 pounds or 36.3 kg

Power Input

100 to 240 V~, 3 A
300 watts or less

Main supply voltage fluctuations not to exceed 10% of the nominal supply voltage.

Temperature

Operating: 15° to 30° C
Storage (non-operating):-10° to 60° C

Humidity

Operating: 10-90% RH, non-condensing
Storage (non-operating):10% to 95% RH

Other

Pollution degree, 2

Installation category, II

Electrical Supply

The electrical supply shall meet the input specified on the instrument label. Voltage fluctuations shall not exceed 10% nominal supply voltage.

Altitude

<2000m

Table 2 Valid ranges for hybridization or stain protocol parameters

Parameter	Valid Range
Hybridization or stain time	0 - 86,399 seconds
Temperature	15 - 50° C
Number of Wash cycles	0 - 99
Mixes per Wash cycle	1 - 99

4. Save the edited protocol:
   - To save the parameters under the same protocol name (overwrites the old protocol), click **Save**.

- To save the parameters under a new protocol name, enter a new name in the Protocol Name field, then click **Save**.

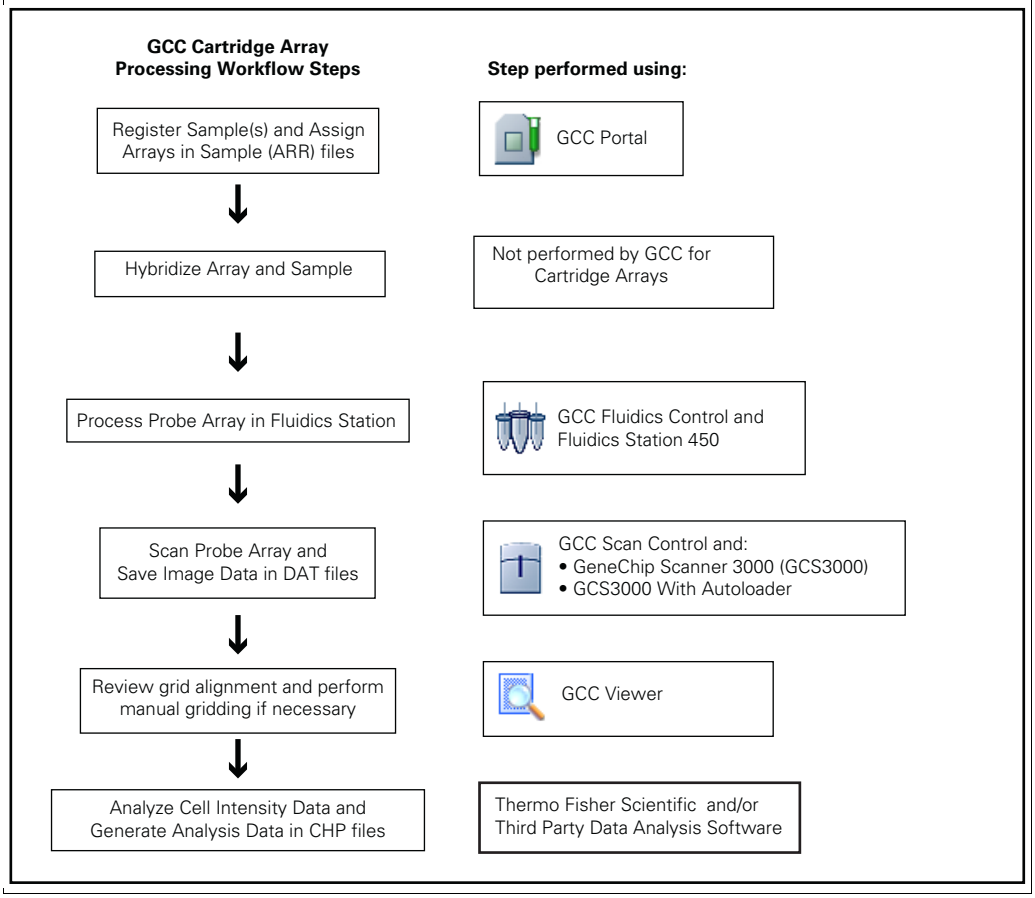
  This adds the new protocol name to the drop-down list.

5. Click **Defaults** to return the parameter settings to the default values.

7 Scanning cartridge arrays

After processing in the Fluidics Station, the arrays need to be scanned. (Figure 209)

Figure 209 Workflow for the Cartridge Arrays



Scanning can be done with the following scanners:

- The **GeneChip Scanner 3000 (GCS3000)** can be loaded with one chip at a time for scanning.
- The **GCS3000 with AutoLoader (Autoloader)** has a carousel that can be loaded with up to 48 chips. The chips can then be scanned in sequence without operator attention.

The scanners are controlled by with the GCC Scan Control software.

This chapter contains the following sections:

IMPORTANT! Read all the material in this chapter before running the scanner.

You can set things up to provide email notification when scans are complete or problems develop. See Appendix E, "Notification e-mails" on page 367 for more information.

GCC scan control software

The GCC Scan Control software is introduced in the following sections:

IMPORTANT! Please make sure that the data roots used in GCC software on the instrument control workstations do not contain files that have non-Thermo Fisher Scientific file extensions (example: DLL, TMP, CPP, ASPX, OUT, etc).

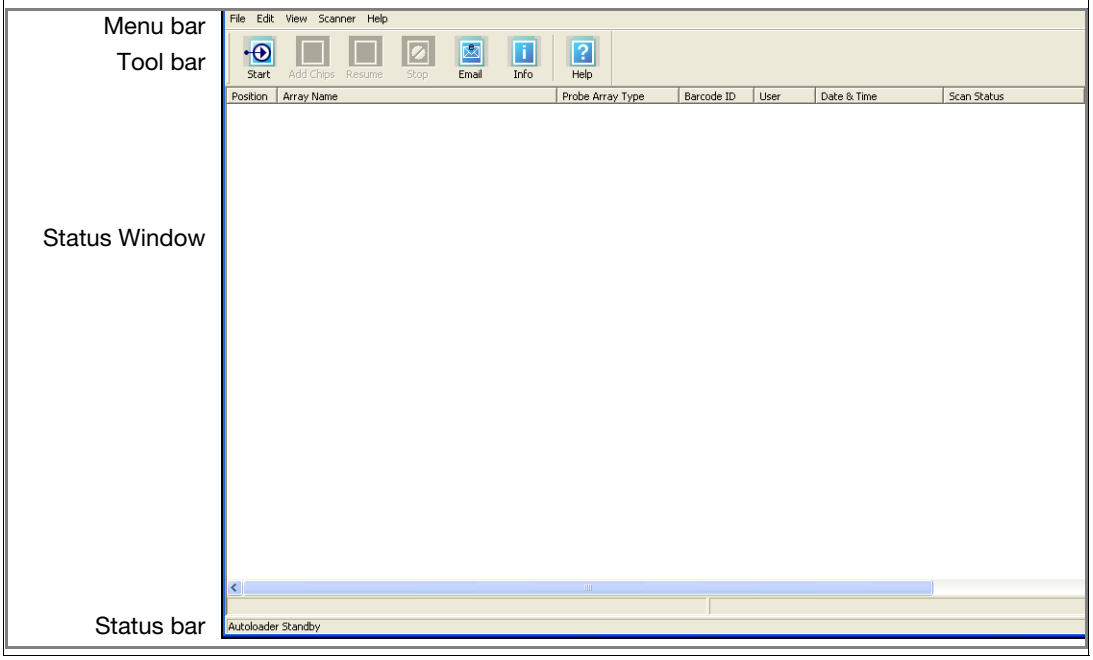
Starting the GCC scan control software

1. Click the GCC Scan Control icon  in the Launcher; or

   Click the **Start** → **Thermo Fisher Scientific** → **Command Console GCC Scan Control**.

   The GCC Scan Control window opens (Figure 210).

Figure 210 GCC Scan Control window



Components of the GCC Scan Control window:

- **Menu bar**: Access to functions of the software.
- **Tool bar**: Quick access to commonly used functions.
- **Status Window**: Displays list of scanned arrays with information on their status.
- **Status bar**: Displays information about the status of the AutoLoader and the scan in progress.

Hiding or displaying the tool bar

1. From the View menu, select **Toolbar** → **Standard Toolbar**.

Adding text labels to the tool bar buttons

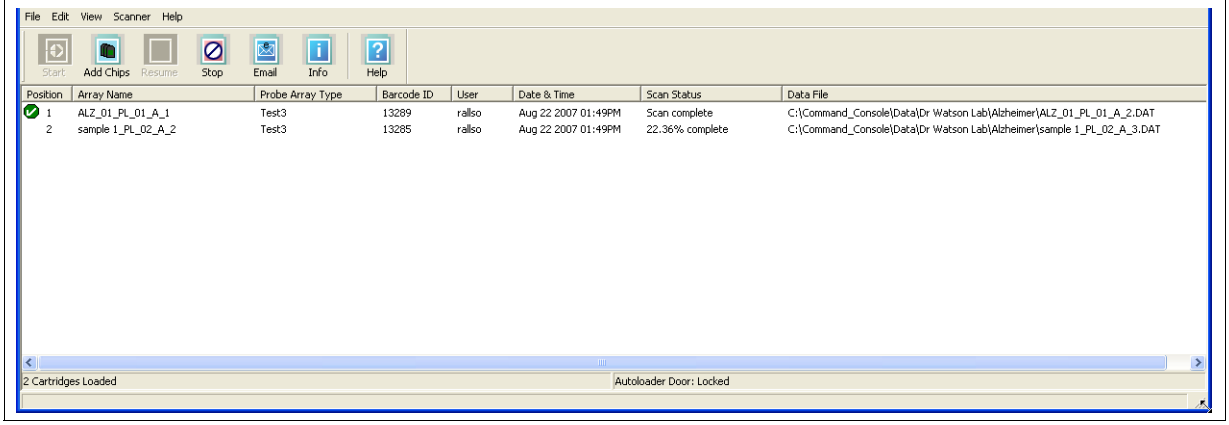
1. From the View menu, select **Toolbar** → **Text Labels**.

Hiding or displaying the status bar

1. Click → **View** → **Status Bar**.
   The Status window appears. (Figure 211)

Status window information

Figure 211 Status window



The Status window (Figure 211) displays the following information:

Position Position occupied by a given cartridge in the AutoLoader carousel.
Completed scans are marked with a green check mark.
Interrupted or failed scans are marked with a red X.

Array Name Array name assigned to the array.

Probe Array Type The probe array type for the scan associated with a given cartridge position.

Barcode ID The unique identifier in the barcode for the scan associated with a given cartridge position.

User Name of the user (array owner) for the scan associated with a given cartridge position.

Date & Time Date and time of the scan.

Scan Status The status of the scan. (Autofocus, scanning). This field displays all scanner status strings associated with the scan and retrieved from the scanner.
The message strings that may appear in this field are listed below. **Note:** Not all of the following messages will appear during each AutoLoader run.

- Autofocus
- Scan Status - % of lines scanned
- Scan Complete status
- Autofocus Errors
- The array XXX has already been scanned
- Chip load failures
- Invalid barcode errors
- Array does not exist errors
- AutoLoader door open errors

Data File Location and name of data file.

The Default folder is designated by the user as the automatic location of all files created during drop and scan operation, and for DAT and CEL files when the Sample

(ARR) file is located on network data storage.

For more information on Network Data Storage option, see Appendix A, "Networking" on page 338.

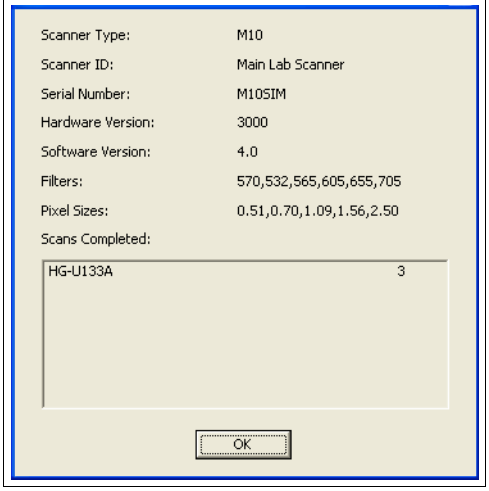
For more information about designating the Default folder, see "Specifying a default folder" on page 90.

For more information about transferring data to network data storage, see "Uploading data to network data storage" on page 91.

Reviewing scanner information

1. From the Scanner menu, select Information of click the Info button.
   The Scanner Information box opens (Figure 212).

Figure 212 Scanner Information box



The box displays information on:

- Scanner Type
- Scanner ID, if assigned (see "Setting Up the Scanner ID" on page 184)
- Serial Number
- Hardware Version
- Software Version
- Filters
- Pixel Sizes
- Scans Completed

Setting Up the Scanner ID

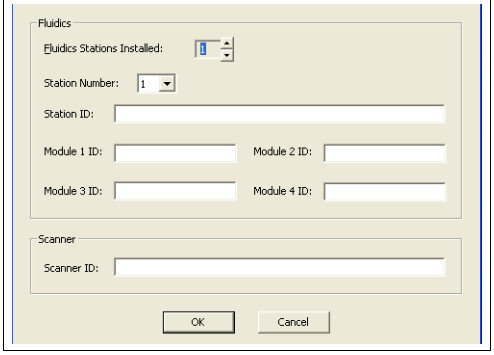
You can add an ID label to the scanner which enables you to identify it when email notification is activated.

Adding a label to a scanner

1. From the **Edit** menu, select **Scanner ID..**.

   The Instrument Configuration dialog box opens. (Figure 213)

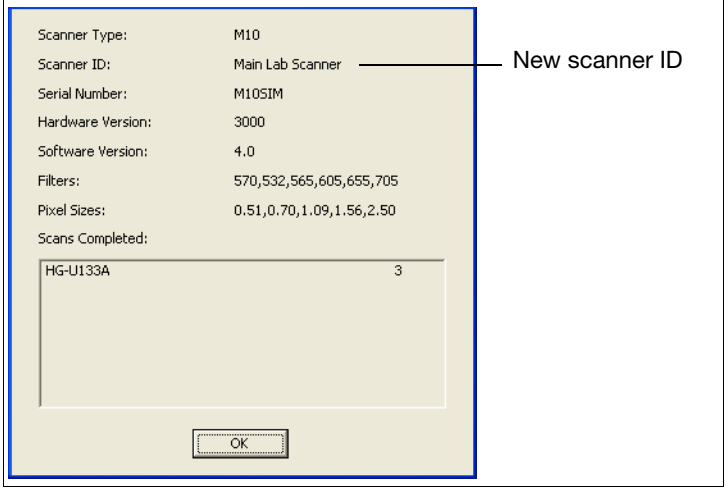
Figure 213 Instrument Configuration dialog box



2. Enter a label for the Scanner in the Scanner ID box.
3. Click **OK**.

   The label can be seen in the Scanner Information dialog box. (Figure 214)

Figure 214 Scanner Information dialog box



Applying Tough-Spots to prevent leaks

Tough-Spots™ are chemically inert polyvinyl labels that adhere to all plastics. Applied Biosystems recommends using 3/8-inch circle diameter Tough-Spots to prevent leakage from the array septa.

Before loading the probe array, follow this procedure to prevent the leaking of fluids from the array during scanning.

Even if you have already applied Tough-Spots to the array prior to hybridization or after washing, you must remove the old Tough-Spots and apply new ones before you load them into the AutoLoader.

Thermo Fisher Scientific recommends the use of Tough-Spots P/N 64-0158

or from

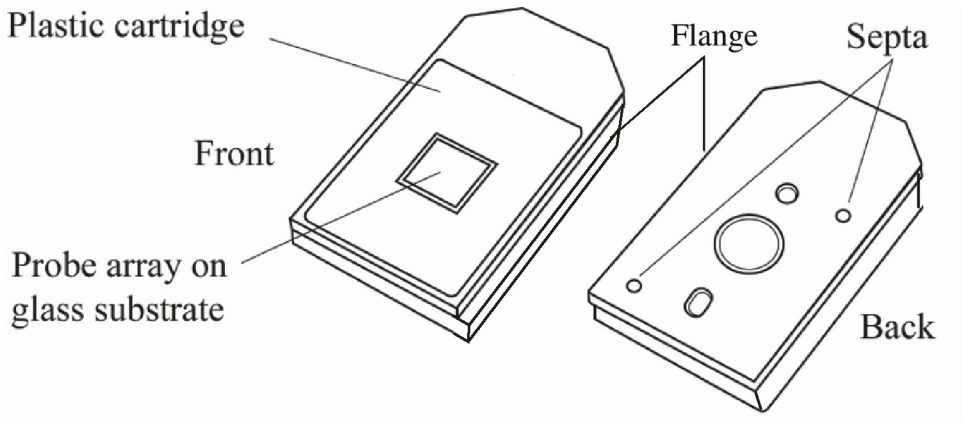
USA Scientific, Inc. P.O. Box 3565 Ocala, FL 34478 (800)LAB-TIPS P/N 9185-0000

WARNING! To reduce the risk of leakage, do not use excessively large pipette tips to pierce the septa.

Using Tough-Spots

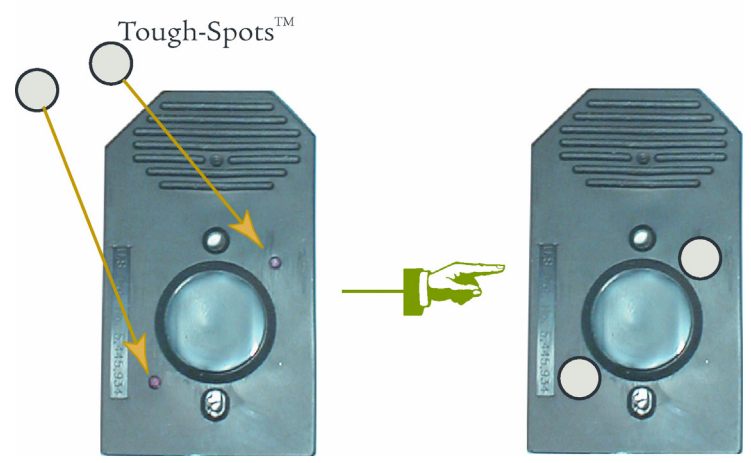
1. On the back of the probe array, clean excess fluid from around septa (Figure 215).

Figure 215 The GeneChip probe array



2. Carefully apply one Tough-Spot over each of the two septa. Press to ensure that the spots remain flat. If a Tough-Spot does not apply smoothly; that is, if you observe bumps, bubbles, tears or curled edges, do not attempt to smooth them out. Remove the spot and apply a new one. (Figure 216)

Figure 216 Applying Tough-Spots to array septa



Using GeneChip Scanner 3000

The GeneChip Scanner 3000 (GCS3000) is used to scan GeneChip probe arrays. It enables you to load and scan one array at a time.

Figure 217 The GeneChip Scanner 3000

WARNING! ONLY authorized personnel may service this equipment. The GCS3000 Scanner contains an incorporated Class 3B laser. Use of controls or adjustments or performance of procedures other than those specified herein may result in hazardous radiation exposure.

WARNING! The GCS3000 Scanner contains an incorporated Class 3B laser with the following specifications: Wavelength = 532nm +/- 1 nm; Beam Divergence (full angle) = <8mrad; Output Duration = Continuous Wave; Maximum Power Output = 500mW.

Do not remove the cover of the scanner. Use the scanner only as instructed in this User Guide. Do not attempt to service the instrument.

WARNING! Laser in use during scanning.

IMPORTANT! Read all material in this section before running the GCS3000.

This section contains the following material:

Laser safety

The laser is equipped with an automatic shutter that inhibits its output beam and ensures safe operation under conditions encountered in normal operation. The instrument covers, the array access port, and protective shutters ensure that during instrument operation no directed or stray laser light leaves the instrument.

IMPORTANT! The scanner is a Class 1 laser product when the laser is enclosed in scanner case. The laser itself is a Class 3B laser product.

DANGER
Laser radiation when open.
Avoid direct exposure to laser beam.
The lasers can cause serious injury if the instrument is not operated in accordance with instructions in this user guide.

CAUTION
Use laser safety glasses when servicing
DO NOT STARE INTO LASER BEAM.

Class 1 Laser Product

The green laser is a 532nm solid-state laser. This is a Class 3B laser and has visible outputs greater than 5mw but not more than 500mw. It must never be operated in an exposed manner. Any object in the direct path of the laser beam may be damaged. Eyes and skin can be seriously damaged by direct exposure to, specular reflections from, or diffuse reflections from this laser. If improperly used, a laser of this type can cause fires. When used according to the instructions in this manual and when all covers are in place, the GeneChip Scanner is classified as a Class 1 Laser Product per IEC 60825-1:2007.

Complies with 21 CFR 1040.10 and 1040.11 except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007.

Always take note of laser safety labels; they indicate areas where exposure to laser beams may be hazardous.

Electrical safety

The scanner will automatically handle any input voltage from 100 to 240 VAC nominal, 50 to 60 Hz.

Note: The scanner's power supply will auto-detect the input voltage source and configure itself.

The power supply cord is used as the main disconnect device. Ensure that the socket outlet is located and installed near the equipment and is easily accessible.

CAUTION! If you use the scanner in a manner not specified in this user guide, you may impair the protection provided by the equipment.

CAUTION! Do not confuse your company's network connections with the dedicated Ethernet port of the scanner-workstation. The proper scanner connection is located near the top of the workstation.

CAUTION! This 10/100 Base T Ethernet communications port is dedicated to the scanner-workstation interface. You cannot connect the scanner to your company's Ethernet communications network.

IMPORTANT! The reset button is the scanner's circuit breaker. The breaker switch will be tripped whenever the scanner experiences an electrical fault condition. Press to reset. If you cannot reset this switch, contact technical support.

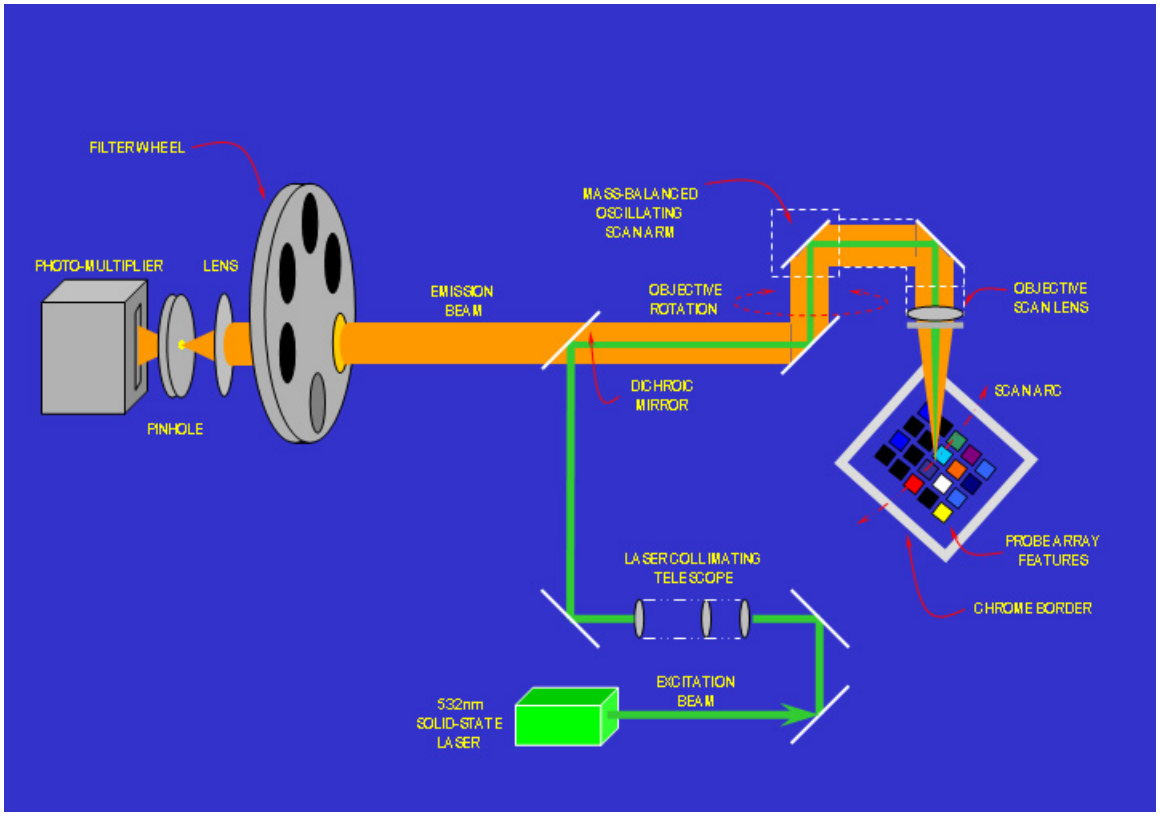
Introduction to the GCS3000

This section contains:

Theory of Operation

The GeneChip Scanner 3000 is a wide-field, epifluorescent, near-confocal microscope. The scanner uses a 532 nm solid-state laser to excite probe array fluorophores. This in turn produces an emission wavelength appropriate for the probe array being scanned, which is automatically specified in the scan parameters for the selected probe array. As the surface of the probe array is scanned, a photomultiplier tube collects and converts the fluorescent emissions into an electrical signal. An analog-digital converter in the scanner converts this signal into corresponding numeric values representative of fluorescent intensities. These digital intensity values are collected from discrete areas on the array surface and are stored on the computer workstation as pixels that comprise the image data file (the DAT file). The patented Flying Objective™ technology represents a radical departure from conventional laser scanners. The optical system comprises a scan arm that rapidly oscillates from side to side scanning the entire width of the probe array in a continuous arc while the probe array is advanced in front of the objective. The acquired image of the array is returned to the computer software as a set of arcs. The software then geometrically corrects these arcs to form a linear image of the array (Figure 218).

Figure 218 Schematic of the scanner design



The laser source excites the hybridized fluorophores and the photomultiplier system simultaneously captures the resulting fluorescent intensities. The optical components direct the fluorescent beam back through the objective lens, through a dichroic mirror and to the PMT. An analog-digital converter transforms the PMT output into 65536 levels of intensity. Each level of intensity is stored in the software as a 16 bit number (2^{16}=65536).

The scanner is equipped with an IEC 320 compliant power entry module located at the rear of scanner.

The scanner is equipped with an RJ-45 interface connector compatible with 10/100 Base T Ethernet for communications with the host workstation.

The GCC application controls the scanner. After the scanner has completed a scan, GCC displays a picture of the image in the image window. The software displays the fluorescent intensity values from each pixel within the probe array feature in a grayscale or pseudo color mode and superimposes a grid on the image to delineate the probe cells.

GCC analyzes the image and derives a single intensity value for each probe cell on an array. This data is automatically generated and saved to the cell intensity file.

Starting the scanner

1. Press the on/off (I/O) switch on the front panel.

   The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

Shutting down the scanner

1. Close the GCC software. This is the best way to shut off the laser. Alternately, press the I/O (on/off) button on the front panel to turn off the instrument.

   Note: The laser also has a sleep mode that activates after 1 hour of inactivity.

Scanning a probe array with GeneChip Scanner 3000

This section shows you how to scan a GeneChip probe array using the GeneChip Scanner 3000.

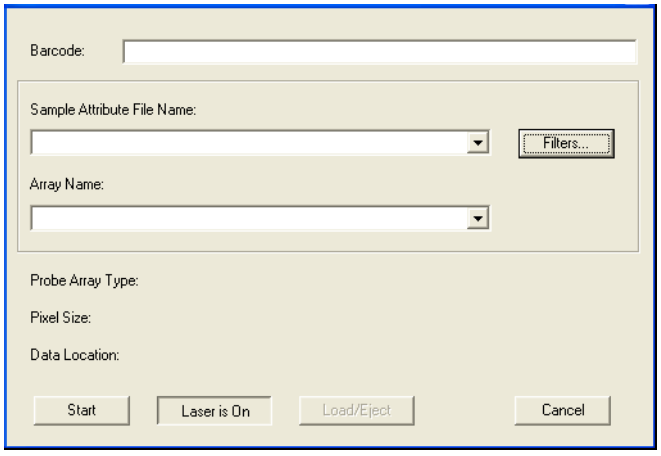
Scanning the probe array

1. Turn on the Scanner-AutoLoader (see "Starting the scanner", above).
2. Start the GCC Scan Control Software (see "GCC scan control software" on page 180).
3. Click the **Start** button  in the main tool bar; or

   Select **Scanner Start Scanner** from the menu bar.

   The Scanner dialog box opens. (Figure 219)

Figure 219 Scanner Dialog box



At this point, you can choose from these options:

- If your array has a valid barcode, you can scan the barcode on the probe array into the barcode field. The software will retrieve the sample file and array name associated with the barcode.

  If the barcode is not associated with an existing Sample file and array, a sample file will be created during scan using Drop and Scan.
- If your array does not have a valid barcode, you can manually select an array as described below:

  a. Select the Sample file name for the probe array you want to scan from the **Sample File Name** drop-down list.

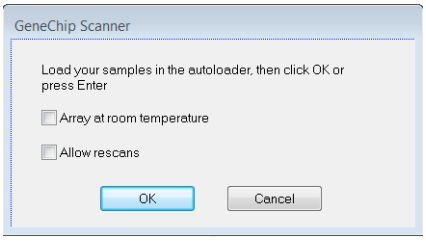
  b. Select the array name of the probe array to be scanned from the **Array Name** drop-down list.

  The **Probe Array Type** field automatically displays the probe array type that was entered while creating the Sample file.

4. Click **Start** in the Scanner dialog box.

   The Start window appears. (Figure 220)

Figure 220 The Start Scanner dialog box

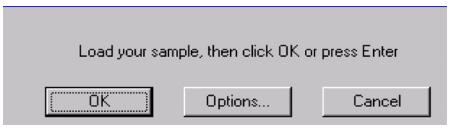


If you want to skip the warm-up period before scanning the first probe array, keep the default check-mark in the **Array at room temperature** check box. If you want to allow rescans, click the **Allow rescan** check box.

5. Click **OK** to start the run.

   The GeneChip Scanner dialog box appears. (Figure 221)

Figure 221 Scanner dialog box

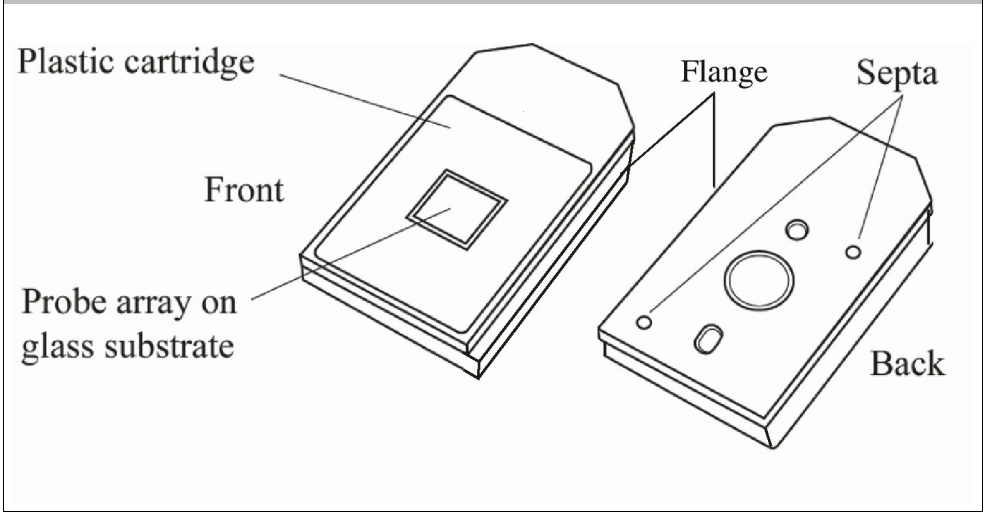


The scanner door opens and the chip transport mechanism raises to accept a probe array.

6. Load the probe array (Figure 222) into the scanner chip transport mechanism. Insert the probe array into the chip transport mechanism such that the front of the probe array (label side) faces to the rear of the scanner.

   Note: The scanner will enter Park mode if it is unattended for 15 minutes and will enter standby, or sleep, mode if it is unattended for 60 minutes (45 minutes after entering Park mode). The green light will turn off and the yellow light will turn on. To reactivate the laser, click **Turn Laser On** in the scanner dialog box and wait 10 minutes.

Figure 222 GeneChip probe arrays. Note the location of the flange, as the scanner accepts the probe array in only one orientation.



CAUTION! Do not force the probe array. If the array does not drop easily into the chip transport mechanism, eject the array and try again. If this does not remedy the situation, see"Troubleshooting" on page 195 or call technical support. Also, if a probe array becomes lodged in the scanner, you can manually remove it. For more information, see "Manually removing a lodged/stuck probe array" on page 196.

In addition, you cannot modify the scanner settings. GCC automatically selects the appropriate settings based on the probe array type specified during experiment setup.

Figure 223 Loading the probe array into the chip transport mechanism. Note that the front of the probe array faces to the rear of the scanner.

7. Click **OK** in the GeneChip Scanner dialog box to start scanning the probe array.

   During the scan, the green light will flash, and the yellow light will be off.

   After the scan starts, the software will start with the auto-focus routine. Data collection starts after successful completion of auto-focus. During the pre-scan state, when auto-focus is complete, but before data collection has started, the software will count downwards.

   Note: When multiple emission filters are used during the scan process, the software will display the scan with a letter followed by the percentage of scan completed. The letter identifies the scan associated with the emission filter.

   After the scan is completed, GCC:

   - Saves the image data.
   - Aligns a grid on the image to identify the probe cells.
   - Computes the probe cell intensity data.
   - Ejects the probe array.

Note: If you leave the scanner idle for an additional 15 minutes, the scanner will also enter “Park” mode. The yellow light is off and the green is light on. The chip transport mechanism will retract and the scanner door will close. You must click the **Eject Chip** button to open the scanner door and raise the chip transport mechanism.

Note: You can track the progress of the grid alignment and cell intensity computation in the GCC Viewer. For more information see Chapter 9, "Using the GCC viewer" on page 267.

Scan Options

This section describes various options when using the GCS3000:

Scanning Four-Color Arrays

The four color scans are performed on GeneChip arrays that have been configured for use with four emission filters. The four emission filters are specified in the GCC scan parameters. when performing a multi-filter scan, GCC scans the array with different emission filters, using the order specified for the array.

A DAT file is created for each of the emission filter scans. To distinguish the different scans, GCC appends a suffix of A, B, C, or D to the DAT files. Different file naming conventions are used in the case of a rescan of an array, depending upon whether the array was manually loaded.

When running multiple scans on an array, the scanner performs autofocus only once, prior to the first scan. This is true whether the scans are performed as part of a four-color scan or as a re-scan.

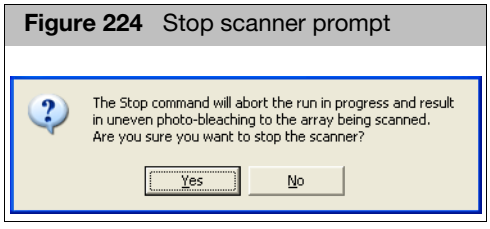
Aborting a scan with a manually loaded array

If scanning is aborted on a manually loaded array, the emission filter scan in progress continues until it is complete, and the DAT data for the completed scans are saved. When the scan is resumed, GCC auto-focuses the scanner and then re-scans and re-creates a DAT file for each emission filter scan, overwriting the previously created DAT files.

Stopping a Scan

1. Click the **STOP** button  or select **Run Stop Scanner** from the menu bar.
2. At the prompt, click **Yes** to stop the scanner or **No** to cancel stopping (Figure 224).

Figure 224 Stop scanner prompt



CAUTION! If you click Yes, the data from a partial scan will be lost. This is different from using earlier software or scanner versions where you could save the data from a partial scan.

If you rescan a probe array that has been partially scanned, the previously scanned area of the probe array may experience fluorophore bleaching. This will result in non-uniform fluorescence intensity across the probe array.

3. After you stop a scan, the scanner will automatically eject the array.

Note: The scanner dialog box has an eject array button. This is reserved for ejecting an array after the scanner goes into sleep mode or when you must manually eject the array for any other reason. If the probe array becomes stuck, see "Troubleshooting" or call technical support.

Troubleshooting

Table 3 Troubleshooting tips

Problem	Possible Cause	Corrective Action
No image when scanning	Power off or cable loose	Check all connections and power.
	Loss of laser power	Contact technical support.
Intermittent problems scanning	Loose cable	Check all rear connections.
Scanner fails with probe array inside	Power failure	Manually extract probe array. Check all connections to scanner. Turn scanner on, restart software.

For additional troubleshooting information, see:

- "Issues relating to the scanner's operation" on page 195
- "Manually removing a lodged probe array" on page 218

Issues relating to the scanner's operation

The table below lists some issues and problems that you may encounter while using

the GCS3000.

Issue	Explanation
If communications are interrupted during a scan (by a faulty cable connection or power being lost at the scanner, for example)	GCC will properly note the failure and present a message “Cannot connect to Scanner.” However, there are two issues to note. First, GCC will report such a failure only after a network time-out of about 30 seconds. Second, rarely, if communications have been lost, GCC and the Scanner may not be able to automatically restore communications once the problem is rectified, and both may become unresponsive. To restore proper operation, verify that the scanner is on, that communication cables are properly connected, and close and restart Microsoft® Windows® then restart GCC. If the system remains unresponsive, disconnect and reconnect power to the scanner, restart the scanner normally, close and restart Microsoft® Windows® and GCC.
Repeated attempts to send commands (Start, Turn Laser On, etc.) from GCC to the Scanner while GCC is reporting the scanner “Offline” may result in GCC becoming unresponsive until communications are restored	If communications cannot be re-established, please follow the recommendations of item 1
If the Scanner experiences multiple auto-focus failures, the system may enter an unresponsive state.	Follow the recommendations of item 1 to restore communications and correct operation.
Laser warm-up lasts for ten minutes, during which time the “Turn Laser On” button will remain unchanged and GCC will display the status message “Warm-up”.	Simply note that this is normal operation.
If no array is inserted and a scan started.	The scanner will attempt go through the first parts of the auto-focus routine and then report “Failed to find chrome border”.
The scanner should be in the park mode to eject the array.	
Auto focus will fail if salt deposits accumulate on the array.	Use Tough-Spots to prevent leaks in the GeneChip probe array. See the quick reference card, p/n 08-0076.

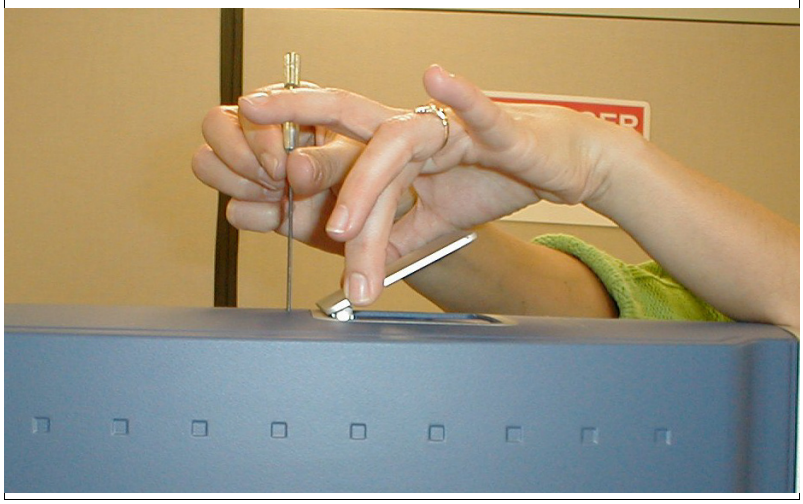
CAUTION! Heavy object. Two people are required to lift the scanner.

Manually removing a lodged/stuck probe array

In the event that a probe array becomes lodged in the array transport mechanism, follow the procedure outlined below.

1. Turn off the scanner.
2. Insert a paper clip or small Allen wrench into the rescue hole on top of the scanner and press to partially lift the array loading door.

Figure 225 Using the rescue hole



3. Using your fingers, gently lift the front edge of the door. As you lift the front edge, lift the back edge approximately 1/4” to open the door straight up to expose the rescue screw in the front.
4. Using a standard (-) screwdriver, turn the rescue screw clockwise to raise the array transport mechanism.
5. Continue to turn the screw until the probe array ascends sufficiently to grab it.

Figure 226 Turning the rescue screw

Note that the screw is fine pitched and requires a number of turns. Stop if you encounter screw resistance. Do not over torque.

6. When the array has ascended sufficiently, remove it.

Figure 227 Removing the array

7. Re-screw the array transport mechanism until it descends completely, or until you encounter resistance. Do not over torque.
8. Close the door.

GCS3000 Specification

GCS3000 Specification table:

Item	Parameter	Value
Weight	Shipping	approx 74 pounds (35.4 Kg)
	Free -standing	63 pounds (28.6 Kg)
Dimensions	Width	-13.25 in
	Depth	-27.5 in
	Height	-18.25 in
Power	Voltage Current Line Frequency	100 - 240 V – 4 - 2 A 50 - 60 Hz
Working Environment	Temperature	59°F-85°F (15°C-30°C)
	Humidity	10-90% Non-condensing
	Clearance	2 in.(5 cm) on side, back and top
	Pollution Degree	2
	Installation Category	II
	Altitude	<2000m
Electrical Supply Main Supply Voltage Fluctuations	Provide voltage, frequency or power rating per unit label Are not to exceed ±10% of the nominal supply voltage	

Using the GCS3000 with AutoLoader

The GeneChip Scanner 3000 with AutoLoader (AutoLoader) is similar to the GCS3000 with the addition of a carousel autoloader, designed expressly for scanning multiple GeneChip probe arrays. The AutoLoader can scan up to 48 probe arrays automatically without operator presence.

WARNING! Laser in use during scanning.

Figure 228 The GeneChip Scanner 3000 with AutoLoader

Introduction

For more information about the scanner, see "Introduction to the GCS3000" on page 189.

Starting the AutoLoader

To turn on the AutoLoader:

- Turn on the Scanner-AutoLoader by pressing the on/off (I/O) switch on the front panel.

  The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

Shutting down the scanner

1. Close the GCC software. This is the best way to shut off the laser.
2. Press the I/O button on the front panel to turn off the instrument.

Scanning probe arrays with GeneChip Scanner 3000 with AutoLoader

This section shows you how to scan a GeneChip probe array using the GeneChip Scanner 3000 with AutoLoader.

Scanning chips using the AutoLoader

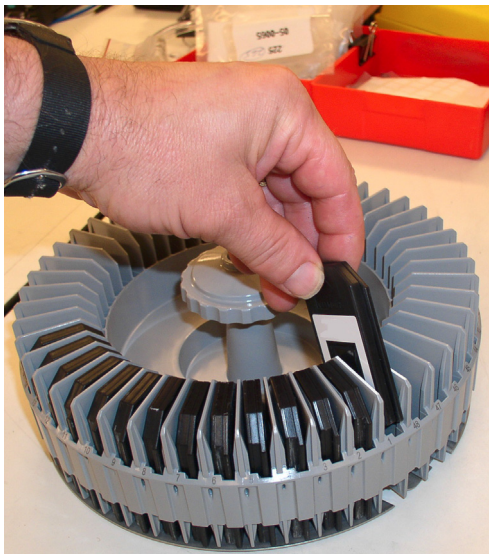
1. Turn on the AutoLoader by pressing the on/off (I/O) switch on the front panel.

   The scanner's onboard computer boots up. The bootup process takes a few minutes. During this time both the yellow and green light will be on. The scanner enters the laser warm-up state. During this warm-up time, the green light will turn off and the yellow light will remain on. You must wait 10 minutes for the laser to stabilize.

2. Load your cartridges into the carousel (up to 48). Note that only one orientation is possible (Figure 229).

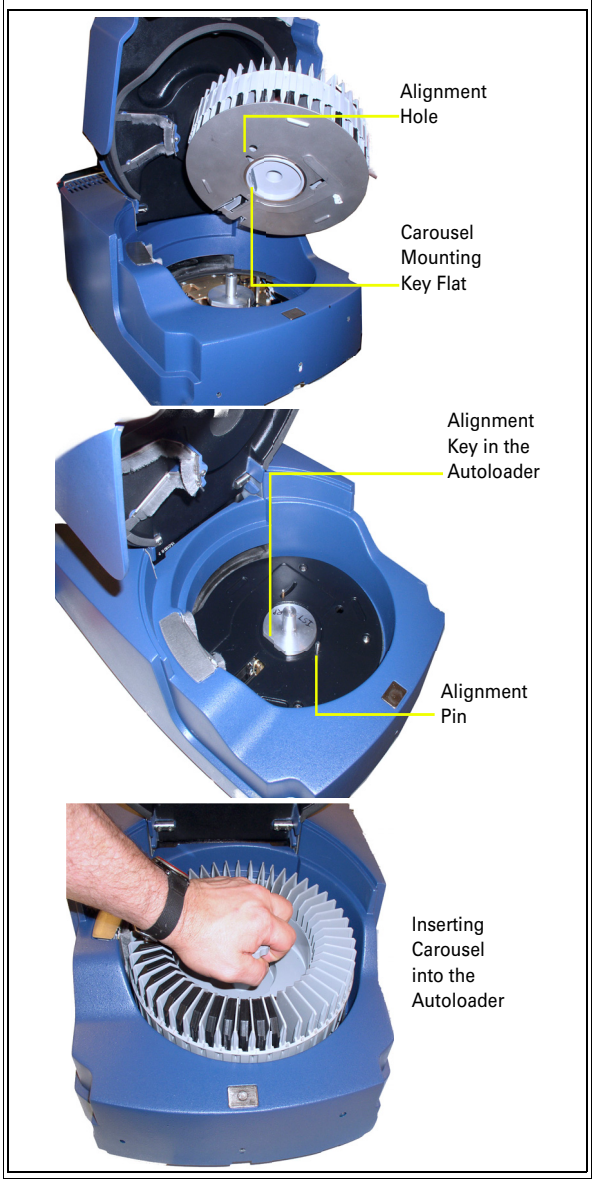
   Cartridges should be loaded into the carousel starting at position #1. Additional cartridges need not be contiguous. A run will stop after 48 cartridges OR when the same barcode is read within the same run.

Figure 229 Loading the array into the chip carousel. Each slot is numbered, 1 through 48, and each array can fit in only one orientation



3. Load the carousel into the AutoLoader by inserting the carousel into the AutoLoader and turning the carousel until the alignment pin seats into the alignment hole. (Figure 230)

Figure 230 Loading the array carousel into the AutoLoader



4. Turn the carousel clockwise until the carousel mounting key flat seats gently into the AutoLoader alignment key. You may have to turn the carousel several times before it will seat into the alignment pin and alignment key. When seated properly, the carousel will be flush with the AutoLoader housing.
5. Close the AutoLoader door. (Figure 231)

Figure 231 Inserting and turning the carousel. the carousel must be seated and flush with housing.

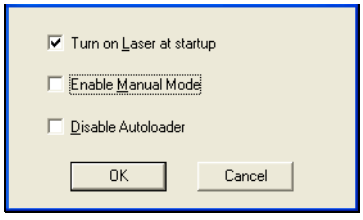
Note: The seating of the key flat is confirmed by a gentle falling of the carousel into the key.

Note: If all probe arrays have valid, associated barcodes, you can run the AutoLoader in auto-mode.

Note: If there exists an identical barcode within the database from an earlier AutoLoader run, and you want to rescan the current probe array with that same barcode, check the Allow Rescans box. This will create additional DAT files. The original DAT file WILL NOT BE OVERWRITTEN. A new DAT file is created, and the file name for the new file has an underscore and incremental number added to it, beginning with _2. If the AutoLoader encounters the same barcode within the same run, the run will terminate.

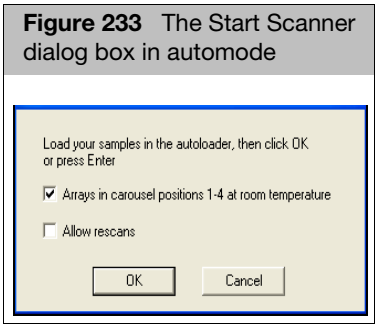
6. Start the GCC Scan Control software (see "Starting the GCC scan control software" on page 180).
7. Set the default settings.
   a. Click **Edit Options**.
   b. **Clear** the **Enable Manual Mode** check box.
   c. Click **OK**.

Figure 232 Scanner Options dialog box with Enable Manual Mode check box cleared



8. Click the **Start** button in the main tool bar; or
   Select **Scanner Start Scanner** from the menu bar.
   The Start window appears. (Figure 233)

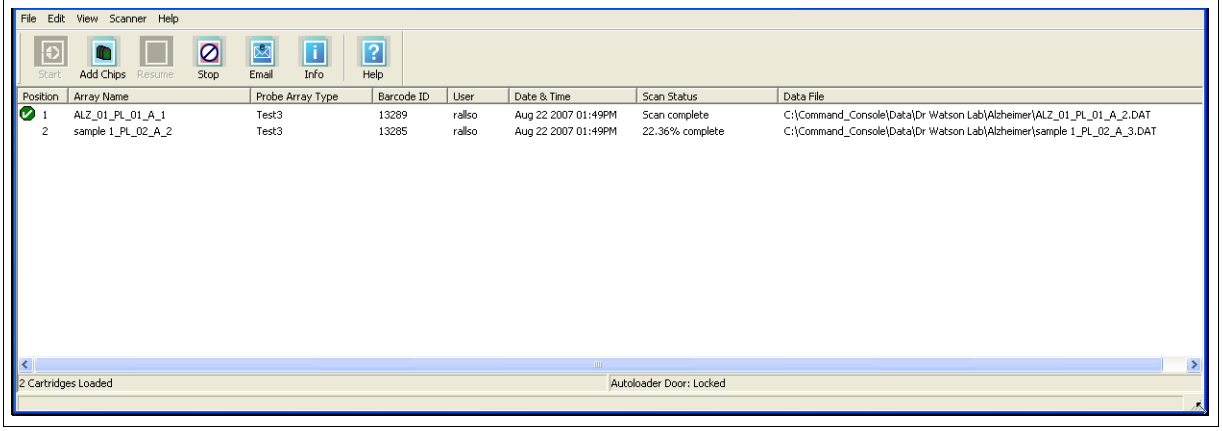
Figure 233 The Start Scanner dialog box in automode



   If you want to skip the warm-up period before scanning the first probe array, keep the default check in the **First four arrays at room temperature** box.

9. Click **OK** in the Start Scanner dialog box to start the run.
   - The AutoLoader blue indicator light will light up signifying that the AutoLoader door is now locked.
   - The carousel automatically homes itself and performs inventory to determine the number and position of cartridges present.
   - The scanning run begins. During the scan, the green light will flash, and the yellow light will be off.
   - The AutoLoader completes the autofocus operation before scanning each of the probe arrays. This takes approximately two to three minutes. The scanner cannot be stopped during this period.
   - The run will stop automatically when the last array is scanned.
   - At the completion of each scan, the GCC software will attempt grid alignment. If it is successful, the scan data will be automatically advanced to the Grid Alignment processing state.
     The progress of the scan data can be tracked using the Review Window of the GCC Viewer (see Chapter 9, "Using the GCC viewer" on page 267).
   - The progress of each scan is displayed in the Scan Status window (Figure 234).

Figure 234 Scan Status window during autoloader run.



- The window displays a list of the arrays as they are being scanned with the information displayed in the Status window (see "Status window information" on page 182)

After the scan is completed, GCC:

a. Saves the image data to an image file (*DAT).

b. Ejects the probe array.

c. Aligns a grid on the image to identify the probe cells.

d. Automatically computes probe cell intensities and saves the data to the cell intensity file (*CEL).

Note: You can track the progress of the grid alignment and cell intensity computation in the GCC Viewer.

Arrays with barcodes that are not associated with a Sample file and array will have a sample file created using Drop and Scan.

The AutoLoader will **skip** probe arrays if the AutoLoader encounters:

- Arrays with unreadable or invalid barcodes or without barcodes.
- Arrays that have been previously scanned if the **Allow Rescans** check box is cleared.

10. Close the GCC Scan Control software. This is the best way to shut off the laser.
11. Press the I/O button on the front panel to turn off the instrument.

Special scan options

The following sections describe various options for running the scan:

Drop and scan

The Drop and Scan feature lets you scan a set of GeneChip probe arrays without first creating a Sample (ARR) file for them. A Sample file is created automatically during Drop and Scan, with the probe array barcode used as the file name.

1. Start the GCC Scan Control software.
2. Start the scanner.
3. Load the arrays in the scanner.
4. Click the Start button.

   If the arrays have valid barcodes, they are scanned. The ARR, DAT, and CEL files are named using the barcode and placed in the designated Default folder.

   For more information about the Default folder, see:

   - "Default folders" on page 33
   - "Specifying a default folder" on page 90

   If the scanner cannot read the barcode, or if there are no library files on the system for chips with that part number, the chip is ejected and an error notice appears.

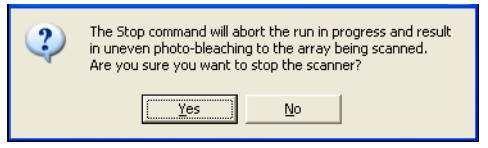
Stopping an AutoLoader run

The Stop button is only available after you have clicked the Start button. Click this button if you want to abort a scan or run in progress.

Note: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo-bleaching. This could potentially make the data from the array difficult to compare to other array data.

1. Click the **STOP** tool bar button  or select **Scanner Stop Scanner** from the menu bar.
2. At the prompt, click **Yes** to stop the scanner or **No** to elect not to stop the AutoLoader run.

Figure 235 Stop AutoLoader prompt



A window displays the message “The scanner will not stop until autofocus has finished.”

3. Click **OK**.

   After you stop a scan, the scanner automatically ejects the array.

Adding cartridges during a run

The software provides you with a button that will enable you to unlock the AutoLoader door and add additional probe array cartridges while in the middle of an AutoLoader run. You have two choices:

- To add cartridges immediately even while a scan is in progress (in which case the DAT file is discarded and replaced with a newly collected one after the AutoLoader run is resumed).
- To add cartridges after a scan has completed (in which case the DAT file is saved).

  Note: The Add Chips button is enabled only after the AutoLoader has started a run in automatic mode.

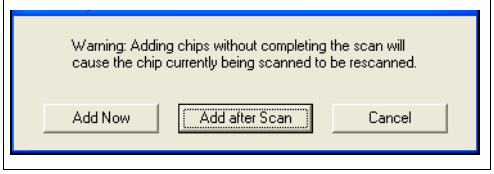
Interrupting a scan in progress

Note: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo-bleaching. This could potentially make the data from the array difficult to compare to other array data.

1. Click the **Add Chips** button  , or select **Run Add Chips** from the menu bar.

   The Add Chips Options dialog box opens. (Figure 236)

Figure 236 The Add Chips Options dialog box



2. Click **Add Now**.

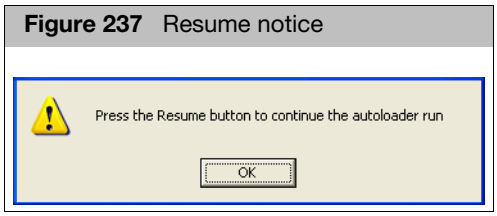
   The blue AutoLoader indicator light will turn off signifying that the AutoLoader door is now unlocked.

If a scan is in progress, the software will continue to record the scan. However, to avoid the possibility of generating a corrupt DAT file, it will discard that scan that was in progress when the door was opened.

3. Open the door and add probe array cartridges to the carousel.
4. Close the scanner door.

   The following window appears. (Figure 237)

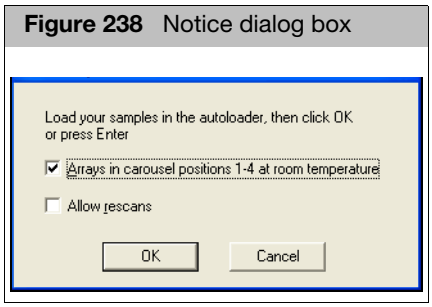
Figure 237 Resume notice



5. Click **OK.**
6. Click the Resume button; or select **Run Resume**.

   The Notice dialog box opens. (Figure 238)

Figure 238 Notice dialog box



7. Select the Allow Rescans option, if desired, then click **OK**.

   The blue AutoLoader indicator light turns on signifying that the door is locked. The software homes the carousel and inventories the number of present probe arrays. **The carousel then moves to that last previously scanned probe array (when the door was opened) and continues the scanning run by rescanning that probe array**.

   The array is rescanned and a new DAT file overwrites the previous DAT file.

IMPORTANT! Do not load an array into the same carousel position that was occupied by the array that had just been scanned, i.e., do not replace cartridges.

Adding chips without interrupting a scan

1. Click the **Add Chips** button, or select **Run Add Chips** from the menu bar.

   The Add Chips Options dialog box opens. (Figure 239)

Figure 239 The Add Chips selection buttons

2. Click **Add after scan.**

   The Interrupt After Scan Complete notice appears. (Figure 240)

Figure 240 Complete Scan notice

3. Click **OK**.

   The AutoLoader will wait until the current probe array has undergone the autofocus and scan procedures before unlocking the door.

   The blue AutoLoader indicator light turns off when the AutoLoader door is unlocked.

4. Open the door and add probe array cartridges.
5. Close the scanner door.

   The Resume Notice dialog box opens. (Figure 241)

Figure 241 Resume notice

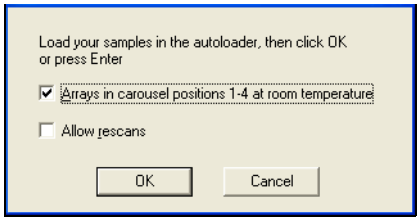
   The GCC status bar displays a “waiting to start” status.

6. Click **OK.**
7. Click the Resume  button; or

   Select **Run** → **Resume**.

   The Run Options dialog box opens. (Figure 242)

Figure 242 Run options dialog box



8. Select the Allow Rescans option, if desired, and click **OK**.

   The blue AutoLoader indicator light turns on signifying that the door is locked. The software homes the carousel and takes inventory of the probe array cartridges present. The carousel then proceeds to the next array position following the previously scanned probe array. The AutoLoader continues the run from that array position.

   Note: If you click the **Cancel** button in the Run Options dialog box, the AutoLoader will not resume the scan.

Scanning a Probe Array in Manual Mode

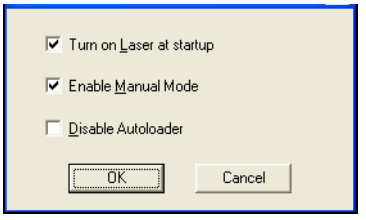
In the AutoLoader Automode, each probe array requires a valid barcode in order to be scanned. The manual mode feature enables you to scan one probe array at a time without the requirement of a barcode. This is useful if you must scan probe arrays that have invalid or absent barcodes.

1. Set the scanner options.
   a. From the Edit menu, click **Options**.

      The Scanner Options dialog box opens. (Figure 243)

   b. Check **Enable Manual Mode**.
   c. Click **OK**.

Figure 243 Scanner Options dialog box, Enable Manual Mode checked

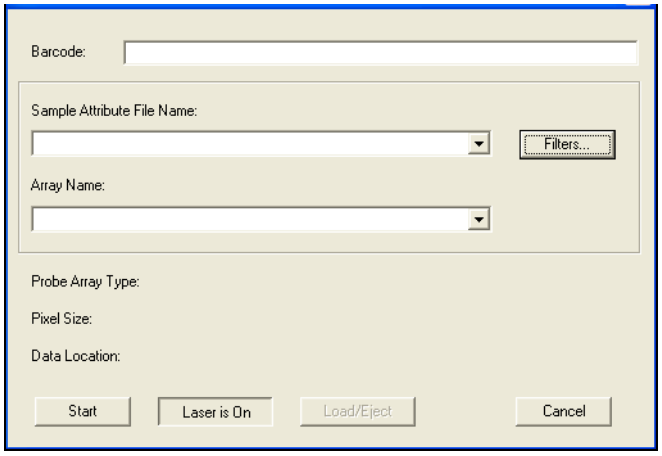


2. Click the **Start** button  ; or

   Select **Scanner Start Scanner** from the menu bar.

   The Scanner dialog box opens. (Figure 244)

Figure 244 Scanner Dialog box



At this point, you can choose from a number of options:

- You can click **Start** without selecting an array name. If your array has a valid barcode, the software will get the barcode from the array in the AutoLoader and select the correct Sample file and Array name.
- If your array has a valid barcode, you can scan the barcode on the probe array in to the barcode field. The software will retrieve the Sample Attribute File associated with the array.
- If your array does not have a valid barcode, you can manually select an array as described below:

– Select the Sample file name for the probe array you want to scan from the **Sample File Name** drop-down list.

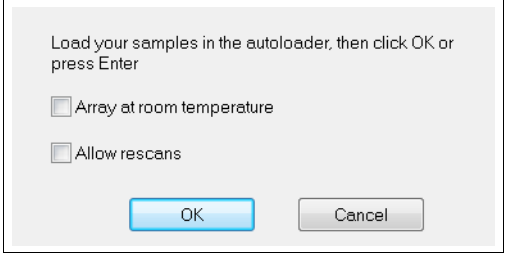
– Select the array name of the probe array to be scanned from the **Array Name** drop-down list.

The **Probe Array Type** field automatically displays the probe array type that was entered during experiment setup.

3. Click **Start** in the Scanner dialog box.

The Start dialog box appears. (Figure 245)

Figure 245 The Start Scanner dialog box



Note: If you want to skip the warm-up period before scanning the first probe array, keep the **Arrays at room temperature** check box marked as checked.

Note: You can eject or load an array by clicking on the Load/Eject button at any time except when the scanner is engaged in the autofocus operation or the scanning run.

4. Load the probe array into slot number 1.

   Note: The array slot at position number 1 is the only slot available in Manual Mode.

5. Click **OK** in the Start Scanner box (Figure 245) to start the autofocus routine. This takes approximately two to three minutes. The scanner cannot be stopped during this period.

   During the scan, the green light will flash, and the yellow light will be off.

   After the scan is completed, GCC:

   a. Saves the image data to an image file (DAT).
   b. Aligns a grid on the image to identify the probe cells.
   c. Automatically computes probe cell intensities and saves the data to the cell intensity (CEL) file.

      Note: You can view the status of the cell intensity computation in the GCC Viewer.

   d. Ejects the probe array.

Ejecting a probe array

The probe array will automatically eject after a run.

Using GCC with the AutoLoader disabled

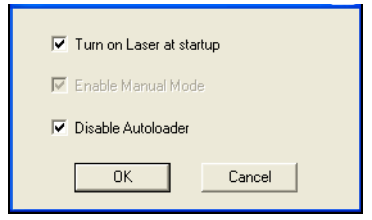
If you have a working scanner but the AutoLoader is not operating, you can still use the scanner, but you must check the Disable AutoLoader option in the Defaults window. This will disable the AutoLoader and enable you to use the scanner alone as you would in manual mode.

1. From the Edit menu, click **Options**.

   The Scanner Options dialog box opens. (Figure 246)

2. Check **Disable AutoLoader**.
3. Click **OK.**

Figure 246 Disable AutoLoader checked



A window will appear asking that you reboot the scanner.

Figure 247 Reboot notice

4. Press the scanner front panel I/O button once to turn off the scanner. Wait a few moments, the press the I/O button to turn on the scanner.
5. Open the AutoLoader door.
6. Manually load a probe array into the slot.
7. Close the AutoLoader door.
8. Scan the probe array in the same manner as the AutoLoader in manual mode. See "Scanning a Probe Array in Manual Mode" on page 210.

   After scanning the probe array, you must manually remove the probe array from the AutoLoader. See Steps 7 though 13 in "Manually removing a lodged probe array" on page 218.

Scanning four-color arrays

Four color scans are performed on GeneChip arrays that have been configured for use with four emission filters. The four emission filters are specified in the GCC scan parameters. when performing a multi-filter scan, GCC scans the array with different emission filters, using the order specified for the array.

A DAT file is created for each of the emission filter scans. To distinguish the different scans, GCC appends a suffix of A, B, C, or D to the DAT files. Different file naming conventions are used in the case of a rescan of an array, depending upon whether the array was manually loaded (see below) or loaded using the autoloader.

When running multiple scans on an array, the scanner performs autofocus only once, prior to the first scan. This is true whether the scans are performed as part of a four-color scan or as a re-scan.

Aborting a four-color scan with a manually loaded array

If scanning is aborted on a manually loaded array, the emission filter scan in progress continues until it is complete, and the DAT data for the completed scans are saved. When the scan is resumed, GCC autofocuses the scanner and then re-scans and re-creates a DAT file for each emission filter scan, overwriting the previously created DAT files.

Aborting a four-color scan when using the autoloader

If scanning is aborted on an array loaded using the autoloader, the emission filter scan in progress continues until it is complete, and the DAT data for the completed emission scans are saved. When the scan is resumed, GCC auto focuses the scanner and then re-scans and re-creates a DAT file for each emission filter scan. GCC does not overwrite the previously created DAT data, but creates a new set of DAT files, adding a suffix of “_nX” to the DAT file name, where n identifies the rescan number and 'X' is the letter assigned for the emission filter. A 4-color array scanned a second time will produce DAT files with the following suffixes: _2A, _2B, _2C, _2D.

Note: When using the "Add Chips Now" function of the autoloader, if the door is opened in the middle of a scan acquisition, GCC treats the scan as an abort request. After the emission filter scan in progress completes, scanning halts and the DAT and CEL files for the completed emission filter scans are saved. Upon resume, the GCC auto-focuses the scanner and rescans the array for each emission filter. To avoid the rescan of the array, it is recommended that the "Add Chips Later" function be used.

Autorotation: The AutoLoader is equipped with a heater to warm up the cartridges prior to scanning in order to reduce condensation and fogging of the probe array window. This autorotation routine is used for temperature stability but only after the AutoLoader run is complete or during a power failure as described below.

Autorotation

Autorotation occurs during a power failure only if the uninterrupted power supply (UPS) is included as an accessory. The UPS provides power to the scanner/ AutoLoader during a power failure. If the power fails during the scan of an array, that scan is completed and then the system turns off the heater and enters the autorotation mode to conserve power and cool the chips in the carousel. The system will also attempt to send an e-mail to notify the user of the power failure.

During an AutoLoader run, the carousel is rotating as the chips are processed to introduce the next array to the scanner, so autorotation is not needed. After the AutoLoader run is complete the heater is turned off and the carousel is rotated to get even cooling of the chips.

Terminating a scan run

The AutoLoader run will terminate under certain normal circumstances. Table 4 outlines under what conditions a scan run will or will not terminate.

Table 4 Summary of scan run termination conditions

The scan run will terminate if:	The scan run will not terminate if:
You press the Stop button. Caution: If you stop the scanner while a probe array is in the process, you will lose all scan information from that probe array. If you rescan the array, it may be affected due to uneven photo-bleaching. This could potentially make the data from the array difficult to compare to other array data.	You check Allow Rescans box. When the AutoLoader encounters a probe array that was previously scanned in an earlier run, it will rescan that probe array and will create additional DAT files (DAT1, DAT2, etc.).
The AutoLoader detects a probe array with the same barcode in the current run, i.e., in the currently loaded carousel. The probe array will not be rescanned.	You clear the Allow Rescans box. When the AutoLoader encounters a probe array that was previously scanned in an earlier run, it will log the probe array but will not rescan it. It will continue the run.

Table 4 Summary of scan run termination conditions

The scan run will terminate if:	The scan run will not terminate if:
The AutoLoader detects 48 scanned cartridges in the same run.	You click the Add Now button. The AutoLoader door will unlock to accept new probe array cartridges. The scan in progress will complete. When you close the door and continue, the AutoLoader will home, take inventory and move to the same probe array that was in the process of being scanned when the door was opened. It will discard the earlier DAT file and rescan that probe array. Note: this has nothing to do with the Allow Rescans check box.
	You click the Add After Scan button. The AutoLoader door will wait until the scan in progress is complete then unlock the door. When you close the door and continue, the AutoLoader will home, take inventory and move to the next probe array from that which was in the process of being scanned when the door was opened.

Troubleshooting

Troubleshooting tips are given in the table below and in the following sections:

- "AutoLoader error messages" on page 216
- "Manually removing a lodged probe array" on page 218

Problem	Possible Cause	Corrective Action
No image when scanning	• Power off or cable loose	Check all connections and power.
	• Loss of laser power	Contact technical support.
	• Image display disabled	Enable image display
Intermittent problems scanning	• Loose cable	Check all rear connections.
Scanner fails with probe array inside	• Power failure	Manually extract probe array. Check all connections to scanner. Turn scanner on, restart software.
Carousel does not automatically home	• Check for stuck array • Carousel not seated on D ring • Alignment Pin not engaged in Carousel • Door is open or ajar • Door is open when blue LED is off.	
Carousel does not rotate	• Door is open or ajar • System is warming up, array in heater • Carousel not seated on D ring • Alignment Pin not engaged in Carousel • Laser in Scanner is warming up. GCC has Start grayed out in this case	
Carousel misses next array	• Array UP sensor not working, call technical support.	
Stuck array		See "Manually removing a lodged probe array" on page 218
AutoLoader freezes up	• Door is open or ajar	

Problem	Possible Cause	Corrective Action
AutoLoader overheats	• Heater Failure • TE failure • TE hot fans vent blocked	Call technical support. Call technical support.
Autofocus routine fails to conclude		• Try to rescan array. • Check for salt on chrome border. If still error, call technical support.
The array does not descend into scanner.	• Carousel not seated correctly • Door is open or ajar • Heater is waiting until array is at temperature.	

AutoLoader error messages

The following error messages indicate a serious malfunction of the scanner with AutoLoader. Your probe arrays, or the data generated from them, may be at risk. You should shut down the AutoLoader and remove the carousel. Do not continue to use the AutoLoader in Automode and call technical support. However, if the AutoLoader appears to be operating normally, you can continue to use the AutoLoader in Manual Mode. See "Scanning a Probe Array in Manual Mode" on page 210.

HEATER_LOW	“Warning: The warming chamber temperature is low. Refer to the troubleshooting guide.”
COLD_CHAMBER_LOW	“Warning: The cold chamber temperature is low. Refer to the troubleshooting guide.”
COOL_HOTSIDE_HIGH	“Warning: The cooler hot-side temperature is high. Refer to the troubleshooting guide.” Note: Before calling technical support, check around the ventilation vents to ensure that nothing is blocking them.
COLD_CHAMBER_HIGH	“Warning: The cold chamber temperature is high. Refer to the troubleshooting guide.” Note: Before calling technical support, check the AutoLoader door to ensure that it is not open.
HEATER_HIGH	“Warning: The warming chamber temperature is high. Refer to the troubleshooting guide.”

E-mail messages

If the e-mail system is enabled, the instrument control software sends an e-mail alert for conditions that may occur during an AutoLoader run.

Note: For information on enabling the email system see Appendix E, "Notification e-mails" on page 367

In case of a fatal error:

1. The software sends an e-mail to the specified set of e-mail addresses or to the Outlook distribution list.
2. The software provides you with the ability to send an e-mail without your intervention.

3. Each e-mail message contains the following information:
   a. Date and Time
   b. Scanner ID
   c. All experiment information displayed in the status window. You select error messages to be sent in the e-mail configuration.

Manually removing a lodged probe array

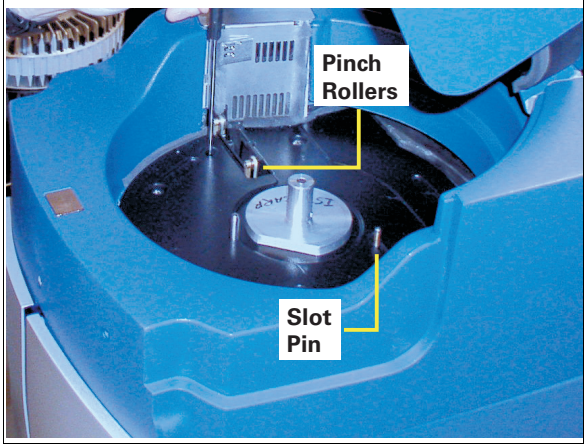
In the event that a probe array becomes lodged in the array transport mechanism, follow the procedure outlined below.

1. Turn the AutoLoader off and remove the power cord from the back of the unit.
2. Open the AutoLoader door on top of the unit.
3. Remove the carousel from the system. (Keep cartridges in carousel at proper temperature while recovering the array still in the scanner).
4. Remove the hole plug, which is just in front of the array slot in the base piece of insulation. In Figure 248, the screwdriver is inserted into this hole.

Figure 248 Locating the rescue hole

5. Using a standard, flat (-) screwdriver, (13-0257) gently slide it down through the hole making sure not to damage the shaft and spring that are protruding into the hole. When the screwdriver stops, it should be in contact with the scanner Y stage screw. Slowly turn the screwdriver until you feel it engaging the slot on the screw of the scanner Y stage.
6. Slowly turn the screw clockwise until it hits a hard stop and cannot turn further. (Do not try to turn it further or use excessive force because it will break the Y stage in the scanner). The Y stage has now ascended to its maximum position.
7. Using your fingers, slowly slide the slot pin, which is sticking through the slot in the base piece of insulation, to the right until it stops. You should see the little pinch rollers near the array slot close a little as you do this. (Figure 249)

Figure 249 Pinch rollers and slot pin



8. Insert a 3/16” hex driver (13-0255) into the hole that is located on the front of the AutoLoader housing on the left. You should feel it engage a coupling. (Figure 250)

Figure 250 Finding the coupling

9. Turn the hex driver counter clock wise until you see the array appear through its opening. (The array should stay up if you stop turning the hex driver). If you don't see the array after turning the hex driver ten seconds go to step 11.

10. Grab and hold the array with your fingers. Using your other hand slowly slide the slot pin (Step 7) back to the left. This should open up the pinch rollers. Pull the array out.

    If you do not see the array after turning the hex driver for 10 seconds, stop.

11. Using tool (13-0256) (Figure 251) with the hook down and toward the back, slide it vertically down against the front of the array opening, about 1.5 inches. (There is a small groove made for this tool in the middle of the front array guide).

Figure 251
Tool

12. Pull the top finger grip of the tool toward the front of the unit, and then pull it up while still putting pressure towards the front. The array should come up with the tool. When you see it, grab the array and pull it out of the unit.

    If you cannot get the array out after doing this procedure, call technical support.

13. Put the hole plug back into the hole in the base piece of insulation.
14. Plug the scanner back in and turn it on.
15. Load the carousel after the scanner boots up.

    If cartridges continue to become lodged in the AutoLoader, you should call technical support

GCS3000 with AutoLoader specification

GCS3000 with AutoLoader Specification Table

Table 5 Item	**Table 6** Parameter	**Table 7** Value
Weight	Shipping	approx 115 pounds (52.2 Kg)
	Free-standing	approx 100 pounds (45.4 Kg)
Dimensions	Width	~13.25 in.
	Depth	~21.25 in.
	Height	~32 in.
Power	Voltage Current Line Frequency.	100 - 240 V ~ 4 - 2 A 50 - 60 Hz
Working Environment	Temperature	59°F-85°F (15°C-30°C)
	Humidity	10-90% Non-condensing
	Clearance	2 in. (5 cm) on side, back 12.5 in. on top
	Pollution Degree	2
	Installation Category	II
	Altitude	<2000m
Electrical Supply	Provide voltage, frequency or power rating per unit label	
Main Supply Voltage Fluctuations	Are not to exceed ±10% of the nominal supply voltage	

Regulatory

This device complies with Part 15 of FCC Rules (Table 8). Operation is subject to the following two conditions: (1) This device may not cause harmful interference, and (2) This device must accept any interference received, including interference that may cause undesired operation.

This device complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007.

This Class A digital apparatus meets all requirements of the Canadian Interference-Causing Equipment Regulation.

Cet appareil numérique de la classe A respecte toutes les exigences du Règlement sur le matériel broullier du Canada.

Table 8 Regulatory Certifications

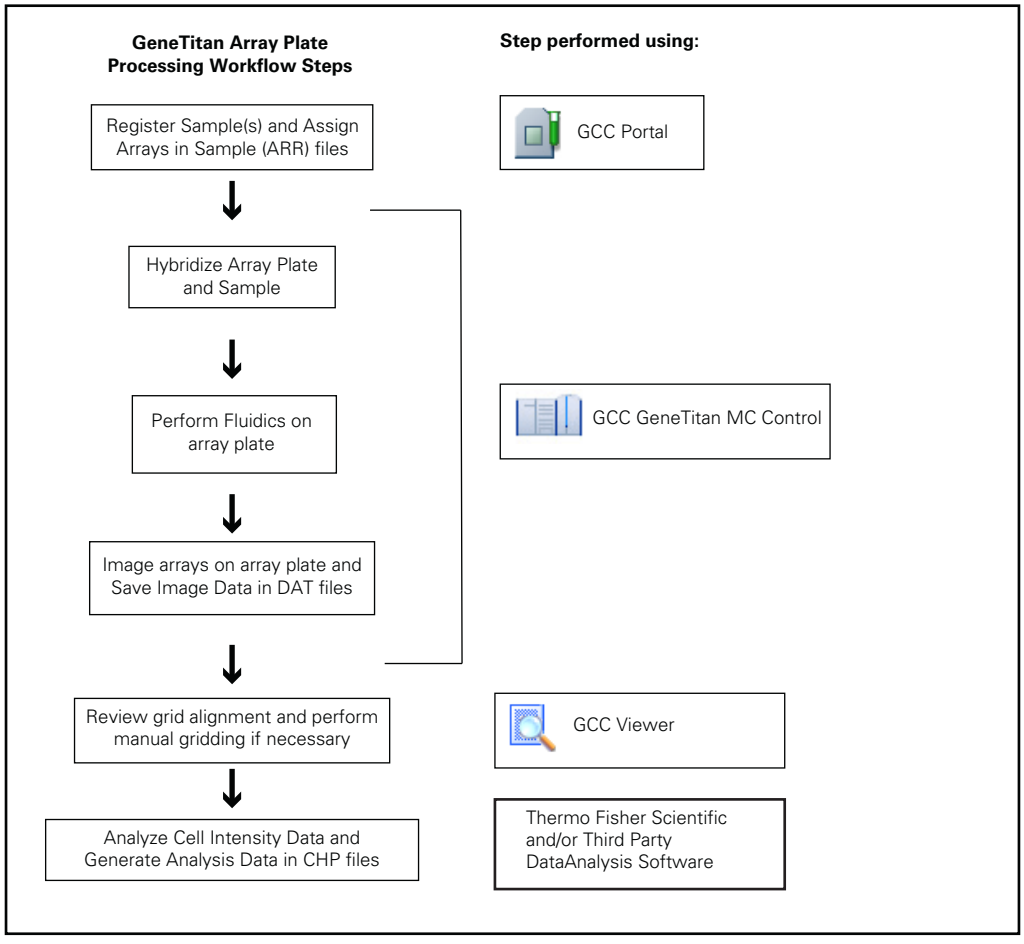
Regulatory Agency	Certification
CE	
Class 1 Laser Device	Complies with EN 60825-1:2007 Complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007
Hand held barcode reader is a Class 2 laser device	Complies with EN 60825-1:2007 Complies with FDA performance standards for laser products except for deviations pursuant to Laser Notice No. 50, dated June 24, 2007
	Compliant with directive 2002/96/EC (WEEE)

8 Controlling the instruments

The GeneTitan MC instrument array plates need to be run through the following steps (within the array plate processing workflow), as shown in Figure 252.

- Hybridization
- Washing and Staining
- Imaging

Figure 252 Recommended Array Plate Processing Workflow for GeneTitan System



GeneTitan array plates are processed using the GeneTitan Multi-Channel (MC) instrument, for genotyping and expression array plates.

There are differences in the workflows for genotyping array plates and expression array plates. This chapter describes the functions of GeneTitan Instrument Control that are common to both genotyping and expression array plates:

- "GCC GeneTitan instrument control software"
- "GCC GeneTitan scanner"
- "The GeneTitan MC instrument"
- "Overview of the GeneTitan workflow"
- "Tracking the array plate through the workflow"
- "Aborting a run"
- "Unload plates"
- "Using the wash-scan-resume workflow"
- "Using the wash only workflow"
- "Drop and scan with array plates"
- "Insufficient disk space notice"
- "Resetting the lamp life clock"
- "Computer practices, maintenance and troubleshooting"

Information specific to Expression Arrays is given in the Expression Assay Manuals.

Information specific to genotyping array plates is given in Axiom Genotyping Assay User Guide (P/N 702830).

See the GeneTitan Multi-Channel Instrument User's Guide (PN 08-0308) for a a detailed description of the instrument itself.

GCC GeneTitan instrument control software

The GCC GeneTitan Instrument Control software is used to control the GeneTitan Instruments.

Note: A computer used as a GeneTitan workstation requires a user account with specific privilege settings. In addition, some of the other features of Windows 10 Enterprise 2016 LTSB must be set up in particular ways or disabled to avoid causing problems when running GeneTitan IC software. The workstation is initially set up for use with GeneTitan has a default user account with these privileges and features already set.

IMPORTANT! If the GeneTitan workstation becomes unstable during a workflow the cost of an aborted workflow and replacement plates is substantial. To avoid this, it is recommended you Rebooting the instrument control computer weekly and follow the procedures described in "Computer practices, maintenance and troubleshooting".

Starting

1. Click the GCC GeneTitan Instrument Control icon  in the GCC Launcher.

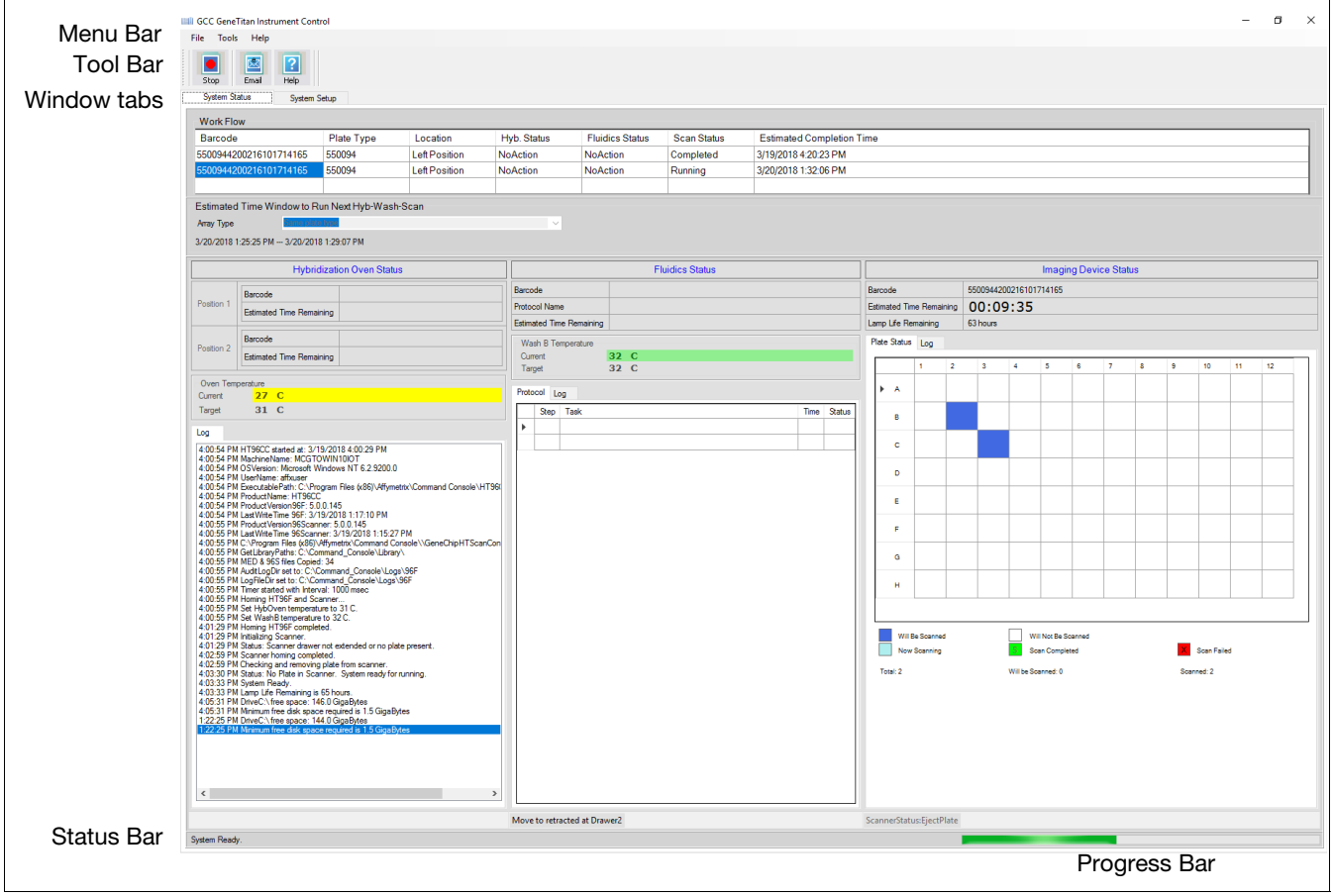
   or

   Click the **Start** → **Thermo Fisher Scientific** → **Command Console GCC GeneTitan Control.**

   The GCC GeneTitan Instrument Control window opens.

   See Figure 253 for 96 array plate GCC GeneTitan Instrument Control window example.

Figure 253 System Status window tab

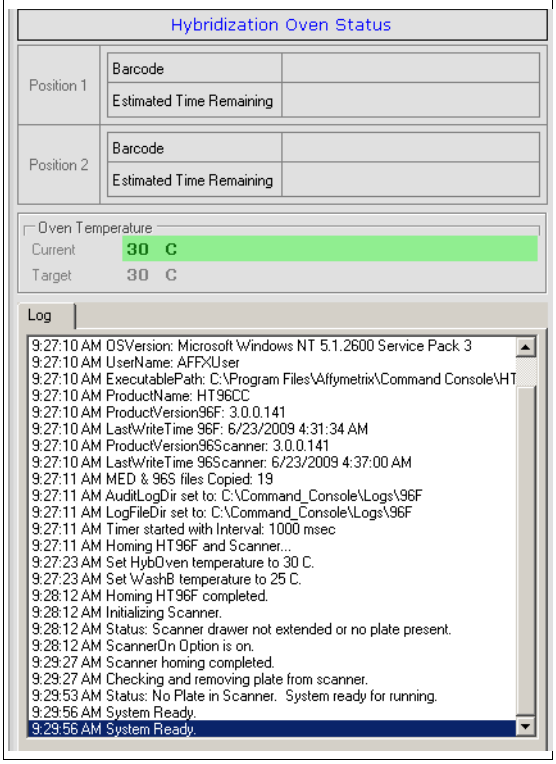


The software goes through the initialization process and starts the GeneTitan instrument.

You can track the initialization process in the Hybridization Oven Status pane (Figure 254).

After the initialization is completed, **System Ready** is displayed in the log, and you can display the Setup tab.

Figure 254 Hyb Oven log with System Ready notice



The following notices may appear:

- **Lamp Life setting** (see "Resetting the lamp life clock")
- **Insufficient Disk Space** (See "Insufficient disk space notice")

Software components

- **Menu bar:** Provides access to IC functions.
- **Tool bar:** Provides buttons to access frequently used functions.
- **System Setup/System Status tabs:**
  - "System status window tab": Use to track the progress of array plates through the workflow.
  - "System setup window tab": Use to set up the GeneTitan Instrument for different workflows.
- **Status bar and Progress bar:** Displays information about the status of the GeneTitan Instrument and the workflow in progress.

Tool bar buttons

The **Stop** button is used to abort the array process. If there are two or more plates running in the instrument, the software will prompt you to select which process is to be aborted. See "Aborting a run".

The **Email** button opens the GCC Email Configuration File Editor, which enables you to send email messages about the instrument status. See Appendix E, "Notification e-mails" for more information.

The **Help** button opens the GCC Online help file.

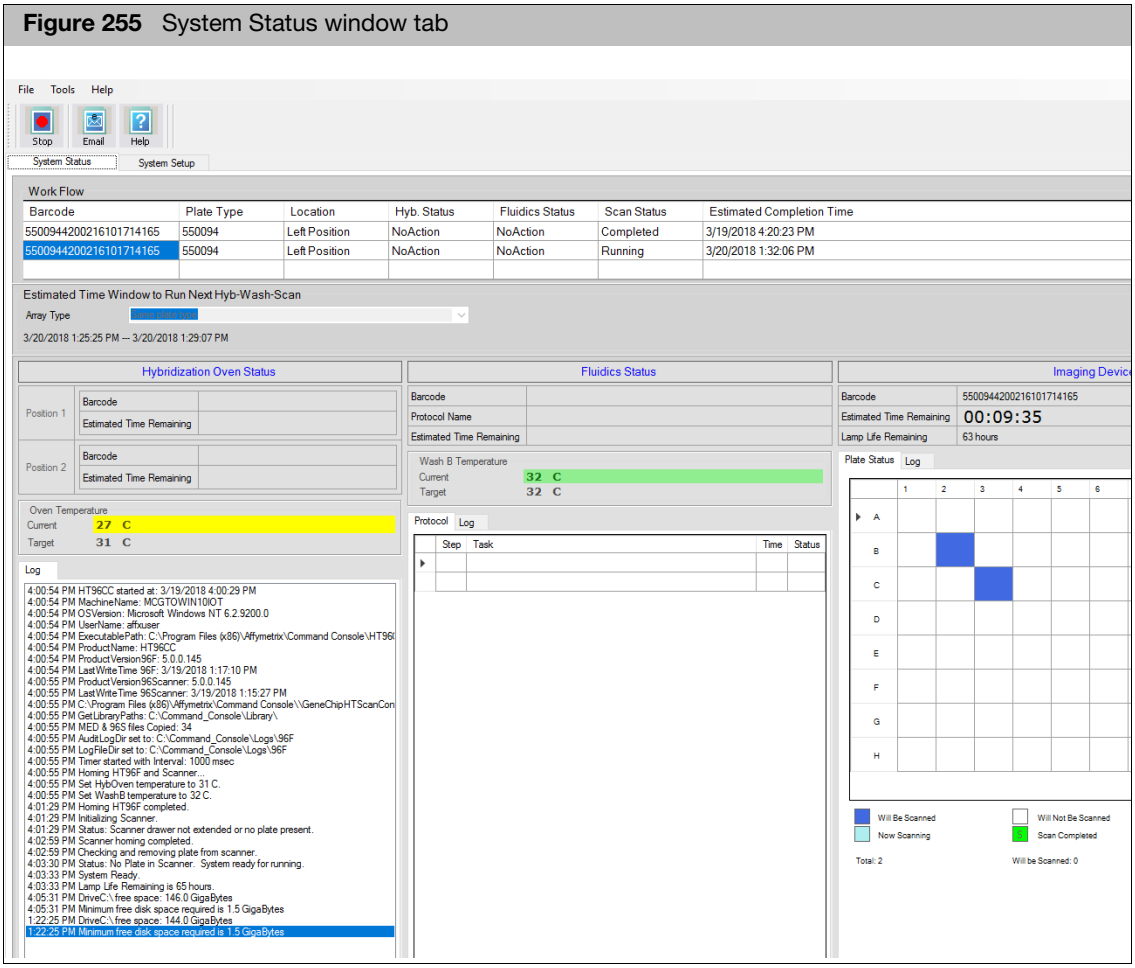
System status window tab

The System Status window tab (Figure 255) displays the progress of any currently loaded array plate(s) and features the following sections:

- Workflow
- Hybridization Oven Status
- Fluidics Status
- Imaging Device Status

The System Status tab is described in more detail in "Tracking the array plate through the workflow".

Figure 255 System Status window tab

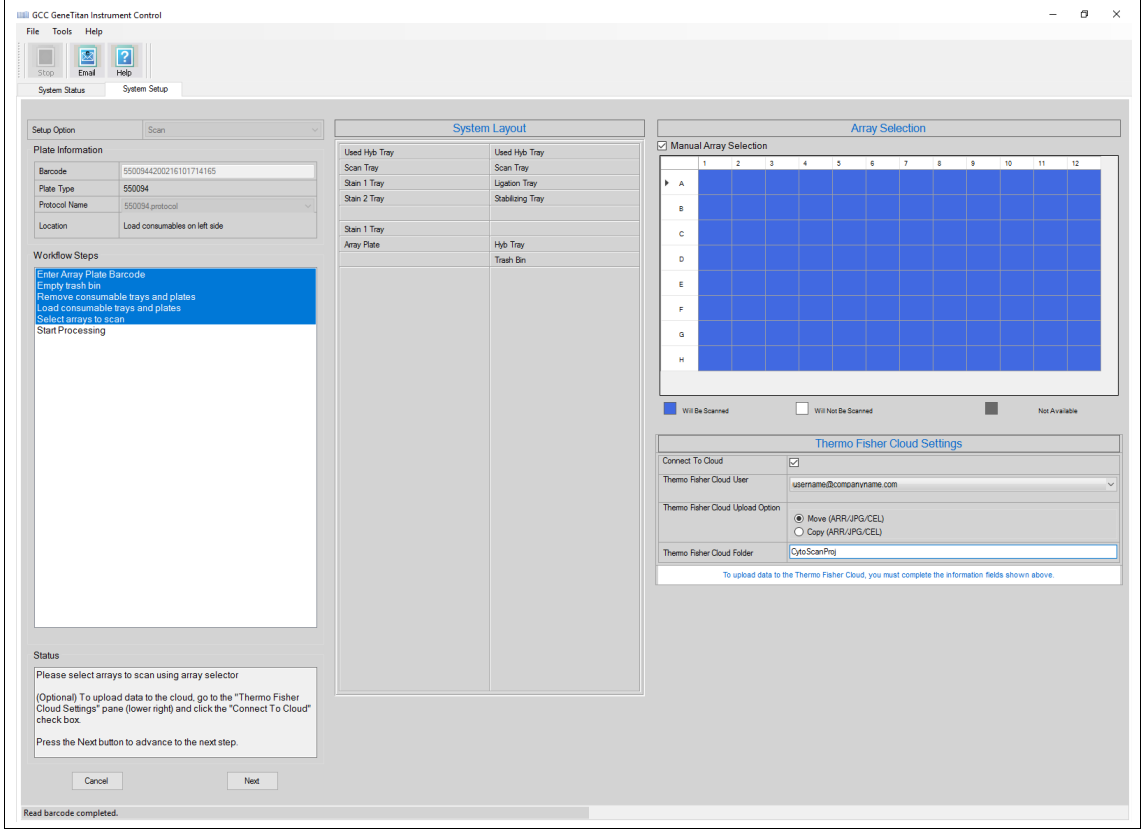


System setup window tab

The System Setup tab is used to:

- Specify the type of workflow you want to perform.
- Enter a barcode for the array plate being processed.
- Unload and load trays and plates.
- Select arrays on the array plate for imaging.
- Upload data results to the Thermo Fisher Cloud.

Figure 256 System Setup window tab for genotyping array plates

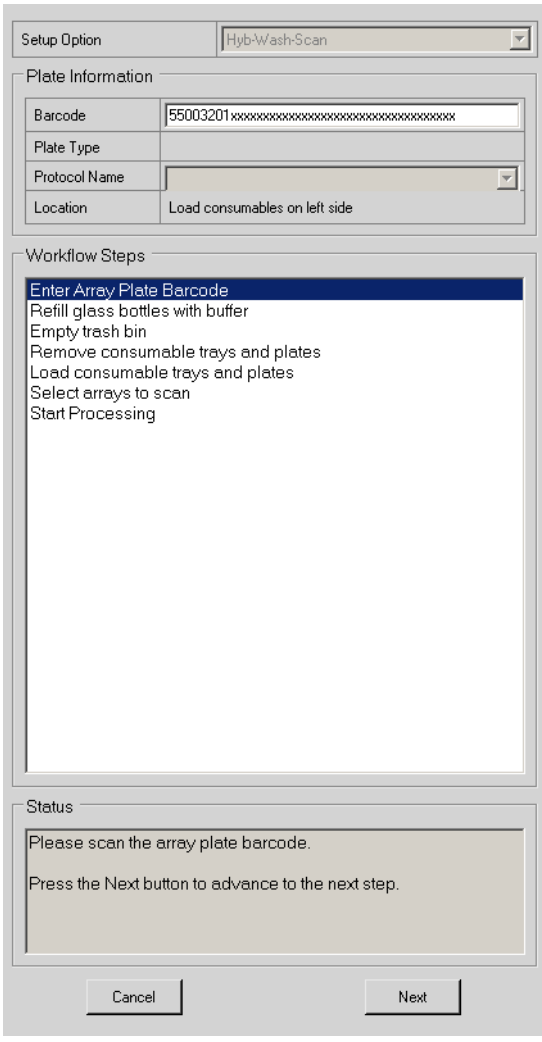


The System Setup window tab features four panes/sections:

- **System Setup:** Use to enter essential information and track progress of the setup and loading of the array plate and trays.
- **System Layout:** Indicates the drawers where different trays and array plates should be loaded. **Note:** The system layout changes based on whether Genotyping or Expression arrays are being processed.
- **Array Selection:** Enables you to select individual arrays on the array plate for imaging.
- **Thermo Fisher Cloud Settings:** Upload data results to the Thermo Fisher Cloud.

System setup

Figure 257 Setup Option pane



The Setup Option pane (Figure 257) has the following controls and displays:

Setup Options [drop-down meu]	Select from the following workflow options: • Hyb-Wash-Scan • Hyb-Wash • Wash-Scan • Wash-Scan-Resume • Wash Only • Scan • Unload Plates See "Running a series of array plates" for more information.
Plate Information	
Barcode	Barcode of the array plate.
Plate Type	Array Plate type.
Protocol Name	Name of protocol used for array plate processing.
Location	Side of drawer to load consumables.
Workflow Steps	Lists the steps to be performed during the operation.
Status	Displays information on the specific step to be performed, with • The plates and trays that need to be removed or placed. • The drawer position the plates and trays should be place in.
Cancel	Cancels the setup.
Next	Proceeds to the next step (not displayed when performing a step that requires you to press the **Confirmation** button on the front of the instrument.

System layout

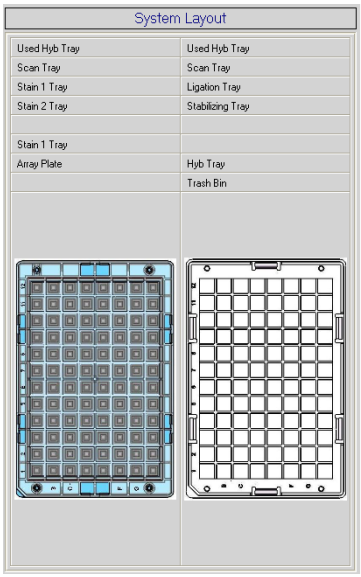
The System Layout pane (Figure 258) displays:

- Schematic view of the drawers to be loaded
- Indication of plate/tray position in drawer

  Note: Different reagent trays are loaded when processing genotyping array plates and expression array plates. The correct trays are selected for display when the array barcode is entered, as shown in the figure below.

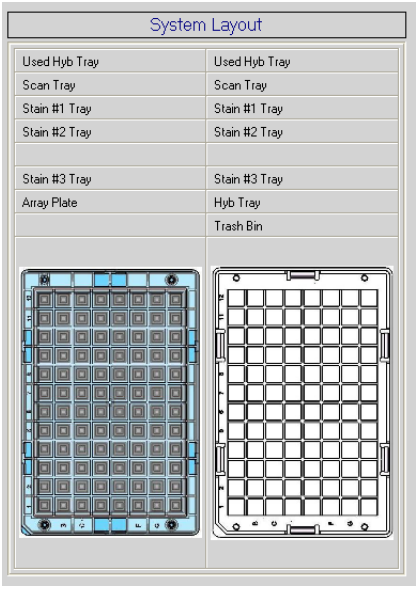
Figure 258 System Layout pane for genotyping (96 and 384) and expression arrays (96 only)

For genotyping arrays (96)



For genotyping arrays (384)

For expression arrays (96)



IMPORTANT! When running a series of array plates through the instrument, you must be careful to remove and load the proper array plate and trays and pay careful attention to the software prompts that tell you which side of the open drawer to remove or place a plate or tray.

Array selection

Figure 259 Array Selection (96- and 384-Array Plate layouts shown)

The Array Selection pane (Figure 259) displays the arrays to be scanned on the array plate:

- Manual array selection check box
- Plate Layout indicator, where you can:
  - Review the arrays available on the array plate.
  - Determine which are to be scanned.
  - Manually select arrays to be scanned on the plate. **Note:** By default, all arrays are selected for imaging.

The array selection process is described in the instructions for loading array plates in:

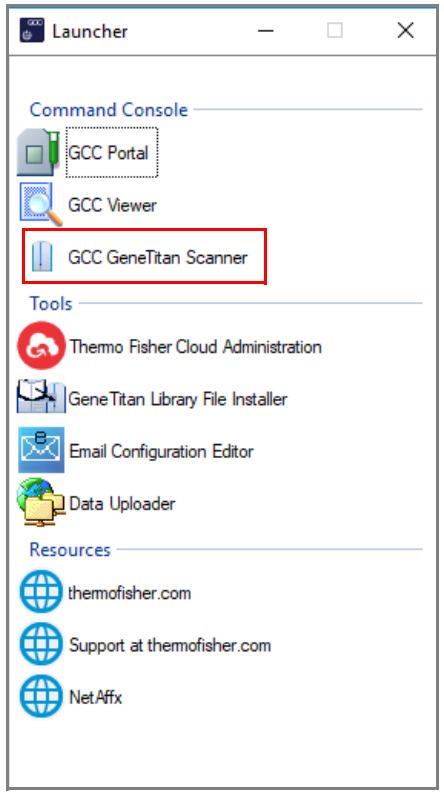
- Expression Assay Manuals
- Axiom Genotyping Assay User Guide (P/N 702830)

GCC GeneTitan scanner

1. Click **Start** →**Thermo Fisher Scientific** → **GCC Launcher** or double-click the **GCC Launcher** shortcut on the desktop.

   The Launcher window appears. (Figure 260)

Figure 260 GCC Launcher menu - GCC Standalone Scanner Control



Command Console

- **GCC Portal** (See "GCC portal home page")
- **GCC Viewer** (See Chapter 9, "Using the GCC viewer")
- **GCC GeneTitan Scanner** (See "Launching the scanner")

Tools

- **Thermo Fisher Cloud Administration** (See "Monitoring an instrument remotely")
- **GeneTitan Library File Installer** (See Appendix D, "Installing library files and scripts")
- **Email Configuration Editor** (See Appendix E, "Notification e-mails")
- **Data Uploader** (See "Scheduling auto-uploads")

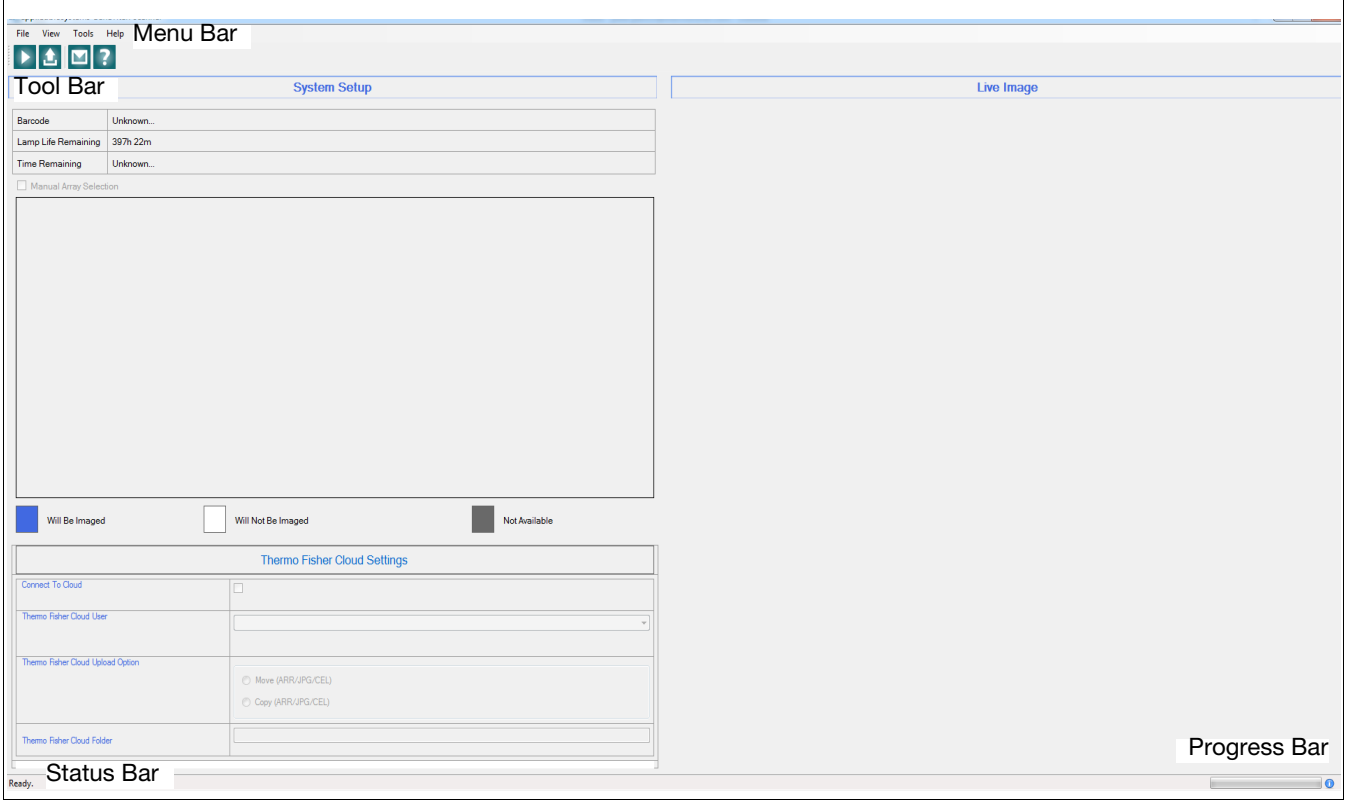
Resources

- **thermofisher.com** (Home page)
- **Support at thermofisher.com** (Services and support page)
- **NetAffx** (Home page)

Launching the scanner

1. Click **GCC GeneTitan Scanner**.
   The following window appears. (Figure 261)

Figure 261 GeneTitan Scanner - Main window



GeneTitan Scanner window options

- **Menu bar:** Provides access to the scanner functions.
- **Tool bar:** Provides the following buttons:
  - = **Start**: Starts the scan process.
  - = **Load**: Loads the plate into the scanner.
  - = **Stop**: Aborts a scan in process.
  - = **Email**: Opens the GCC Email Configuration File Editor. See Appendix E, "Notification e-mails" for more information.
  - = **Help**: Opens on-line help.
- **Barcode:** Displays the barcode of the plate.
- **Lamp Life Remaining:** Remaining lamp life hours.
- **Time Remaining:** Time remaining until the plate is fully processed and complete.

- **Status and Progress bars:** Displays status of the GeneTitan instrument and the workflow in progress.

Using the scanner

1. Click the **Start** button.

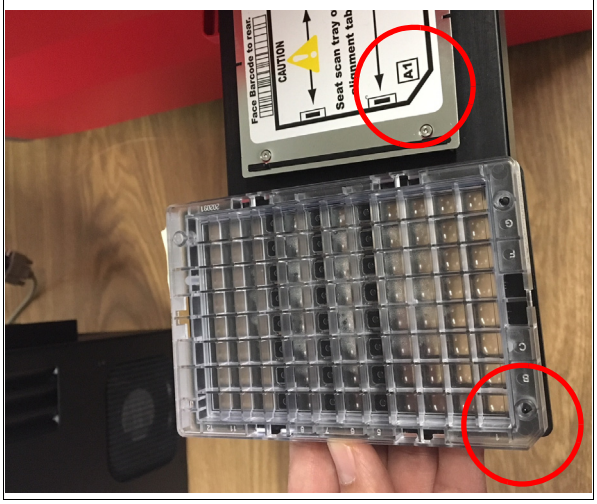
   After a few moments, its side door opens and a drawer slides out. (Figure 262)

Figure 262 Scanner drawer

A message appears (lower right) prompting you to place the plate onto the drawer.

2. Place the plate on the drawer making sure its orientation is correct (Figure 263) and the drawer's pegs match up correctly with the plate's bottom peg holes.

Figure 263 Plate to drawer orientation

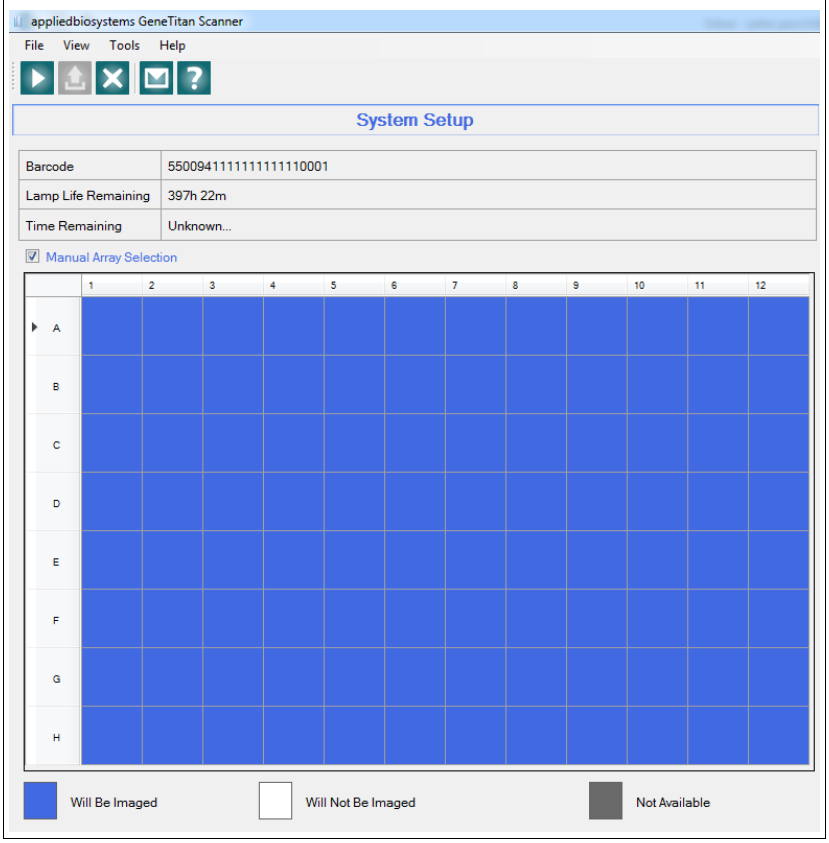


3. After placing the array plate onto the drawer (Figure 264), click the **Load** button.

Figure 264 Scanner drawer

The drawer retracts back into the scanner and the side door closes. After a few moments the barcode is detected and array pane populates, as shown in Figure 265.

Figure 265 Populated System Setup pane



Note: The following notices may appear:

– **Lamp Life setting** (refer to"Resetting the lamp life clock")

– **Insufficient Disk Space** (refer to "Insufficient disk space notice")

4. Click to select the wells you want to scan, as the **Manual Array Selection** check box is checked by default.
5. Optional: If you want to have your scanned data uploaded to the Thermo Fisher Cloud, click the **Connect To Cloud** check box now.

IMPORTANT! You cannot add a user(s) from the GCC Launcher → Thermo Fisher Cloud Administration window (page 37) while the scanner application is open.

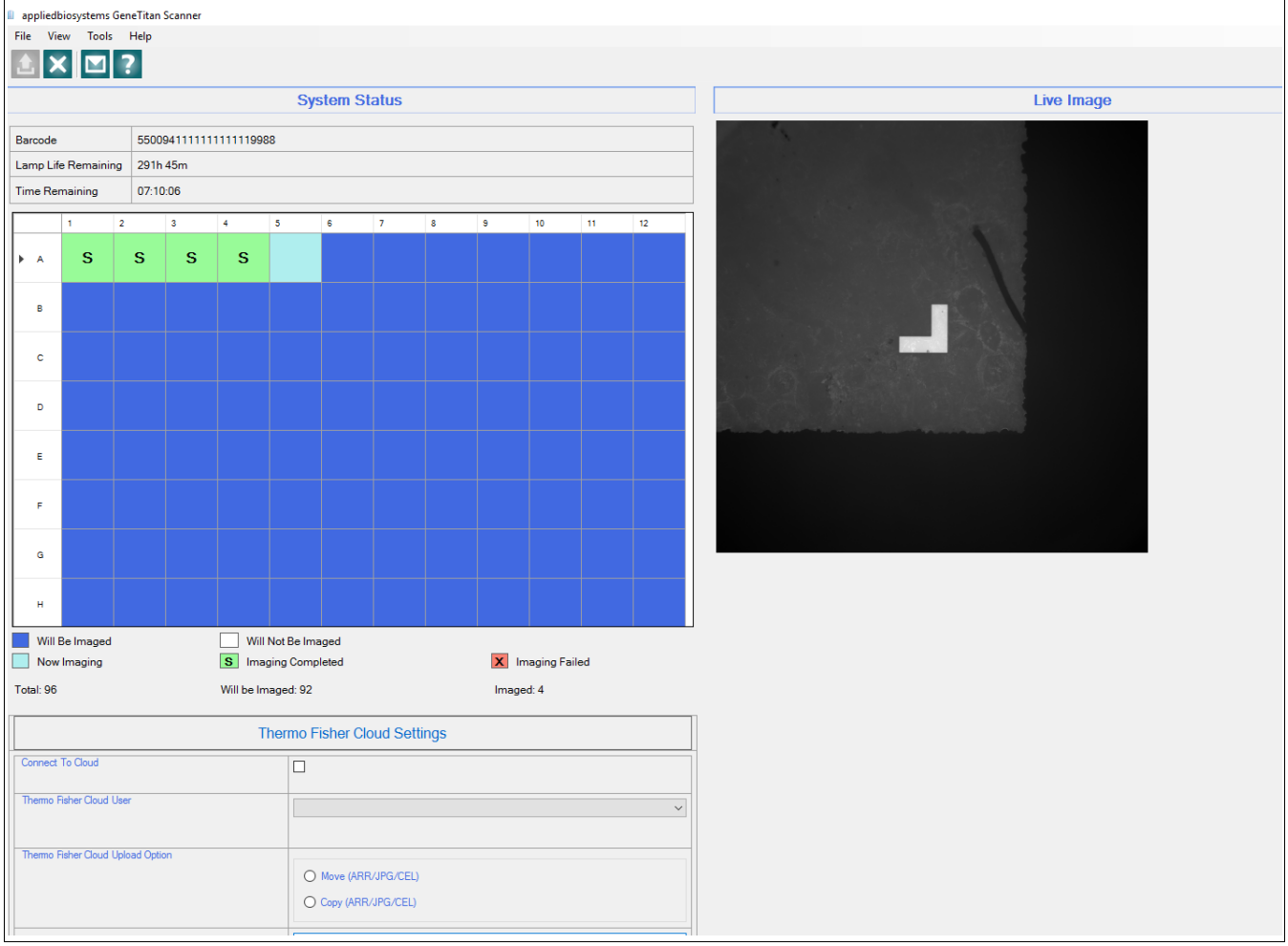
---

6. Click the **Start** button.

   A message appears confirming if you want to continue.
7. Click **OK** to acknowledge the message.

   After several minutes, the GeneTitan Scanner window populates, as shown Figure 266.

Figure 266 GeneTitan Scanner - populated example



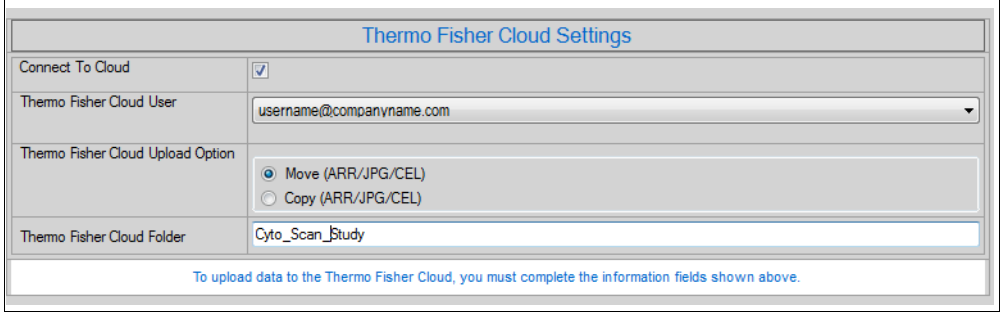
Thermo Fisher cloud settings (optional)

IMPORTANT! To use this option, you must have a Thermo Fisher Cloud account. To register, see "Creating a cloud account".

Make sure you have added the appropriate user account(s), as detailed in "Adding users".

Thermo Fisher Cloud Settings are not applicable for the data registered on network data roots.

Figure 267 Thermo Fisher Cloud Settings pane



Do the following to upload your completed data to your Thermo Fisher Cloud account:

1. Click to check the **Connect To Cloud** check box.
2. From the drop-down list, select a Thermo Fisher Cloud User.
3. Select a Cloud upload option.
   - **Move** - Uploads your files to the cloud. CEL and JPG files are removed from your local drive, while copies of ARR, DAT, and AUDIT files are retained. (Recommended)
   - **Copy** - ARR, JPG, CEL, and AUDIT files are copied and uploaded to the cloud. The original files remain on your local drive.
4. Enter a name for your Cloud folder.
5. Click **Next**.

   Your newly uploaded folder and data now resides on your cloud account's Data Connect web page (left pane/folder view), as shown in "Using the cloud to share data results".

The GeneTitan MC instrument

Overview

The GeneTitan MC instrument is designed to serve medium to high throughput customers. This system supports 16, 24, and 96-format high throughput array plates and will support future array plate formats. The system integrates a hybridization oven, a fluidics station, and an imaging device.

Refer to the GeneTitan Instrument User Guide (P/N 08-0296) for more information.

GeneTitan Multi-Channel (MC) instrument

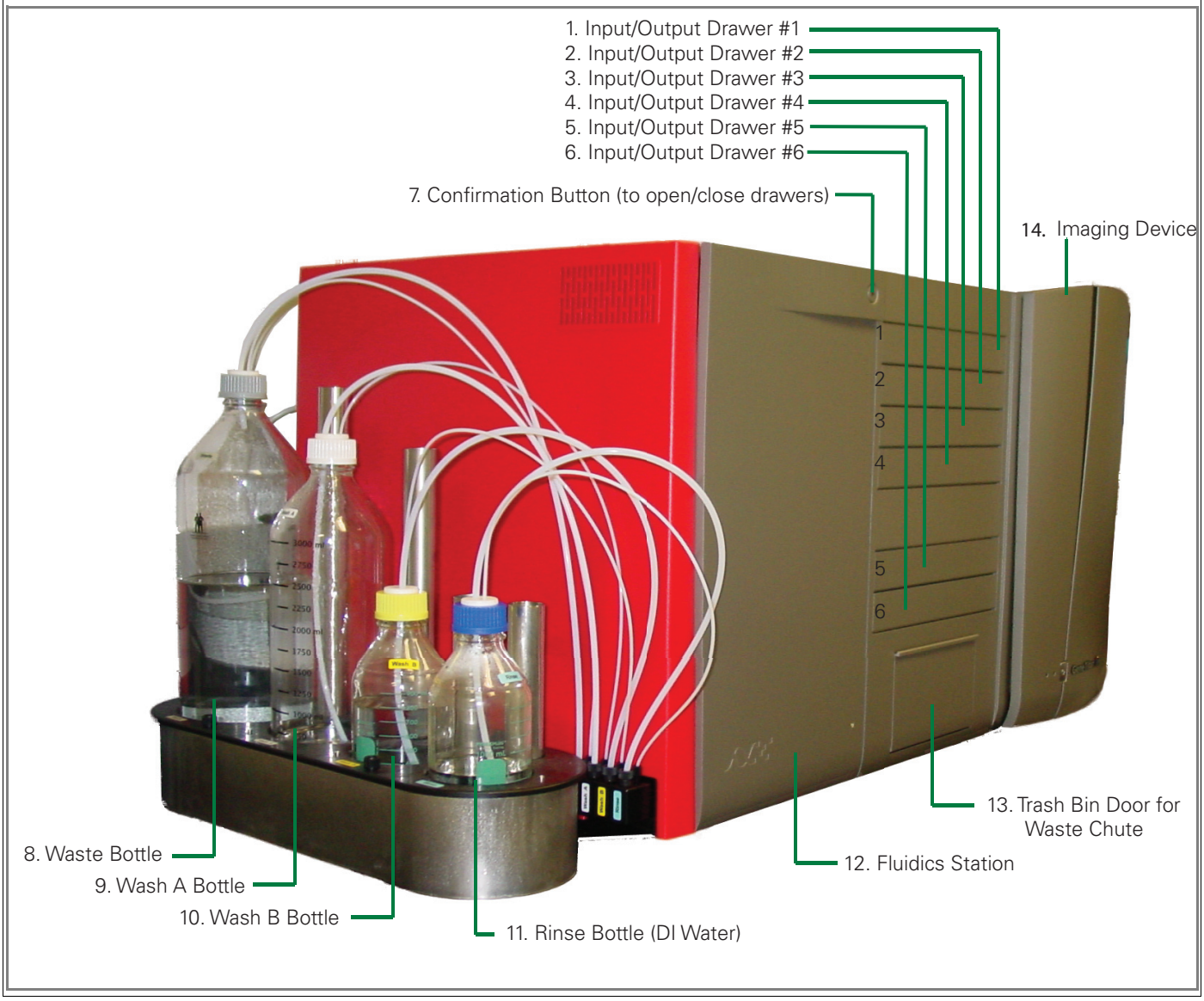
The GeneTitan MC Instrument can process both Expression Arrays and Axiom Assay. The instrument uses an external 300W Xenon lamp and has multiple filters to provide stable, efficient, well-collimated, uniform illumination to the array, optimizing exposure time to minimize photo-bleaching effects and maximize throughput.

Figure 268 GeneTitan MC Instrument

GeneTitan MC instrument controls and indicator lights

The figure below shows the location of the wash bottles, loading drawers, and other controls for the GeneTitan MC instrument.

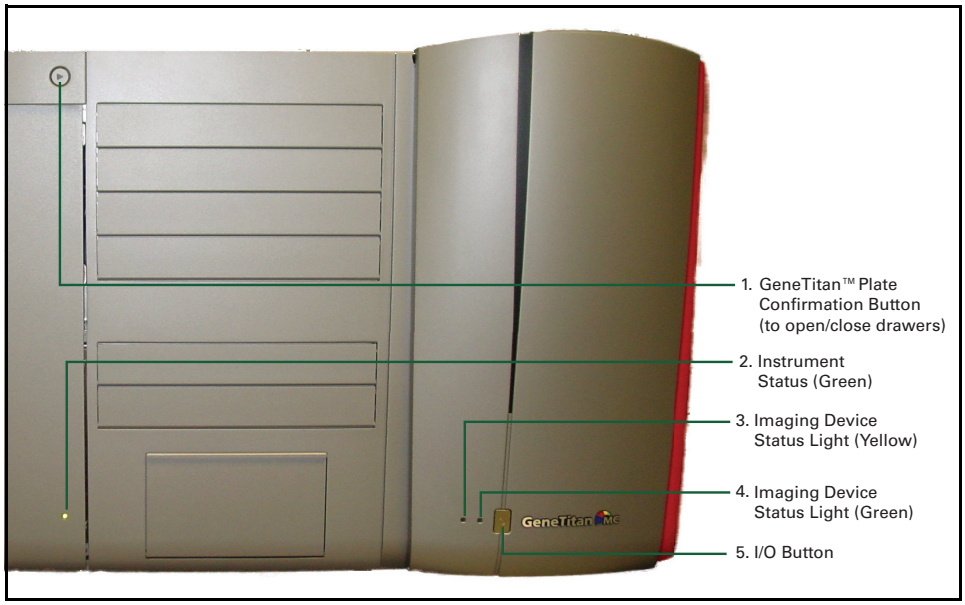
Figure 269 GeneTitan Instrument



WARNING! The bottles are pressurized in normal operation. Wait until you see the prompt that the buffer bottles have been de-pressurized before opening and refilling or emptying the bottles.

The GeneTitan Instrument uses the indicator lights and button below (Figure 270).

Figure 270 GeneTitan Instrument controls and lights.



Confirmation button: Press after completing certain steps for instrument setup, like adding fluids or adding trays and plates.

The button flashes blue when a step is pending.

Instrument Status lights:

- Solid yellow - initialing/homing system
- Solid Green - processing/available to process
- Blinking green - normal operation message box is displayed and requires user input
- Blinking yellow - abnormal event informational message box requires user response

All power to the instrument is turned on when the GCC GeneTitan Control software is started and turned off when the software is shut down. The I/O switch on the front of the instrument is inoperative when the instrument is being controlled using the software.

IMPORTANT! Do not make use of I/O switch on instrument panel to start/stop instrument. Use the menu item in the software.

Refer to the GeneTitan MultiChannel Instrument User Guide (P/N 08-0305) for more information.

Overview of the GeneTitan workflow

Running an array plate through the GeneTitan workflow involves the following sets of steps:

1. Set up the Instrument:
   a. Prepare plates and trays with samples and solutions, including buffer solutions.
   b. Select type of workflow to be performed.
   c. Select the Protocol, if required.
   d. Refill Bottles.

IMPORTANT! Once bottles are refilled, ensure that bottle caps are on tight.

   e. Remove used trays, plates and covers from the instrument.
2. Load new trays, plates and covers.

   There are different procedures for the different array and workflow types:
   - Expression Assay manuals
   - Axiom Genome Wide Human Assay User Manual (P/N 702830)
3. Begin Array processing and track the array plate through the workflow.
4. Empty the instrument.

You can:

- Select only part of the overall processing workflow to run (see "Workflow options")
- Run a series of array plates through the workflow for high-throughput operation (see "Running a series of array plates")

Workflow options

There are three sets of steps performed by the GeneTitan Instrument for array plate processing:

- Hybridization
- Wash and Stain
- Imaging (Scan)

The software enables you to perform all of these steps, or to select an option that runs only some of the steps, as described below.

You can choose from:

- **Hyb-Wash-Scan**

  This workflow performs all the steps on the array being processed.
  - Hybridization
  - Wash and Stain
  - Scan
- **Hyb-Wash**

  The Hyb-Wash workflow enables you to bypass the Scan step, performing only:
  - Hybridization
  - Wash and Stain
- **Wash-Scan**

The Wash-Scan workflow enables you to bypass the Hybridization step, performing only:

- Wash and Stain
- Scan

- **Wash-Scan-Resume**

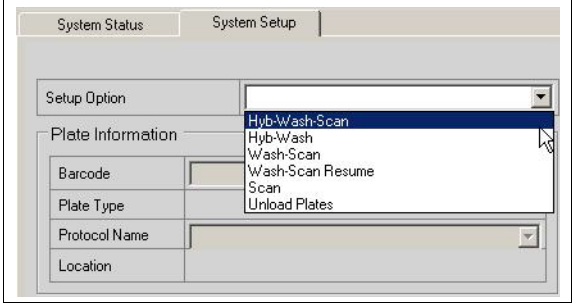
  This enables you to resume an interrupted workflow at any point in the Wash stage. See "Using the wash-scan-resume workflow".

- **Scan**

  The Scan workflow performs the scan only.

Selecting different workflows

Figure 271 Selecting workflow



Selecting the different workflows may require loading the array plate on a different tray (array plate cover, hybridization tray, or scan tray). In addition, there are differences in how the workflows are performed on genotyping arrays and expression arrays.

These differences are detailed in:

- Expression Assay manuals
- Axiom Genotyping Assay User Guide (P/N 702830)

Differences in processing for genotyping and expression arrays

There are two types of Array Plates that can be processed using the GeneTitan instruments

- Genotyping array plates
- Expression array plates

Genotyping array plates

Genotyping Array Plates can be processed only on GeneTitan MC instruments, since they need to be scanned at two different wavelengths.

For genotyping arrays, the reagents trays need to be loaded twenty-four hours after the array plate and hybridization tray have been loaded, after hybridization has completed.

Needed reagents trays are:

- 2 each Stain1 trays with covers
- Ligation tray with cover
- Stain 2 tray with cover

- Stabilizing tray with cover
- Scan tray with holding buffer and cover

See the Axiom Genotyping Assay User Guide (P/N 702830), for more information on running genotyping array plates.

Expression array plates

Expression Array plates can be processed on a GeneTitan MC instrument.

Needed trays/reagents are:

- SAPE 1 Stain tray with cover
- AB Stain Tray with cover
- SAPE 2 Stain tray with cover
- Scan tray with holding buffer and cover

See the Expression Assay manuals for more information.

Running a series of array plates

The GeneTitan Instrument can run two different workflows for the same probe array type at the same time. This enables you:

- To load a series of array plates with hyb trays and consumables for the Hyb-Wash-Scan workflow to process arrays more quickly.
- To run an array plate that was processed using a different system through the scan workflow while another array plate is going through earlier stages of the Hyb-Wash-Scan workflow.

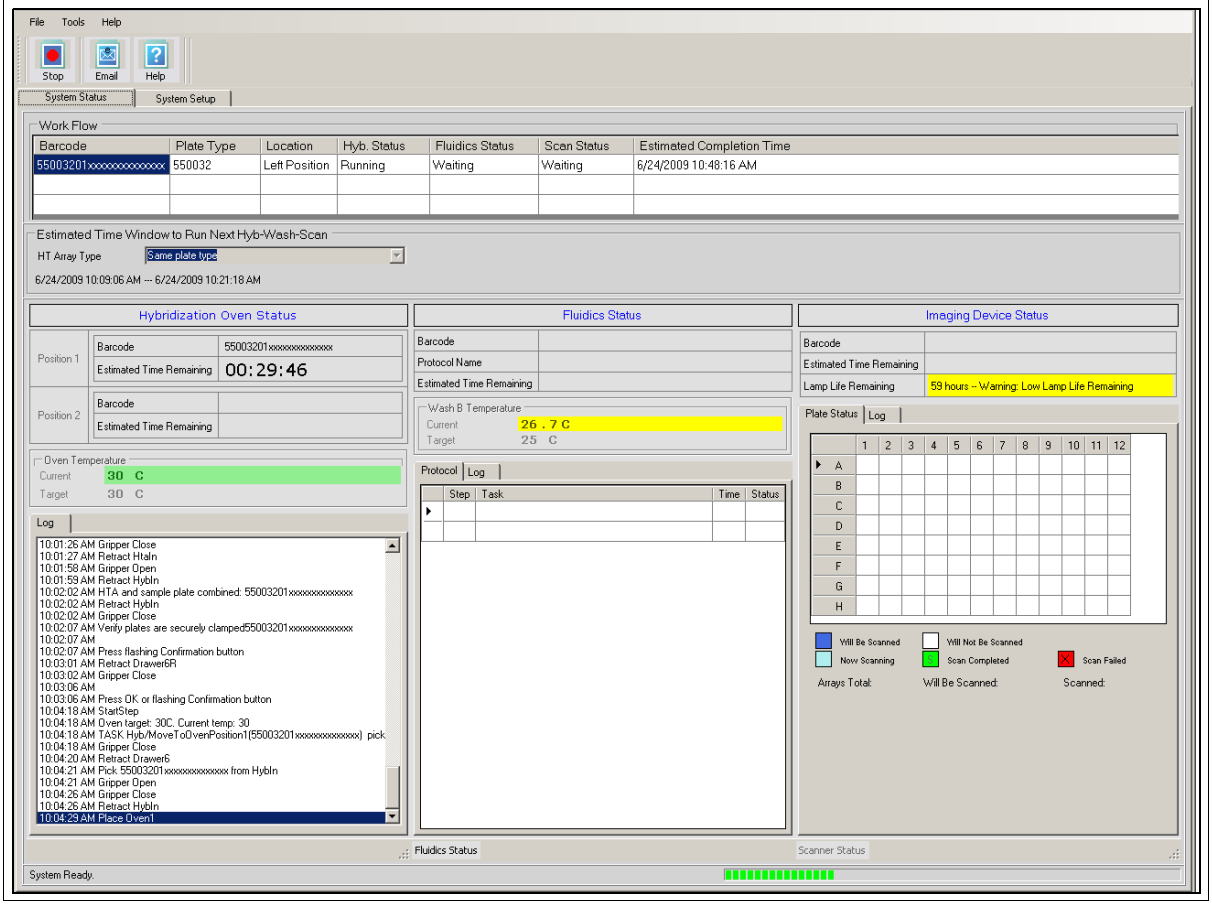
Only certain types of workflows can be run at the same time, and delays may be necessary before starting the second workflow. These restrictions exist because an array plate should be scanned immediately after the wash and stain processing is finished, and GeneTitan scans one array plate at a time. In addition, there are restrictions caused by the differences in workflows for Axiom arrays and Expression arrays, and by differences in the number of arrays on the plates. For more information, see:

- Expression Assay manuals
- Axiom Genotyping Assay User Guide (P/N 702830)

Tracking the array plate through the workflow

You can review the progress of the Workflow in the System Status tab. (Figure 272)

Figure 272 GCC GeneTitan Control software, System Status Tab



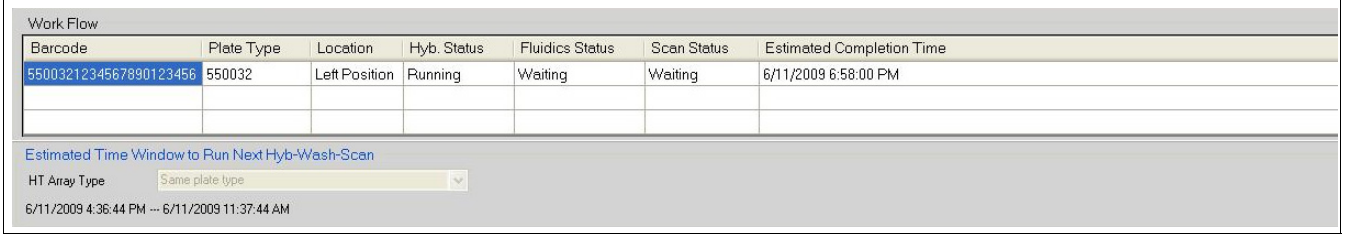
It has the following sections:

- "Workflow status"
- "Hybridization status"
- "Fluidics status"
- "Imaging device status"

Workflow status

The Workflow pane provides an overview of the array processing. (Figure 273)

Figure 273 Workflow pane



The Work Flow table lists the array plates and their status in the workflow, with the following information:

- Barcode of array plates being processed
- Plate Type
- Location
- Hyb. Status
- Fluidics Status
- Scan Status
- Estimated Completion Time

  Note: If more than three arrays are loaded at a time, a scroll bar appears at the right side of the table.

The Estimated Time Window information on when the next hyb-wash-scan workflow can be run

- Array Type

  Note: You cannot select a different array type for the next array to be run.

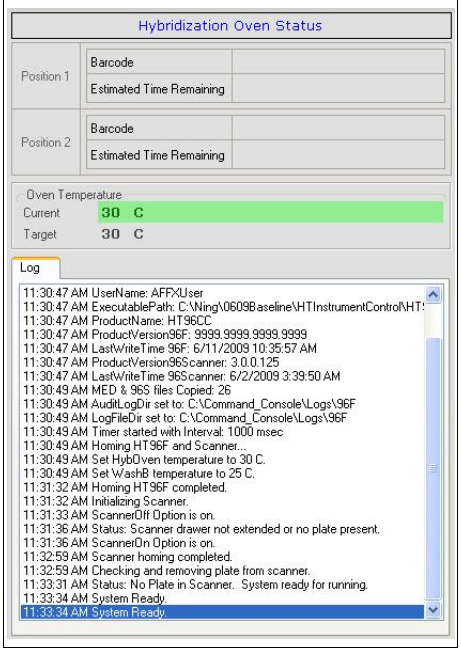
- Time when you can load the next array plate and other consumables.

  Note: When processing genotyping Arrays, once processing begins you have a specified period of time during which you can load another Array Plate and hyb tray. You cannot load another array plate before or after this period of time.

Hybridization status

The Hybridization Status pane displays details of the hybridization operations that have been run. The pane can display information for two array plates that are being processed at the same time.

Figure 274 Hyb Oven Status



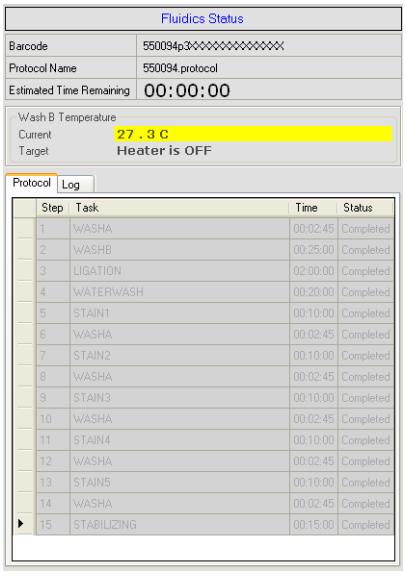
The pane displays the following information:

- **Position 1**
  - Barcode of the array plate(s) being processed
  - Time Remaining
- **Position 2**
  - Barcode
  - Time Remaining
- **Oven Temperature**
  - Current.
  - Yellow: Out of range
  - Green: In range
  - Target
- **Log**
  - Displays history of the operations performed in the Hybridization stage.

Fluidics status

The Fluidics Status window (Figure 275) displays information on the wash and stain operations that have been run or are currently being run.

Figure 275 Fluidics Status



The Fluidics Status window displays the following information:

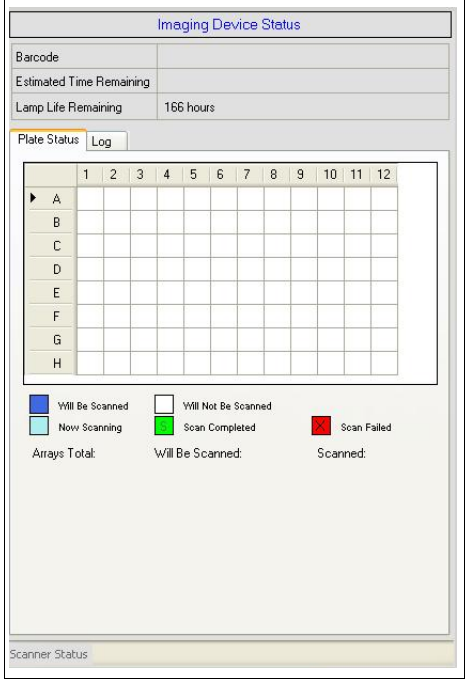
- Barcode of the array plate being processed
- Protocol Name
- Time Remaining
- Temperature for the protocol step
  - Current
  - Yellow: Out of range
  - Green: In range
  - Target
- Protocol tab:

  Displays list of steps in the protocol with:
  - Step
  - Task: short description of the task
  - Time
  - Status: Task pending, in process, or completed?
- Log tab
  - Displays history of the operations performed in the Fluidics stage.

Imaging device status

The Imaging Device Status pane (Figure 276) displays the progress of the scan.

Figure 276 Imaging Device Status



The Imaging Device Status window displays:

- Barcode of the array plate currently being scanned
- Time Remaining for scan
- Lamp Life/Imaging Device Status (see "Lamp Life/Imaging device status notices", below, for details)
- Plate Status tab with:
  - Array Plate Layout

    Each square represents an array with the following options:

(Dark blue)	To be scanned
(Light blue)	Now imaging
(White)	Not to be scanned
(Green	Scan completed
(Red)	Scan failed

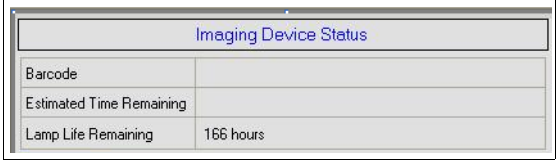
- Log: displays history of the operations performed in the Fluidics stage.

Lamp Life/Imaging device status notices

The Imaging Status pane displays lamp life and Imaging Device status notices for the GeneTitan MC.

In normal operation, the pane displays the hours of life left in the lamp:

Figure 277 Lamp Life above tolerance



It displays a red or yellow notice when the lamp life is getting short:

Figure 278 Lamp Life above tolerance

It also displays a red notice when the Imaging Device is offline:

Figure 279 Imaging Device Offline

Note: The 300 Watt Xenon lamp in the GeneTitan MC instrument is warranted for 500 hours. To replace the lamp refer to the instructions in the GeneTitan instrument manual. After changing the lamp, it is necessary to reset the lamp life clock manually. For more information about the clock, see "Resetting the lamp life clock".

Aborting a run

If necessary, you can abort a run in progress.

IMPORTANT! If you want to abort a run while loading reagents for a genotyping array plate, you must use the Cancel button in the tool bar. During reagent load the abort function will not be available for the plate for which reagent trays are being loaded.

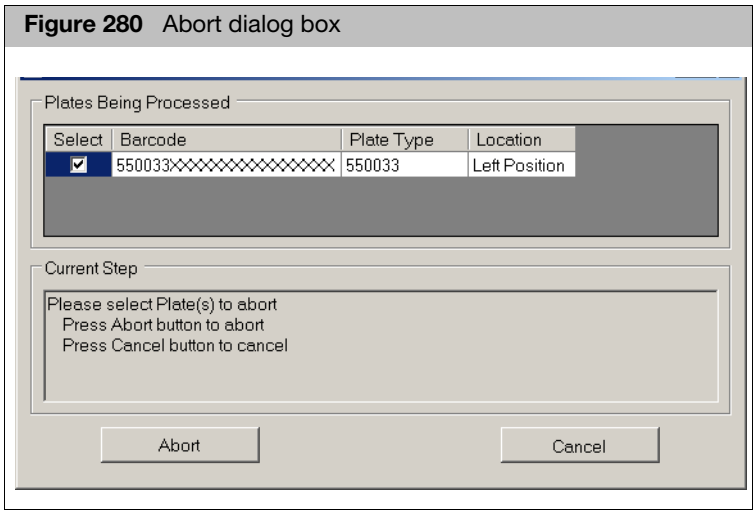
For information on aborting a run because of facility power loss, see "Facility power loss" on page 254.

To abort a run:

1. Click the **Stop** 

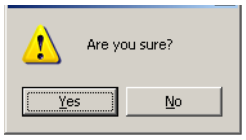
button in the tool bar.
   The Abort dialog box opens. (Figure 280)

Figure 280 Abort dialog box



   The Abort DB has the following components:
   - Plates Being Processed List with the following columns:
     - Select check box
     - Barcode
     - Plate Type
     - Location
   - Current Step: explains the next step in the procedure.
   - Abort and Cancel buttons.
2. Click the Select check box for the plate whose run you want to abort.
3. Click **Abort.**
   The software asks for confirmation.

Figure 281 Abort Confirmation

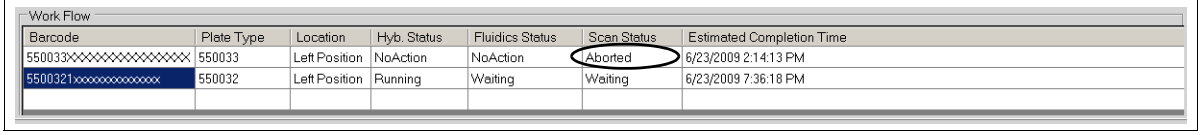


Click **Yes** to continue with the Abort process.

Note: The abort process may take some time to complete. Wait until it is finished before trying to perform any other operations.

When abort is completed, you can see the notice in the Status tab (Figure 282).

Figure 282 Abort notice in Workflow pane



If the array plate is in the Hyb Oven, it is placed in Drawer Number 1

If the array plate is in Fluidics when the abort is ordered, it is placed in the Scan tray.

You will need to unload the loaded plates and trays in a second step, using the Unload function or the unload steps during a setup.

Facility power loss

If facility power is lost and the UPS backup power battery percent remaining drops below 75%, the software will automatically abort all running plates. This automatic abort is intended to protect the plates by bringing all running plates out to the drawers for removal. However, if the user is in the setup tab performing setup steps (loading the machine) the software is prevented from performing the required abort sequence.

If facility power is lost and the user is notified that the UPS power percent remaining drops below 75%, the user should cancel the loading operation to initiate the abort sequence.

Canceling the loading operation and setup

- Select Cancel in the system setup tab.

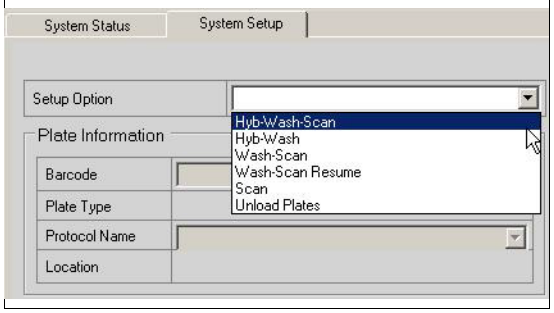
Unload plates

The Unload Plates function can be used to empty the GeneTitan drawers after performing an abort operation.

Unloading loaded plates

1. Select Unload Plates from the Setup Option drop-down list. (Figure 283)

Figure 283 Selecting workflow



The application prompts you to empty the cover trash bin.

2. Perform the following steps:
   a. Open the trash bin door.
   b. Remove and empty the trash bin.
   c. Return the trash bin and close the door.

3. Press the **Confirmation** button to proceed.

   The application prompts you to unload previously loaded plates and trays.

   For each loaded plate or tray:

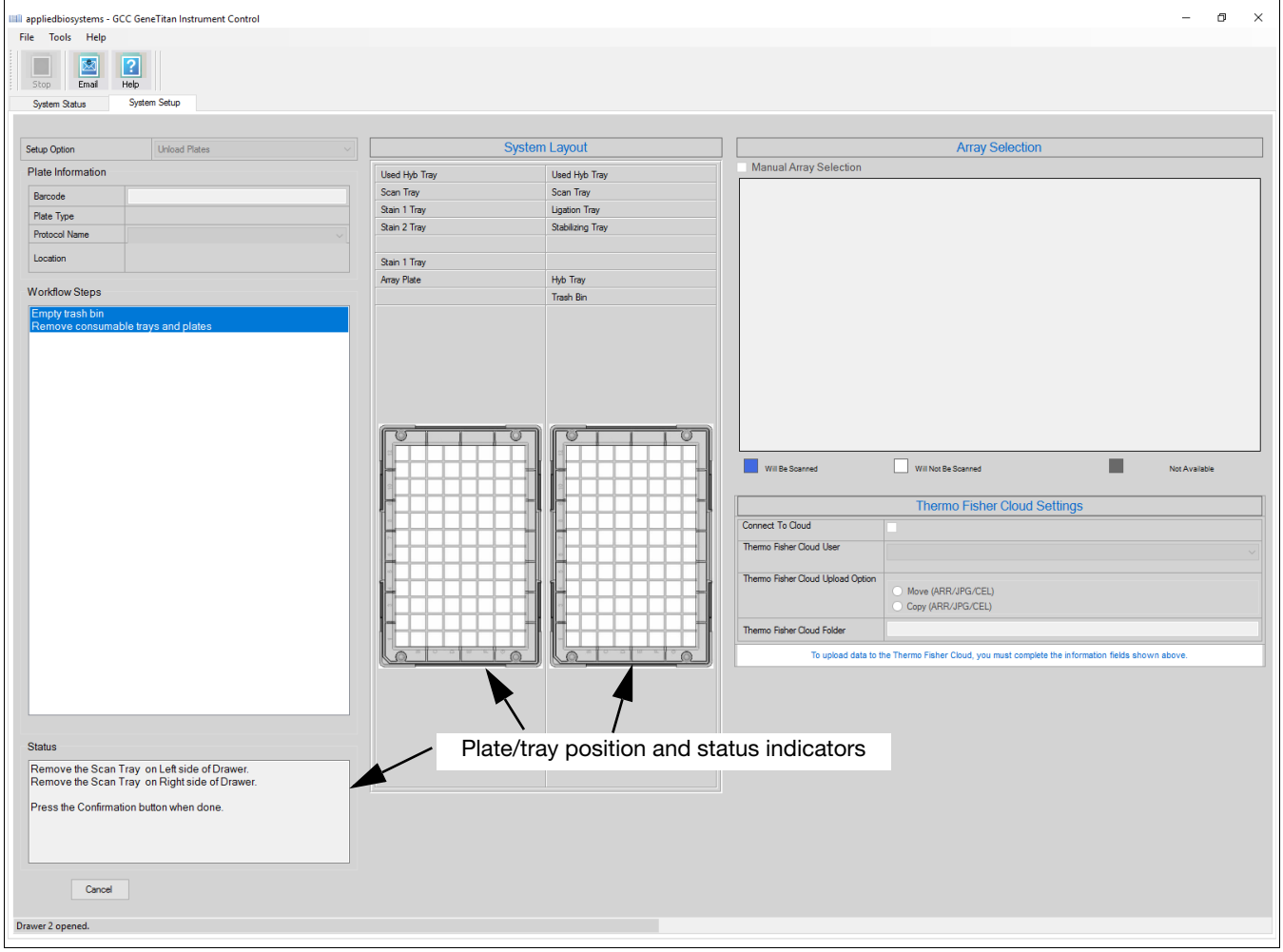
   - The appropriate drawer opens (Figure 284).

Figure 284 Unloading solution trays from Drawer #5

   - The status box prompts you to remove the tray or plate and the system layout indicates the array or tray to remove. (Figure 285)

IMPORTANT! When running a series of array plates through the GeneTitan Instrument, you must be careful to remove and load the proper array plate and trays and pay careful attention to the software prompts that tell you which side of the open drawer to remove or place a plate or tray.

Figure 285 Unload tray(s)



Remove any plate, plate receptacle, or tray from the drawer (Figure 285), then press the **Confirmation** button on the front of the instrument.

When you have finished emptying the old plates and trays, the software prompts you to proceed to the next step.

Using the wash-scan-resume workflow

The Wash-Scan-Resume can be used to resume an interrupted workflow on an array plate.

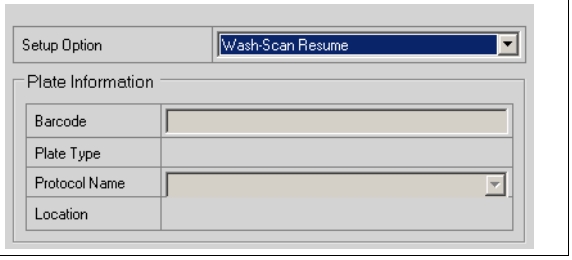
The Abort process places the Array Plate on the Scan Tray. **Note:** You must manually place the array on a blue tray before resuming the workflow.

Applied Biosystems recommends using a new scan tray for the resumed workflow.

Resuming an interrupted workflow

1. Select **Wash-Scan-Resume** in the setup process.

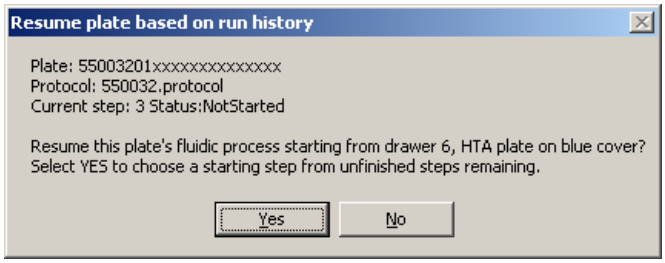
Figure 286 Select Option--Wash-Scan-Resume



2. Enter the barcode for the interrupted array.

   The Resume Plate dialog box appears.

Figure 287 Resume Plate dialog box



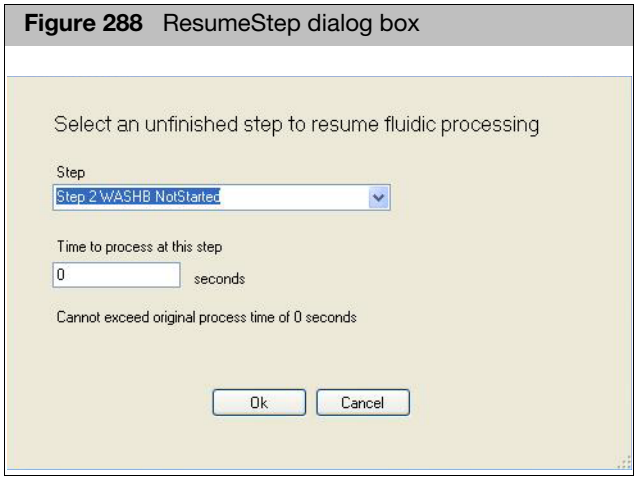
   The Resume Plate dialog box lists:

   - Plate barcode
   - Protocol that had been selected to run the array.
   - Step where the process needs to be resumed.

3. Click **Yes** to proceed with the resume.

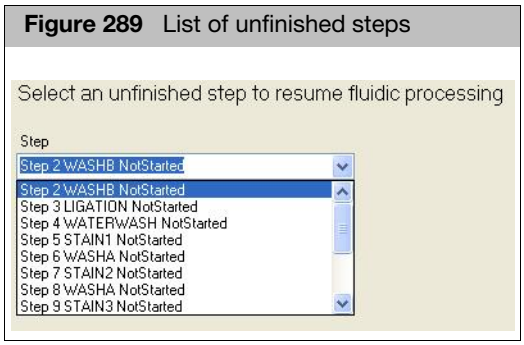
   The ResumeStep dialog box opens.

Figure 288 ResumeStep dialog box



The Steps drop-down list displays the uncompleted steps.

Figure 289 List of unfinished steps



The list of unfinished steps are different for:

- Expression arrays versus Genotyping Arrays
- Arrays interrupted in different parts of the workflow

4. Select the step in the workflow where you want to resume.

   Note: If you have performed certain steps off-line, you need to skip these steps in the workflow.

5. Enter the time you want to run the first step in the Time to Process box.

   You cannot change the processing time for certain steps, and cannot set the time to longer than the protocol specifies.

6. Click **OK** to resume the workflow.
7. Follow the instructions in the software steps for loading the array and trays.

   You must load the array plate on a blue array base.

Figure 290 Array Plate with blue base

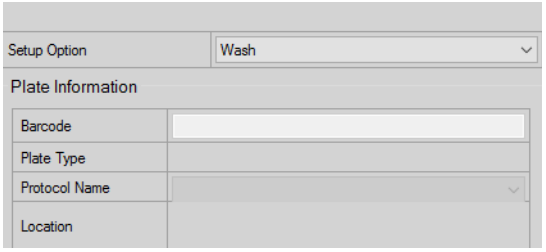
Thermo Fisher Scientific recommends using a new scan tray for the resumed workflow.

You must load all the trays for the original workflow; if you know you are going to skip a particular step, you can load an empty tray in the designated location for that step.

Using the wash only workflow

1. From the Setup Option drop-down menu, select **Wash**.

Figure 291 Select Option- Wash

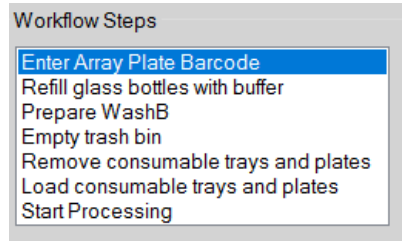


2. Click **Next** (bottom left).

   The Barcode text field is enabled.
3. Enter a barcode.
4. Click **Next**.

   The Workflow Steps pane populates, as shown in Figure 292.

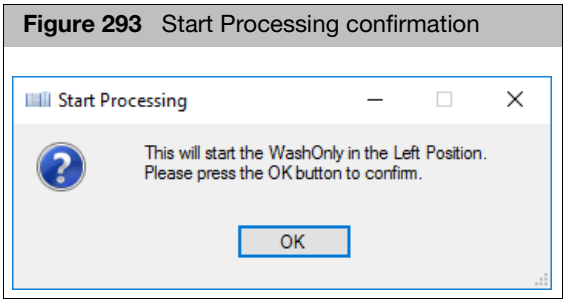
Figure 292 Workflow Steps



5. From the **Protocol Name** drop-down, select an appropriate protocol.
6. Click **Next**.

   After a few moments, a Start Processing confirmation window appears. (Figure 293)

Figure 293 Start Processing confirmation



7. Click **OK**.

   The Wash workflow begins.

   Note: Monitor the Status pane as it continually updates the workflow's progress. Click **Next** when prompted. Completed workflow steps are highlighted in blue.

Drop and scan with array plates

While you can register an array plate and its arrays using the GCC Portal GeneTitan Array Plate Registration before processing, you can also process an array plate that has not been registered by using the Drop and Scan feature for array plates. When using Drop and Scan, the ARR, DAT, and CEL files for each array are named using the barcode and array position.

See "GeneTitan array plate registration" on page 135 for more information about registering an array plate.

Using Drop and Scan

1. Set up and load the GeneTitan Instrument as required for the workflow you are performing.
2. Process the array plate.

   If the array plate has a valid barcode, it is processed and scanned. The ARR, DAT, and CEL files for each array are named using the barcode and array position and placed in the designated Default folder.

   For more information about the Default folder, see:

   - "Default folders"
   - "Specifying a default folder"

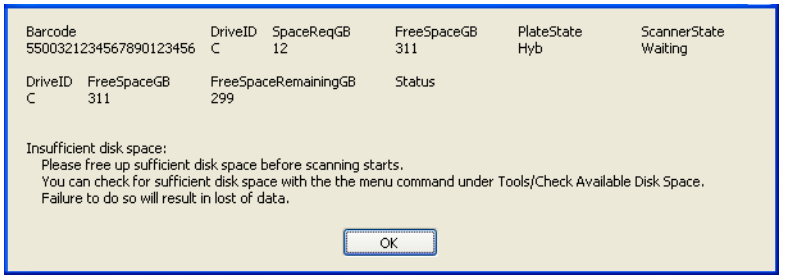
   If the instrument cannot read the barcode, or if there are no library files on the system for array plates with that part number, the array plate is ejected and an error notice appears.

Insufficient disk space notice

If there is not enough memory on the computer's drives to save the data from an array plate, a notice appears when:

- You first initialize the software and instrument
- You select arrays for imaging.

Figure 294 Insufficient Disk Space Notice



If you see this notice, you will need to free up sufficient disk space before imaging starts.

Resetting the lamp life clock

Note: The following resetting instructions can be used for either the GeneTitan or GeneTitan Scanner instrument.

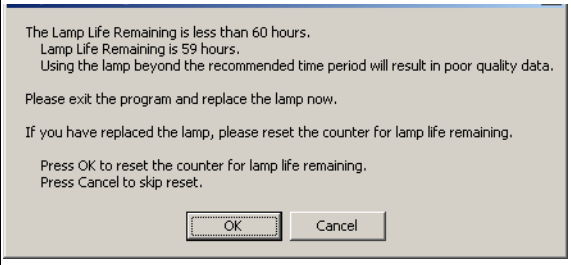
The GeneTitan uses a xenon arc lamp system to provide illumination for imaging the array at two wavelengths. The xenon lamp has a limited lifetime and needs to be replaced at regular intervals.

The GeneTitan Instrument Control software provides a timer that indicates the remaining useful light of the bulb and notifies you when it requires replacement.

The replacement procedure is described in the GeneTitan Instrument User Guide (P/N 08-0296). After replacing the bulb, you will need to reset the time, as described below.

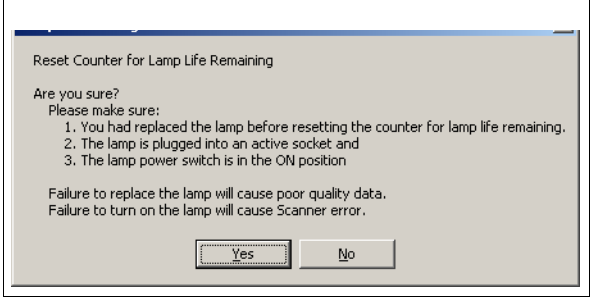
If life of bulb is under a specified limit, the following notice appears (Figure 295) when you launch the software:

Figure 295 Lamp Life Management notice



If you click **OK**, the confirmation notice appears. (Figure 296)

Figure 296 Reset dialog box



Click **Yes** to reset the lamp life timer to the specified time.

Click **No** to cancel.

Computer practices, maintenance and troubleshooting

If the GeneTitan workstation becomes unstable during a workflow the cost of an aborted workflow and replacement plates is substantial. To avoid this Applied Biosystems recommends following certain computer operation practices and preventative maintenance routines.

These are described in:

Computer operation practices

The following computer operation practices are recommended to help prevent problems.

Hard drive

For the instrument control system, it is recommended to keep all drives at a maximum of 50% full. If there is more data on the workstation, the system tends to slow down. If keeping data on the hard drives is absolutely necessary, the drives need to be defragmented regularly (ie: depending on the amount of data, every two weeks or monthly defragmentation is recommended).

USB memory drives/memory stick

When USB drives or memory stick(s) are connected to the workstation, please properly disconnect them (safely remove hardware) before physically pulling them off.

Scanning plates

If the GeneTitan system is scanning a plate or running fluidics, try not to run any other applications while the instrument workstation is running.

Moving data (DAT, CEL, etc.)

When archiving data or moving data off the workstation, it is highly recommended to do this process when scanning or running fluidics is not in process. The scanning process is very slow if data is being moved at the same time.

Preventative maintenance

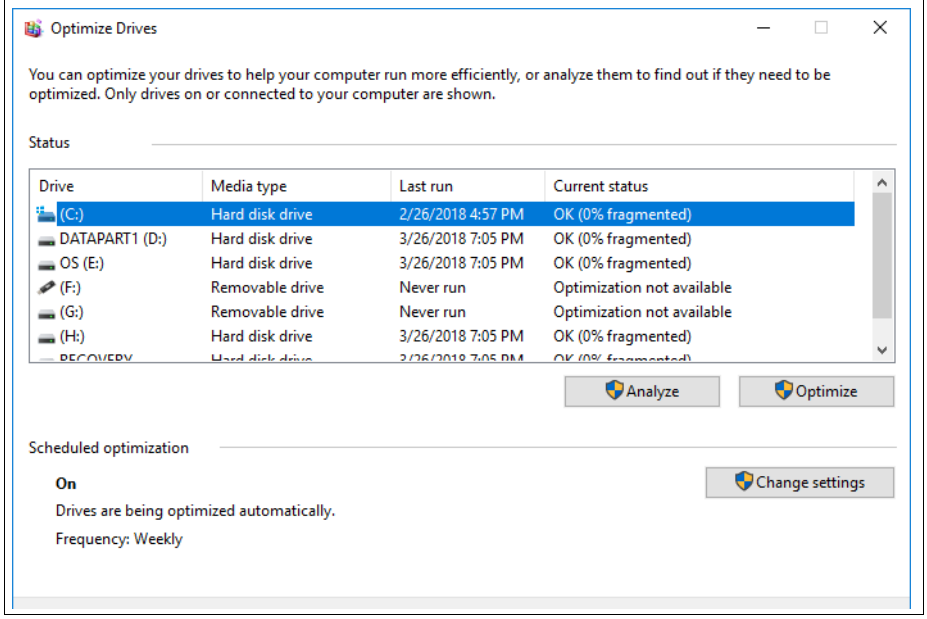
Optimizing your disk drive

The drive(s) on the GeneTitan workstation need to be optimized regularly (ie: depending on the amount of data, every two weeks or monthly optimization is recommended).

1. Click the Search/magnifying glass icon (lower right).
2. In the Search Window text box, type **defrag.**
3. Click on **Defragment and Optimize Drives** selection.

   The Optimize Drives window appears.

Figure 297 Optimize Drives window



The window displays a list of drives with information about capacity and free space.

4. Select the disk you want to optimize.
5. Click **Analyze**.

   The Analyze process runs.

   When the analyzing process is complete, the status of your analyzed drive is displayed in the Current Status column.

   Repeat steps 4-5 for each drive you want to optimize.
6. Close the Optimize Drives window.

Troubleshooting

If the GeneTitan IC window and taskbar icon disappear

The GeneTitan IC window may disappear from the computer screen while, at the same time, the Taskbar icon for GeneTitan IC disappears. If this happens, restore the window and icon by doing one of the following.

Solution 1

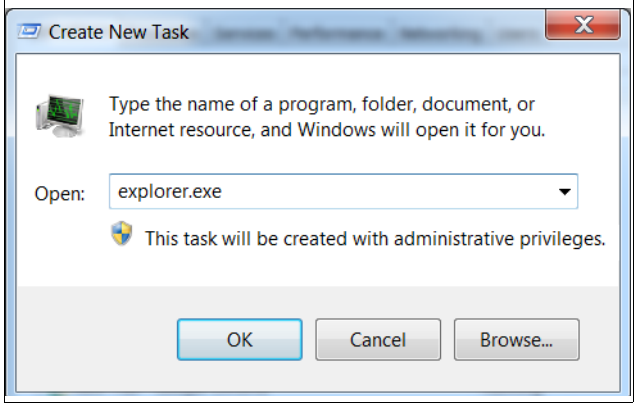
1. Simultaneously press **Ctrl**/**Alt**/**Delete** keys.

   The Windows Security dialog box appears.
2. Click **Start Task Manager**.

   The Windows Task Manager window appears.
3. Click **New Task...**

   The Create New Task dialog box appears. (Figure 298)

Figure 298 Create New Task dialog box



4. Enter **explorer.exe** and click **OK**.

   The Task Bar should be displayed
5. Press the icon for GeneTitan in the task bar to display the GeneTitan window.

   Note: The **explorer.exe** application must be running properly to display the Taskbar at the bottom of the screen. The above procedure will launch explorer.exe to re-display the Taskbar.

Solution 2

1. Simultaneously press the **Alt** and **Tab** keys

   A list of icons for active applications appears.
2. Keep pressing the Alt key while tapping on the Tab key to select the window displaying GeneTitan.
3. When selected, release the Alt key.

   The GeneTitan window re-appears.

Note: For more troubleshooting information, see the GeneTitan Instrument User Guide (P/N 08-0296) or GeneTitan Multi-Channel Instrument User Guide (P/N 08-

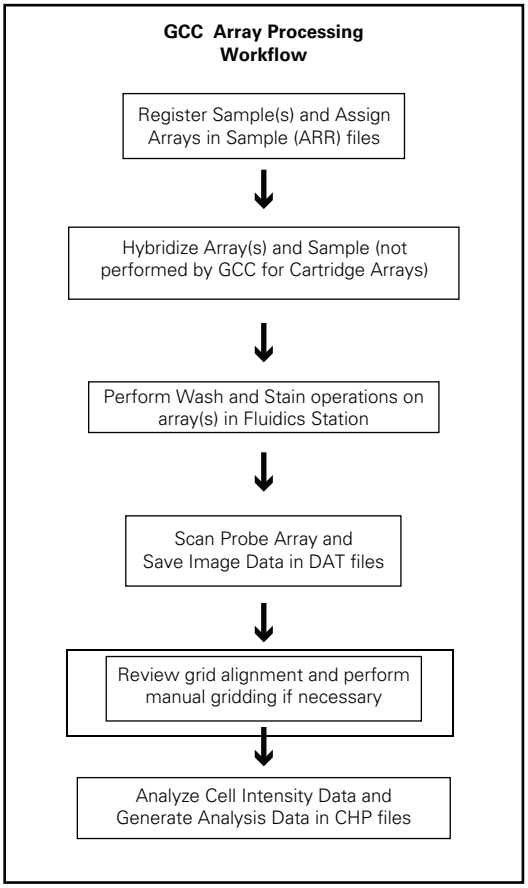
0305)

9 Using the GCC viewer

After the array has been scanned, GCC: (Figure 299)

- Aligns a grid on the Image (DAT) file to identify the probe cells.
- Computes the probe cell intensity data for the array and creates a CEL file.

Figure 299 Array Processing Workflow



The GCC Viewer displays DAT, CEL, and JPG files and enables you to:

- Track the progress of the data through grid alignment and cell intensity generation.
- View the files for quality control purposes, such as detecting scratches and bubbles.
- Check the grid alignment and realign the grid, if necessary.

  See "Checking the grid alignment" on page 310.

Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

- Create a JPG version of a DAT file for archiving.

  See "Exporting images in other formats" on page 322.

This chapter describes the operation of the GCC Viewer in the following sections:

Array and grid types

The Alignment algorithm uses the checkerboard image of the control probes, located at the corners of the probe array, to superimpose a grid on the scan image. The algorithm aligns the grid so that each square in the grid delineates a probe cell.

The alignment of the grid and sub-grids usually takes place automatically after imaging the array. The status of the alignment can be tracked in the Review window. If the alignment algorithm fails you can perform a manual alignment of the main grid and/or sub-grids.

Different types of arrays use different grid types, as described in:

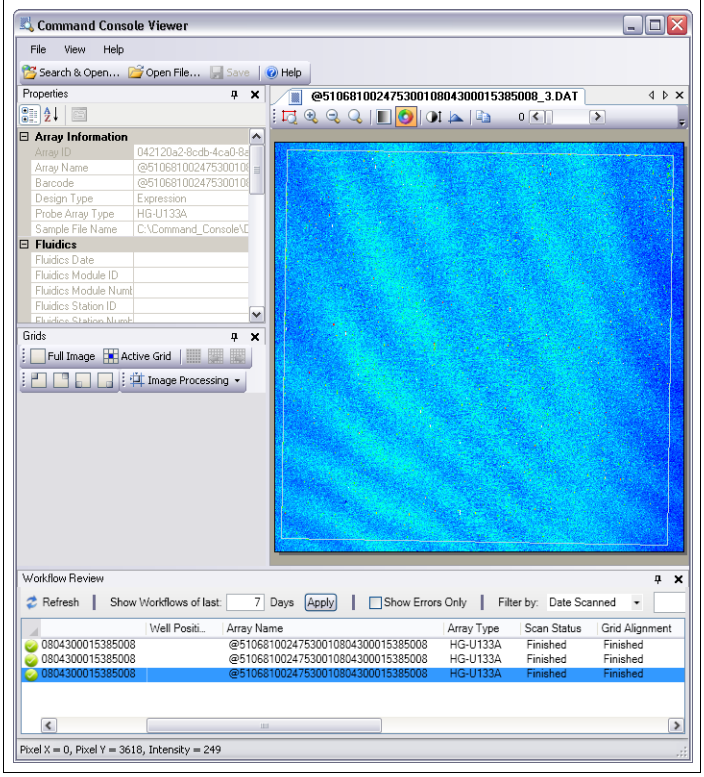
- "Cartridge arrays"
- "GeneTitan array plates" on page 271

Cartridge arrays

Cartridge Arrays can use:

- **Main Grid Only** (Figure 300)

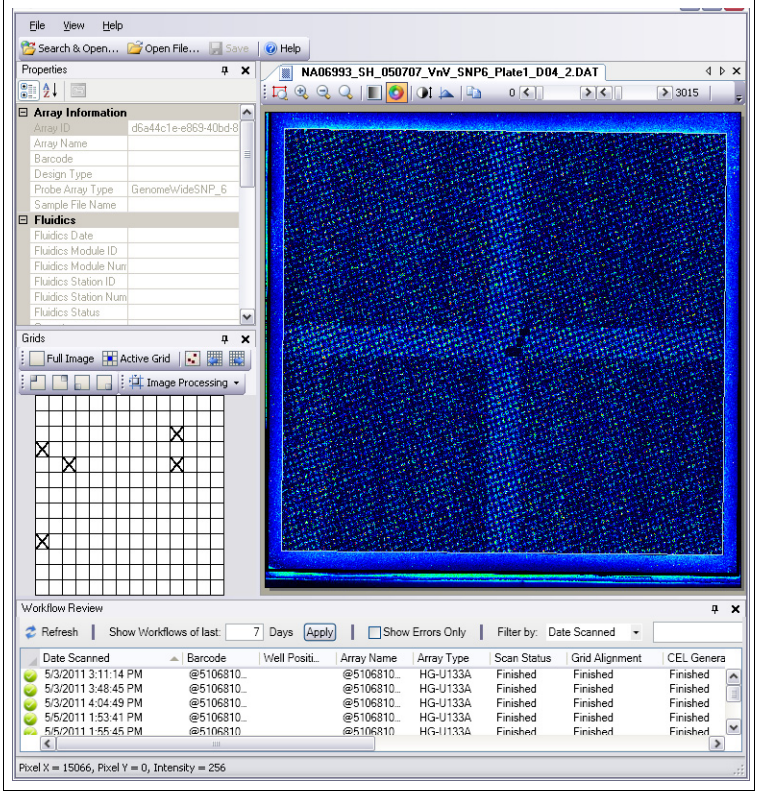
Figure 300 Array with a single grid



- **Main Grid with multiple sub-grids** (Figure 301)

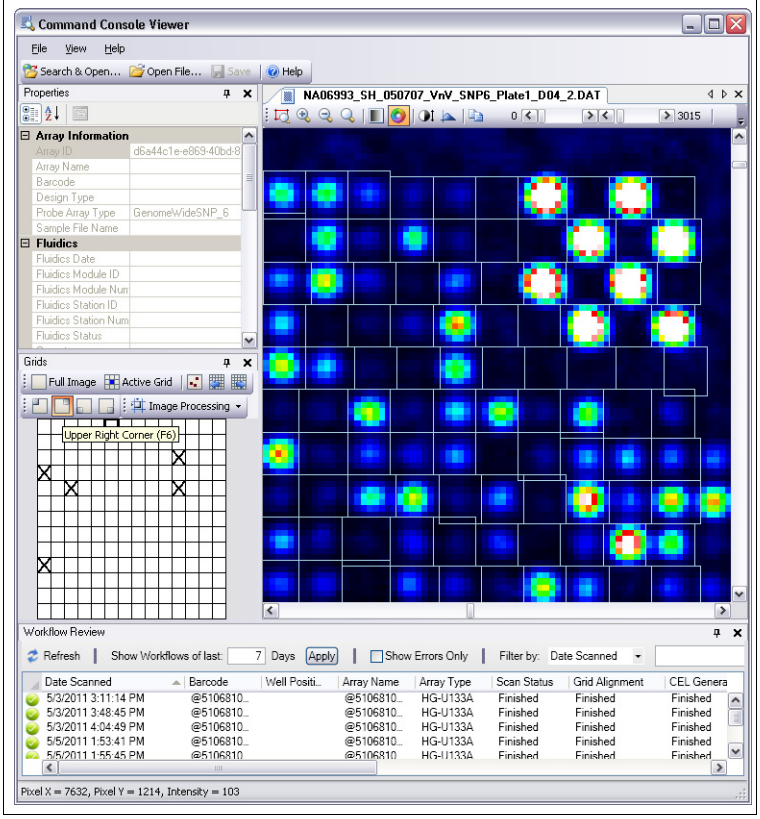
  The position of each sub-grid can be adjusted independent of the other sub-grids.

Figure 301 Main grid with sub-grids



Each sub-grid is identified by its row and column in the main grid. The corners of each sub-grid are marked on the array by specific alignment patterns; the anchors of the sub-grid are aligned to these patterns. (Figure 302)

Figure 302 Corner pattern of a sub-grid



The software uses the corner patterns at the four corners of the array to align the initial main grid. The main grid is then divided into smaller sub-grids. Each sub-grid is aligned on the corner grid patterns in the final steps of the gridding algorithm and in manual alignment.

GeneTitan array plates

Plate Arrays use:

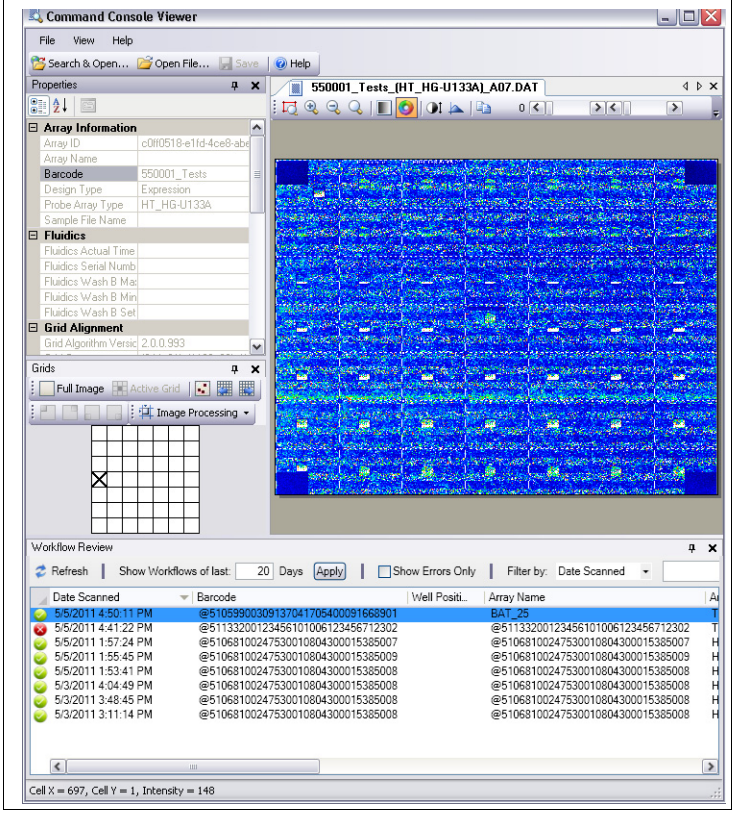
- Sub-grids only without a main grid (Figure 303)

There are two different types of Genetitan array plates:

- "GeneTitan expression array plates" on page 272
- "GeneTitan genotyping array plates" on page 275

GeneTitan expression array plates

Figure 303 GeneTitan Array DAT file



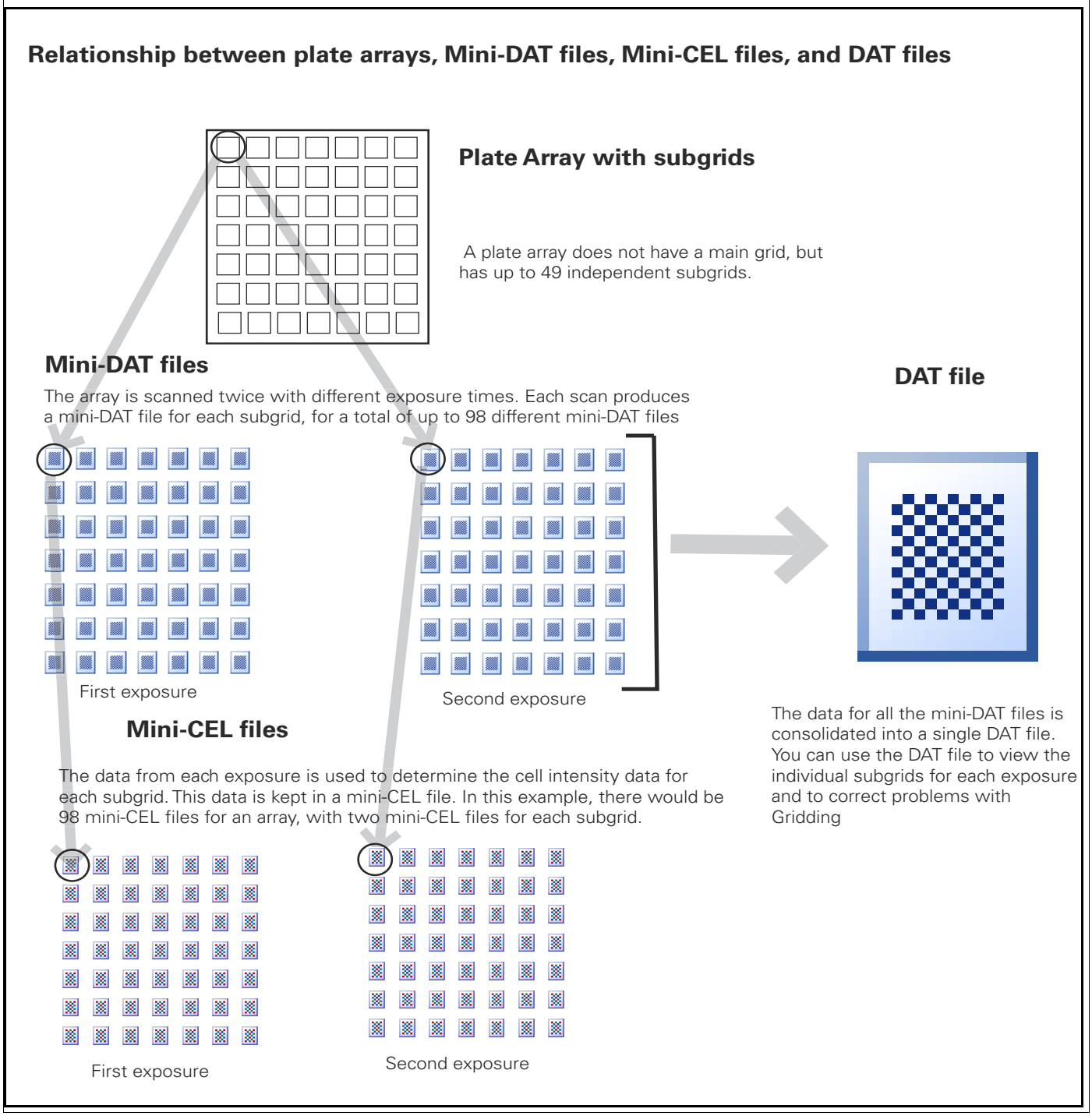
An array plate can have up to 96 arrays (see "GeneTitan array plate registration" on page 135 for more information).

Each plate array on the array plate has multiple sub-grids. Some arrays use a 7 x 7 grid, for a total of 49 sub-grids, while other array types use a 7 x 6 grid, for a total of 42 sub-grids.

These sub-grids are similar to the sub-grids used for some cartridge arrays, but on a plate array the sub-grids are not aligned to a main grid.

In addition, the data for all the mini-DAT files is consolidated into a single DAT file. This DAT file can be viewed in the Image Viewer; the file has all the image and gridding data for each sub-grid and each exposure, and enables you to check the gridding independently for each exposure

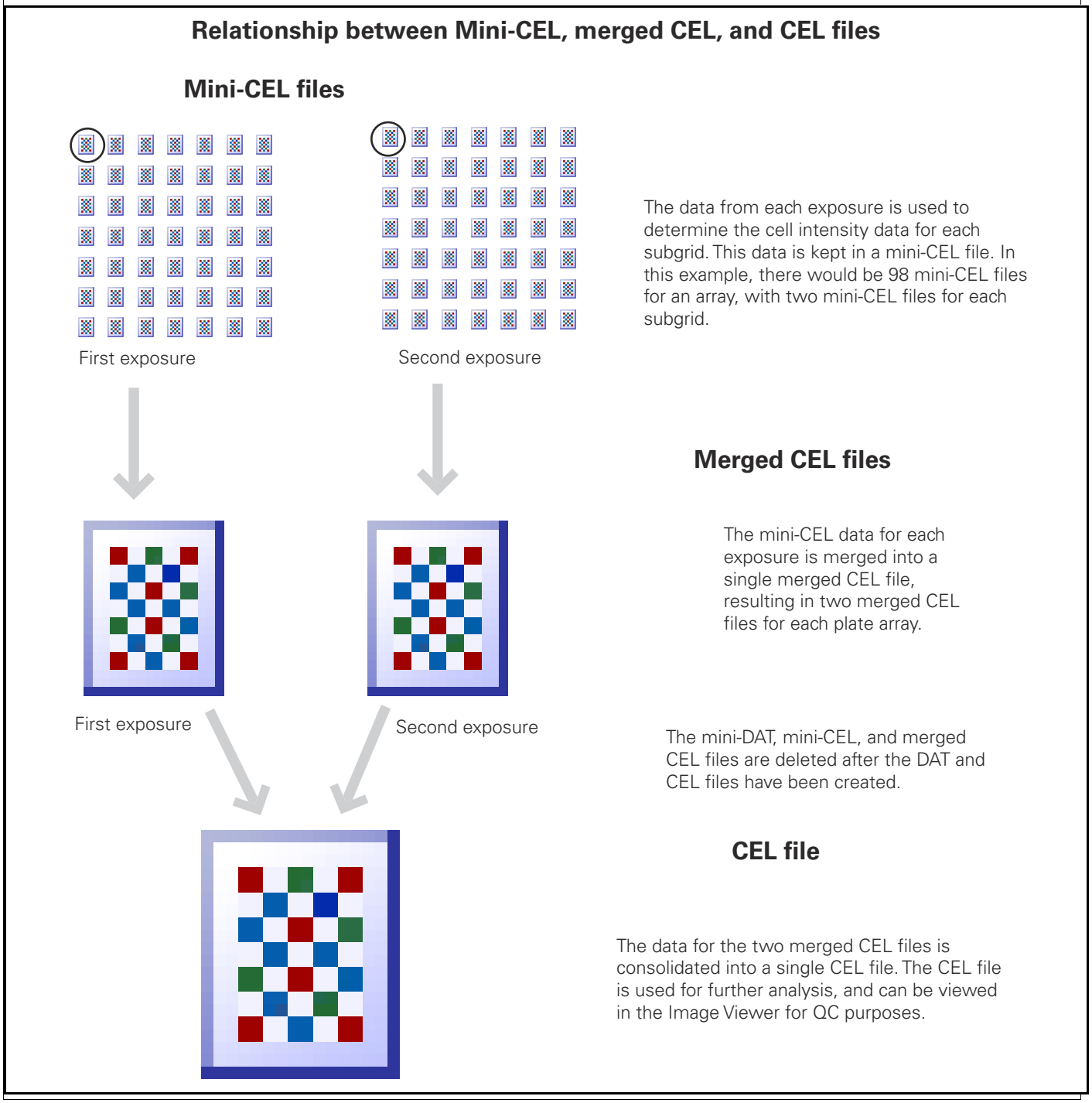
Figure 304 Mini-DAT and mini-CEL files



The mini-CEL files for each exposure are merged into a single merged CEL file (.mgcel) (Figure 305), resulting in two merged CEL files per plate array.

The data in these two merged CEL files is then consolidated in a single CEL file, which is used for further analysis and can be viewed in the Image Viewer for QC purposes.

Figure 305 Mini-CEL merge and consolidation.



The mini-DAT files, mini-CEL files and merged CEL files will be deleted during normal processing. If something goes wrong, you may find these file types in the target folder during a scan.

GeneTitan genotyping array plates

GeneTitan genotyping array plates are handled similarly to the GeneTitan Expression arrays except that the arrays are scanned at two different wavelengths to support the two color assay. At each wavelength genotyping arrays are scanned at two different exposure times where signals from all four DAT files are integrated into a single DAT file to provide an expanded dynamic range.

Introduction to the viewer

You can learn more about the basic functions of the GCC Viewer in:

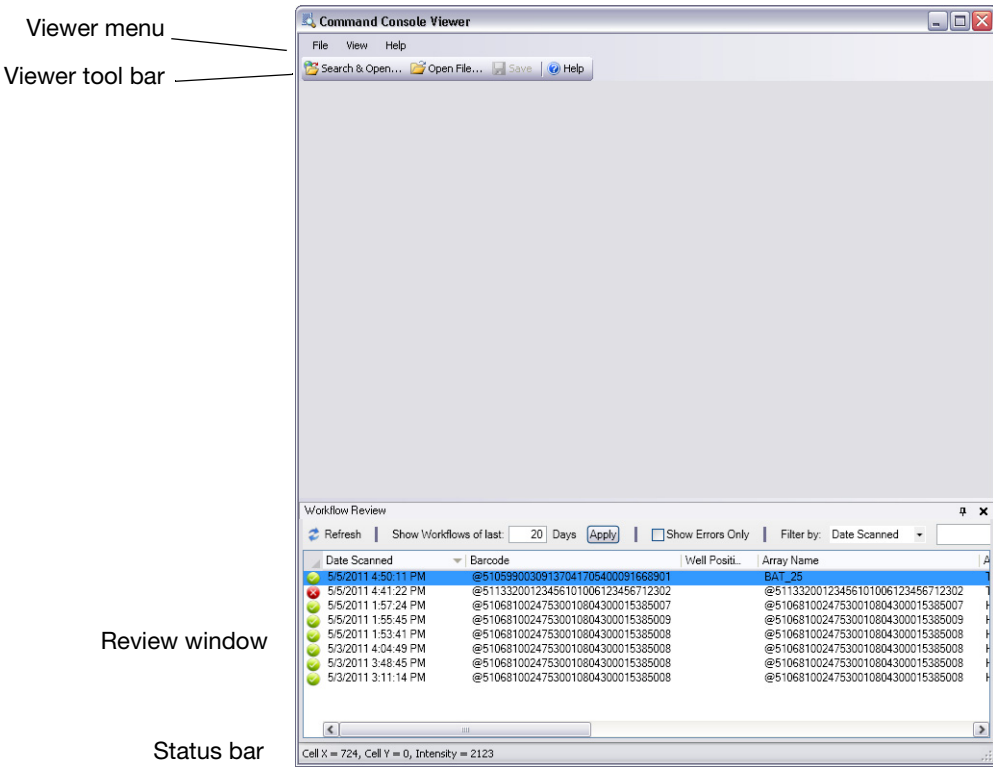
- "Opening the viewer"
- "File display differences" on page 276
- "Moving the components out of the viewer" on page 278
- "Moving the component borders in the GCC viewer" on page 281

Opening the viewer

To start the GCC Viewer:

- In the GCC Launcher, click the GCC Viewer icon  ; or
  Click the **Start** → **Thermo Fisher Scientific** → **GCC Viewer**.
  The viewer opens. (Figure 306)

Figure 306 GCC Viewer with no image displayed

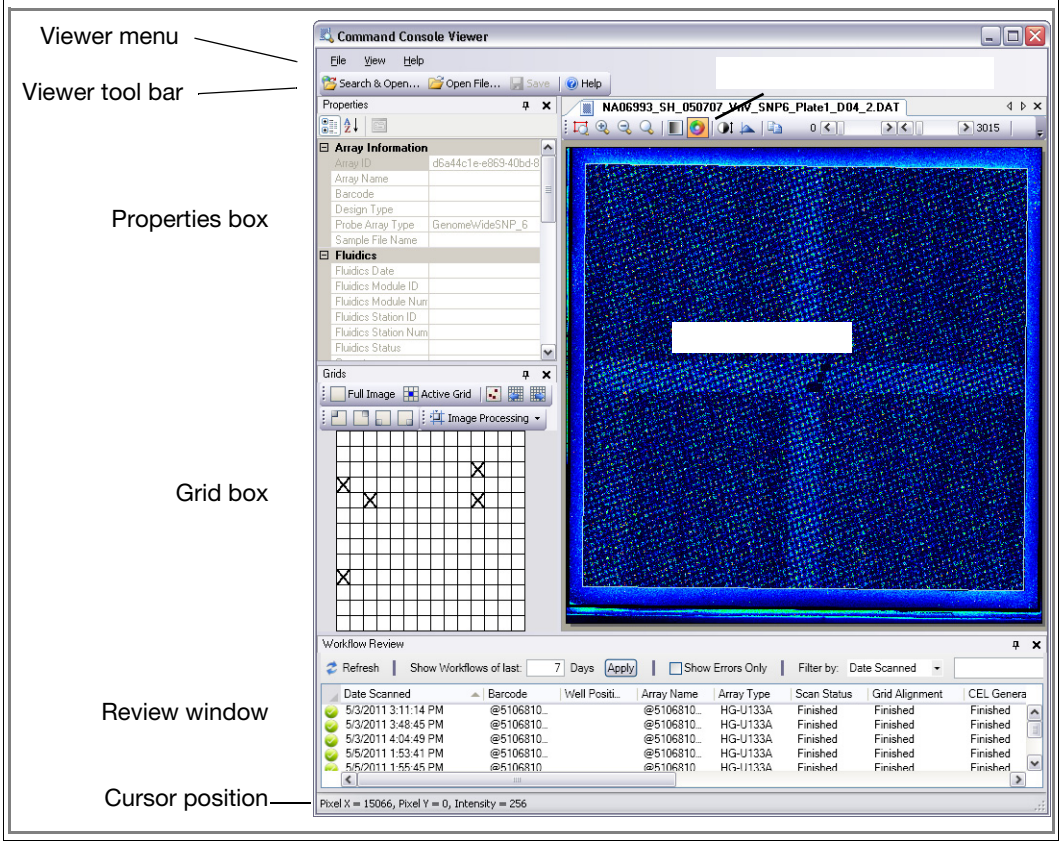


The viewer has the following components when it first opens:

- Viewer menu
- Viewer tool bar
- Review window (optional) (see "Using the review window" on page 283)
- Status bar: displays cursor position and intensity of selected pixel/cell

Additional components are visible when a DAT or CEL file is displayed (Figure 307)

Figure 307 Parts of the GCC Viewer with DAT file displayed



To learn about the Image window tool bar, see "Changing the display of the image" on page 299.

To learn about the Properties box, see "Learning about the image file" on page 307.

To learn about the Grid box, see "Checking the grid alignment" on page 310.

File display differences

The GCC Viewer has different types of functions and options for the different image file types that it displays:

DAT files

DAT files are the image data files, the product of the initial scan.They are used to generate the cell intensity data file after the grid has been aligned.

The DAT file must be opened to perform manual gridding or to run the grid alignment algorithm in the GCC Viewer.

If the cell intensity data (CEL) file has been generated, you can click the **Cell Intensity** button  and view the cell intensity data in the DAT Image window.

GeneTitan expression array plate DAT file exposures

Each array is scanned twice, with different exposure times. The image data from both exposures are in the GeneTitan Array Plate DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303).

GeneTitan MC Genotyping Array Plate DAT File Exposures

In GeneTitan MC each array is scanned twice, with different colors. The image data from both exposures are in the GeneTitan MC Array Plate DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303).

CEL files

CEL files are cell intensity data files, produced using the DAT file data after gridding and feature extraction.

You cannot perform grid alignment or cell generation on a CEL file.

For certain types of probe arrays, failed control features in the array will be masked when viewing the cell intensity data (see "Viewing failed control features", below).

JPG files

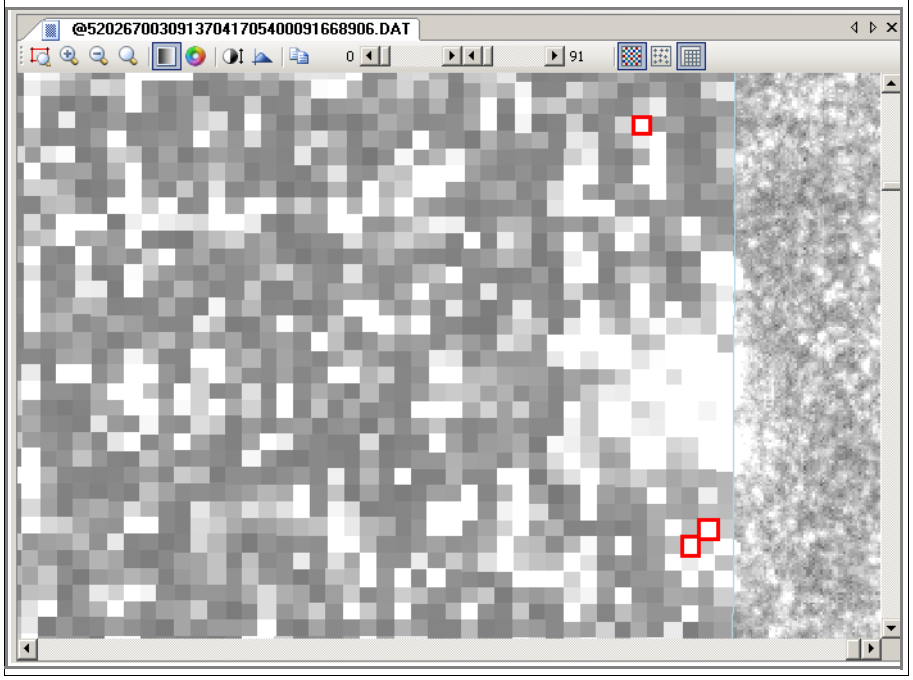
JPG files are a copy of the DAT image in a standard image file format; they provide an image file with a reduced file size for QC inspection, archiving, and publication.

Viewing failed control features

For certain types of probe arrays, the cell intensity analysis also generates a Cell Summary Report. The report has information on the control features on the array that failed certain quality checks.

The failed control features are masked when viewing the cell intensity data in these cases (Figure 308).

Figure 308 Cell intensity data with failed control features masked



See "Changing the grid and intensity display" on page 302 for more information about controlling the grid and intensity display.

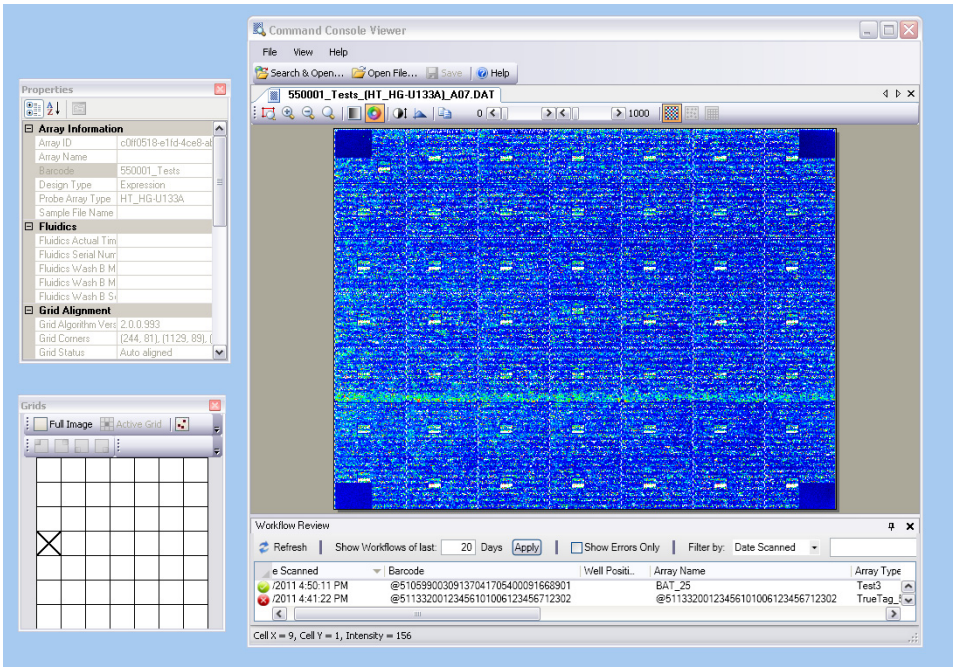
See Appendix C, "Cell summary report" on page 353 for more information about the cell summary report.

Moving the components out of the viewer

You can move the following components to a different location on your screen by clicking in the title bar and dragging the box to the new location (Figure 309).

- Properties box
- Grid box
- Review window

Figure 309 Dragging boxes outside of the GCC Viewer



You can move the Image window outside of the Viewer by clicking on the file name tab and dragging the window out of the viewer.

Docking the boxes back in the GCC Viewer

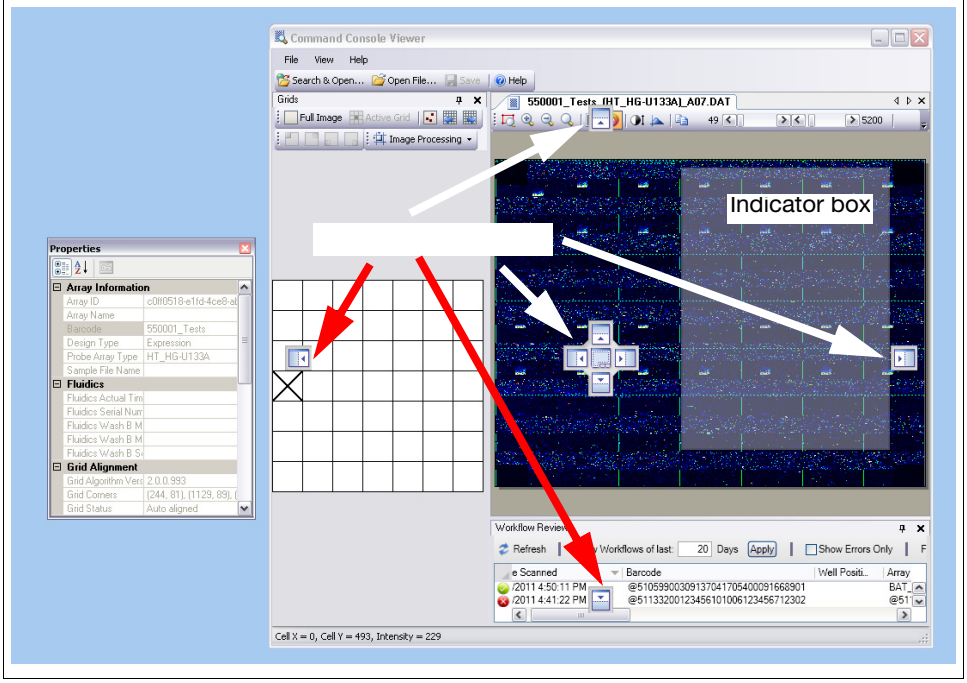
1. Double-click on the box title bar or the file name tab in the Image window.

Choosing a new location for the bo

1. Click on the title bar and drag the box back into the GCC Viewer.

   The docking hints buttons appear in the Viewer. (Figure 310)

Figure 310 Using the Docking Hints buttons



2. Move the Cursor to the docking hint button.

   A gray box appears, showing where the box will dock.

3. Release the mouse button.

   The box is docked in the selected location. The title bar contains two options for the Properties and Grid boxes, Close and AutoHide. (Figure 311)

Figure 311 Box title bars

Closing a box

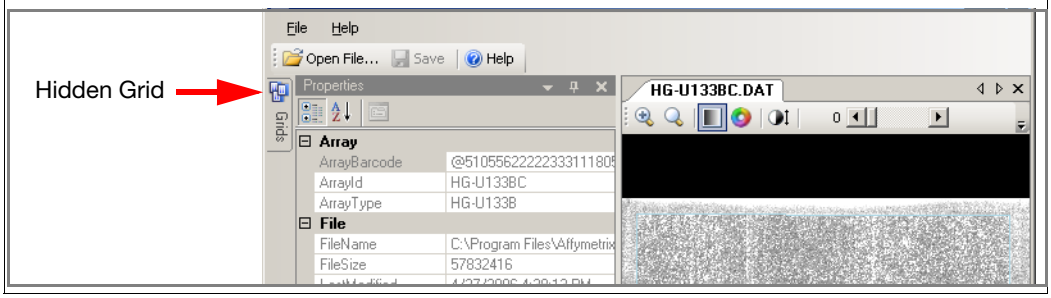
1. Click the **Close** button.

Using the Autohide feature

1. Click the **AutoHide** button in the box.

   The box is closed, but a tab is displayed on the left side of the window (Figure 312).

Figure 312 Hidden Grid Box and tab



Displaying a hidden box temporarily

1. Place your cursor on the tab.

Restoring a hidden box

1. Display the box and click on the **AutoHide** button .

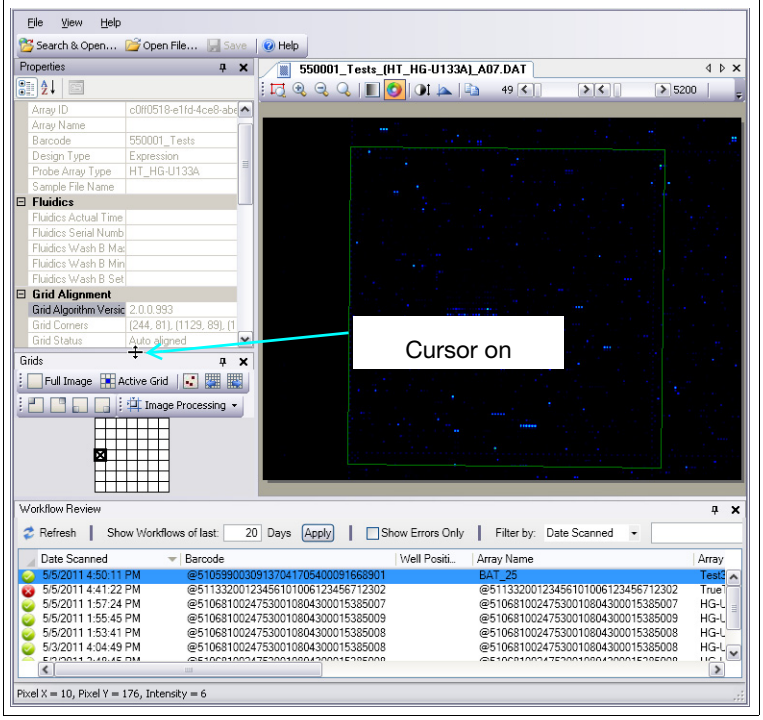
Moving the component borders in the GCC viewer

You can change the relative size of a component in the Viewer by moving the borders of that component.

Changing the size of the component

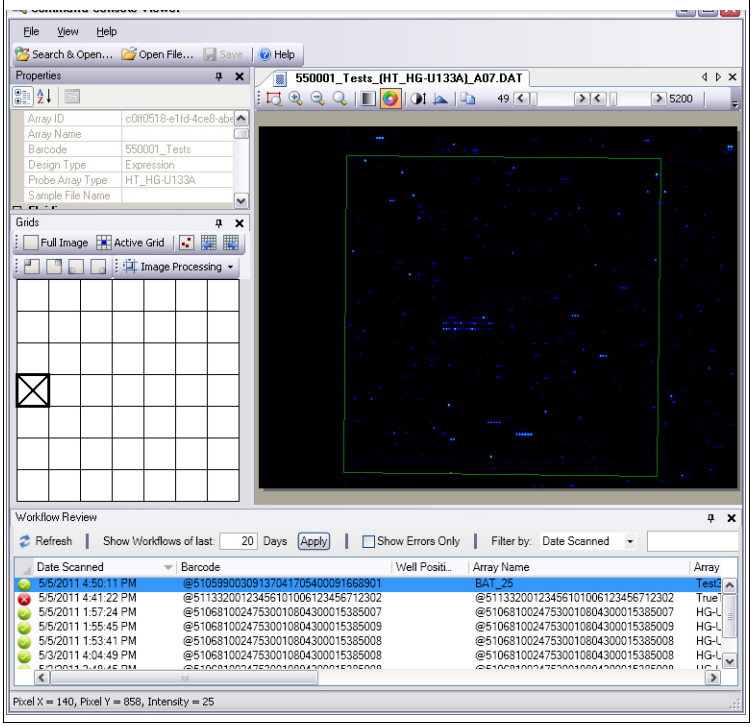
1. Move the cursor over the border until it changes to a double arrow .

Figure 313 Placing cursor on boundary between two components



2. Click and drag the cursor to change the size of the area (Figure 314).

Figure 314 Grid box enlarged.

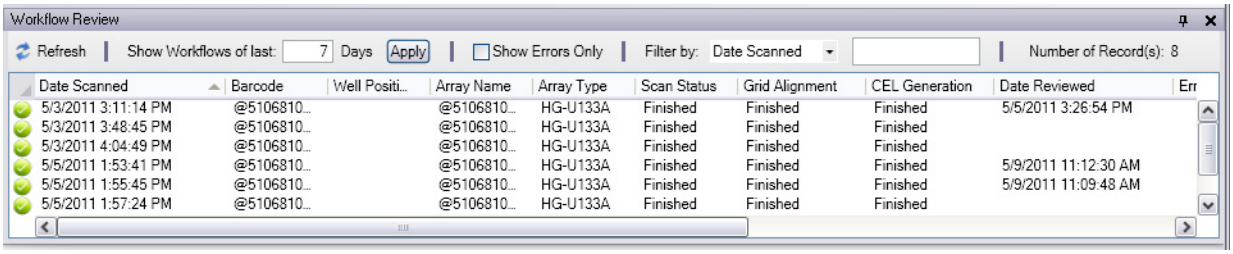


Using the review window

The Review window, at the bottom of the viewer (Figure 315), displays a list of DAT files for scanned arrays. The window includes various information on the DAT files, including the grid alignment and cell generation status.

Figure 315 Review window

Toolbar



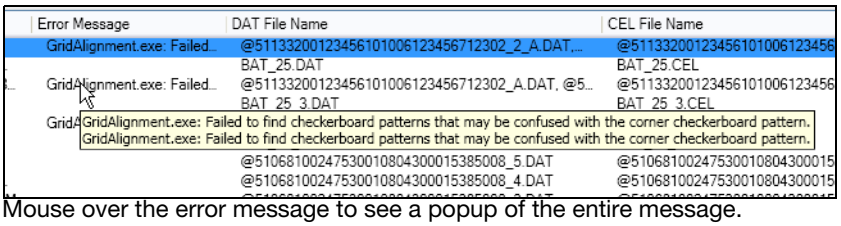
The Toolbar provides access to different functions of the window.

The Review window displays a list of the scans performed along with the following information:

Status Icon	In progress. Finished Failed
Date Scanned	Date and time the array was scanned.
Barcode	Array Barcode.
Well Position	Well Position for Array Plate.
Array Name	Name of the array file created.
Array Type	Probe array model scanned.
Scan Status	Status of scan.
Grid Alignment	Status of grid alignment.
CEL Generation	Status of cell file (CEL) generation.

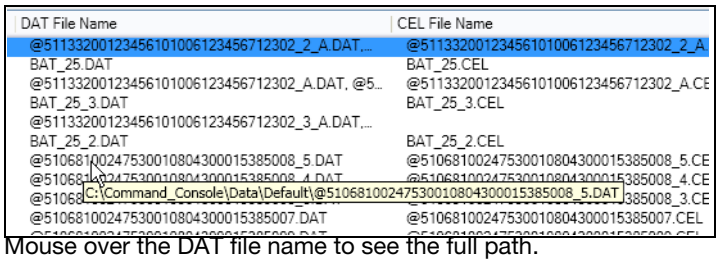
Date Reviewed Data and time the DAT file was last viewed in the Viewer.

Error Message Short message describing the error found [do we need list of codes?].



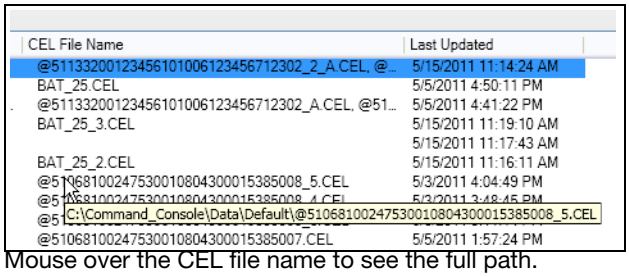
Mouse over the error message to see a popup of the entire message.

DAT File Name Name of the DAT file(s) generated.



Mouse over the DAT file name to see the full path.

CEL File Name Name of the CEL file(s) generated.



Mouse over the CEL file name to see the full path.

Last Updated Date the workflow last ran.

Enable or disable the Review window

1. From the View menu, select **Review Window**.

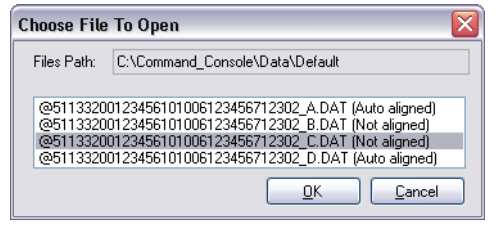
   The Review window displays a list of the scanned arrays with their DAT files and their grid alignment and cell generation status.

Displaying a listed DAT file

1. Double-click on the file in the list.

If the workflow is associated with more than one DAT file, the Choose File to Open dialog box opens (Figure 316).

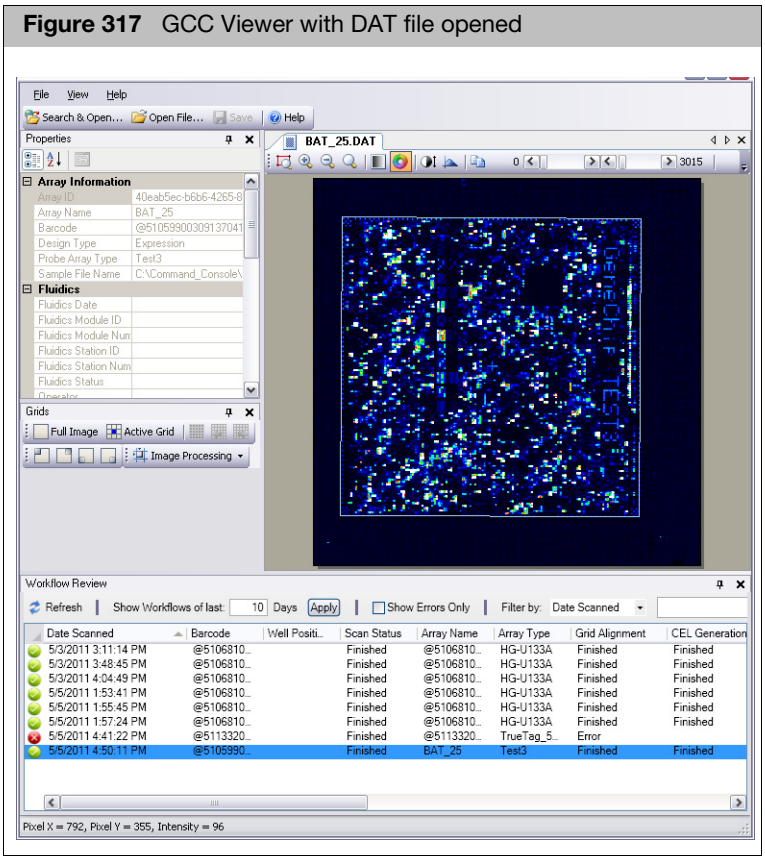
Figure 316 Choose File to Open dialog box



- Select the DAT file to open and click the **OK** button in the Choose File to Open dialog box.

  The image file is displayed in the viewer. (Figure 317)

Figure 317 GCC Viewer with DAT file opened



For information on aligning a misaligned grid, see "Checking the grid alignment" on page 310.

Updating the list

- Click the Refresh button  in the Toolbar.

Sorting the list for a particular parameter value

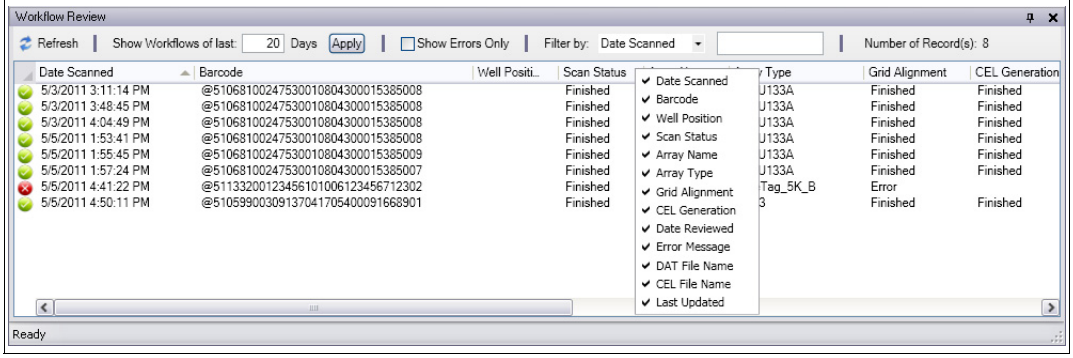
Click in the column header for that parameter.

Selecting columns for display

1. Right-click in any column header.

   A menu of the column headers appears (Figure 318).

Figure 318 Column Header menu



2. Select or deselect the desired parameters to conceal and display them.

Changing the filter settings

The window enables you to filter the workflows to display only the workflows of interest.

You can filter the displayed workflows by:

- Date since workflow ran
- Error Status
- Any of the values in the columns.

It also indicates the number of displayed records in the Workflow Review window.

Filtering by Date since workflow ran

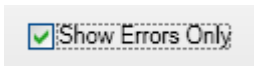
1. Enter a value for the number of days for which you want to display records and click Apply (Figure 319).

Figure 319 Filter by Date controls

Displaying errors only

1. Select the Show Errors Only check box (Figure 320)

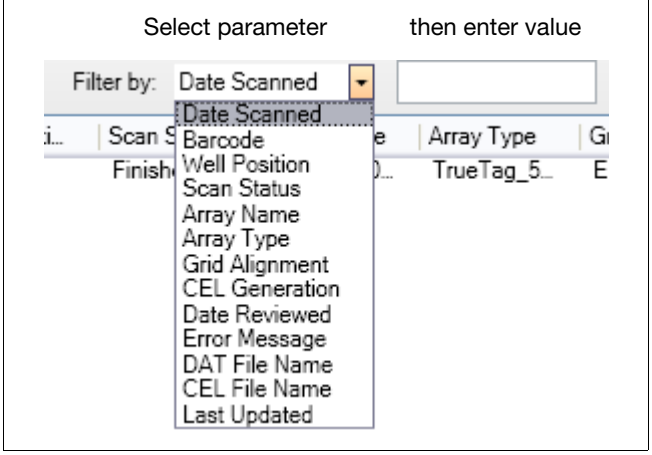
Figure 320 Show Errors Only check box



Filtering by other parameters displayed in the Review window

1. Select the parameter type from the Filter by drop-down list (Figure 321).

Figure 321 Filter by controls



2. Enter a value in the Filter by text box.

   Note: The Filter by function will filter on parameters that are not being displayed in the Review Window. In addition, Only the workflows with parameters matching the entered value will be displayed.

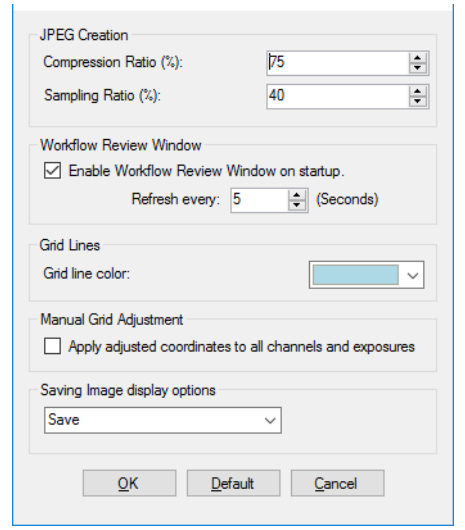
Changing the other settings of the workflow review window

Changing settings for the Review window

1. From the **View** menu, select **Options...**

   The Options dialog box opens (Figure 322).

Figure 322 Options dialog box



2. Select or deselect the following feature:
   - **Enable Review Window on startup**: turns the Review window on whenever the GCC Viewer is opened.

   Note: This change will not take effect until you have stopped and restarted the GCC Viewer.

3. Change the value for the Refresh interval to control the frequency of the Review Window updates.
4. Click **OK** to close the dialog box and enable the changes.

Opening image files

You can display DAT, CEL, and JPG image files in the GCC Viewer. The Viewer has different functions when viewing different types of files (see "File display differences" on page 276).

You have several options for opening files in the Viewer:

- "Using the search and open dialog box", below
- "Using the open dialog box" on page 296
- "Displaying multiple files" on page 297

Using the search and open dialog box

The Search and Open dialog box enables you to search through the files on the GCC system to find the ones of interest.

The Search and Open dialog box enables you to filter the displayed Sample files by:

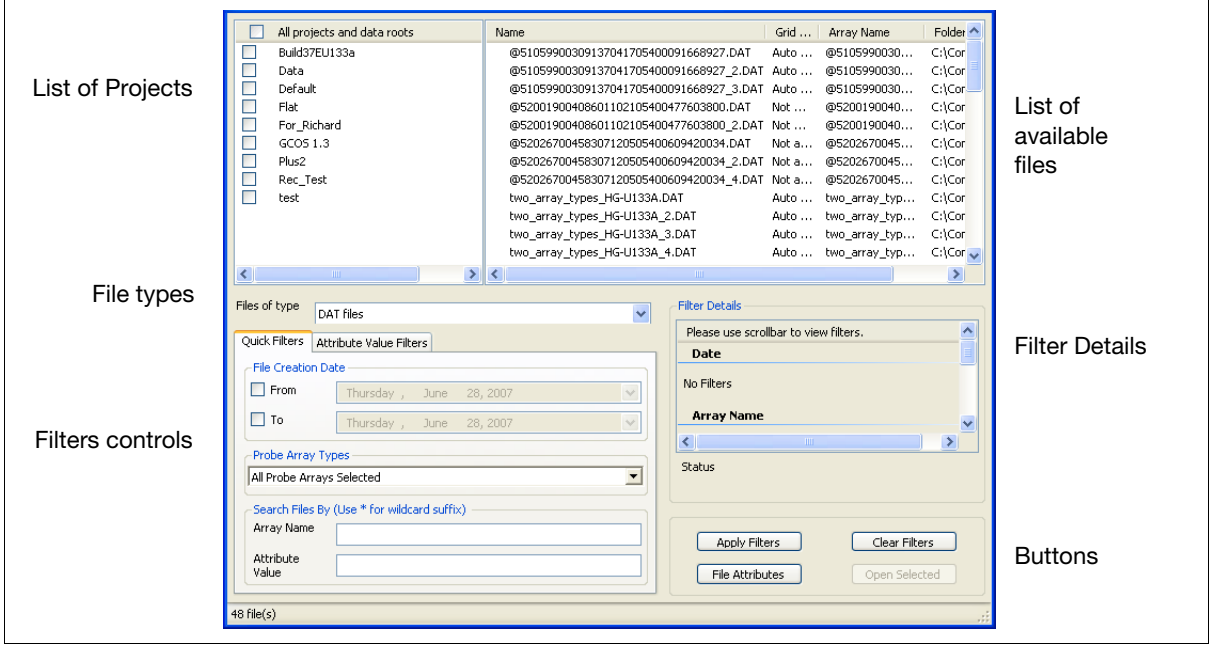
- Projects
- File Type
- File Creation Date
- Probe Array Type
- Array Name
- Attribute Value

1. Click the **Search and Open** button in the Viewer tool bar; or

   From the File menu, select **Search and Open...**.

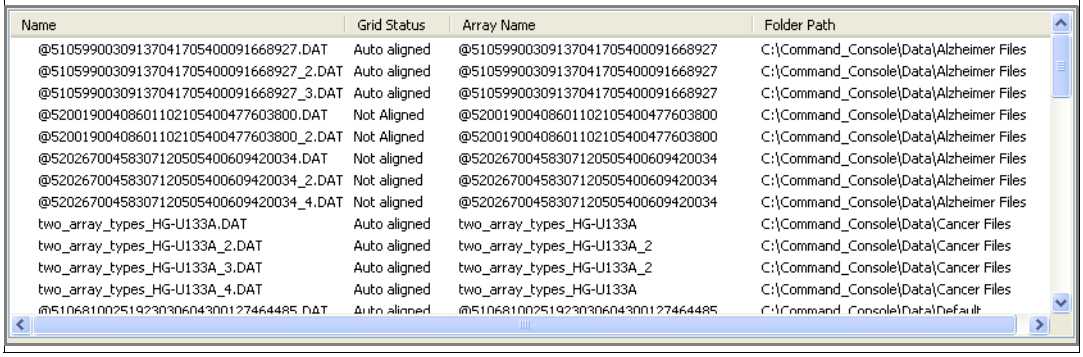
   The GCC File Open dialog box opens (Figure 323).

Figure 323 File Open dialog box



The dialog box displays a list of the files that meet the criteria in the upper right corner (Figure 324). You select the files to display from this list.

Figure 324 Unfiltered file list



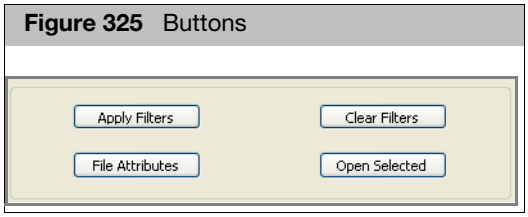
Name	Grid Status	Array Name	Folder Path
@510599003091370417054000916689 27.DAT	Auto aligned	@510599003091370417054000916689 27	C:\Command_Console\Data\Alzheimer Files
@510599003091370417054000916689 27_2.DAT	Auto aligned	@510599003091370417054000916689 27	C:\Command_Console\Data\Alzheimer Files
@510599003091370417054000916689 27_3.DAT	Auto aligned	@510599003091370417054000916689 27	C:\Command_Console\Data\Alzheimer Files
@520019004086011021054004776038 00.DAT	Not Aligned	@520019004086011021054004776038 00	C:\Command_Console\Data\Alzheimer Files
@520019004086011021054004776038 00_2.DAT	Not Aligned	@520019004086011021054004776038 00	C:\Command_Console\Data\Alzheimer Files
@520267004583071205054006094200 34.DAT	Not aligned	@520267004583071205054006094200 34	C:\Command_Console\Data\Alzheimer Files
@520267004583071205054006094200 34_2.DAT	Not aligned	@520267004583071205054006094200 34	C:\Command_Console\Data\Alzheimer Files
@520267004583071205054006094200 34_4.DAT	Not aligned	@520267004583071205054006094200 34	C:\Command_Console\Data\Alzheimer Files
two_array_types_HG-U133A.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_2.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_3.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_4.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files
@510681002519230306043001274644 85.DAT	Auto aligned	@510681002519230306043001274644 85	C:\Command_Console\Data\Default

The upper left corner displays a list of the projects in GCC. The lower left corner displays a set of additional filters you can apply to the file list.

The Filter Details in the lower right corner displays information about the filter criteria that have been applied to the list.

The buttons (Figure 325) allow you to:

Figure 325 Buttons



Apply Filters Apply selected Quick Filter and Attribute Value Filter criteria

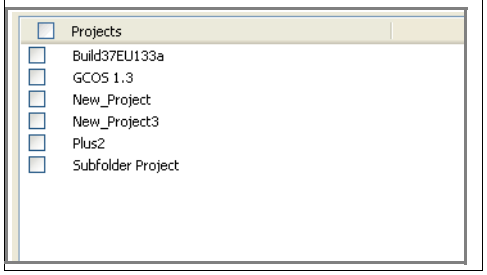
Clear Filters Clear all applied filters

File Attributes Select attributes to be displayed in File list.

Open Selected Open selected files in File list

2. Select the project(s) with files you want to list in the Projects list (Figure 326).

Figure 326 Displaying Project List



3. Select File Types from the drop-down list.

   You can choose from:

   - DAT
   - CEL

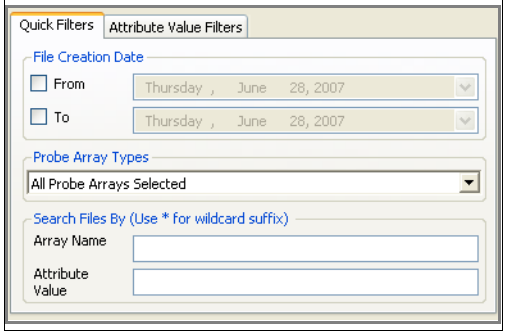
   Changes made in the Projects and Files filters are reflected instantly in the Filter Details part of the dialog box.

   Changes to the Quick Filters and Attribute Value Filters have to be applied by clicking the **Apply Filters** button after selecting.

   The Quick Filters (Figure 327) enable you to filter by:

   - Date of file creation
   - Probe Array Types
   - Array Name
   - Attribute Value

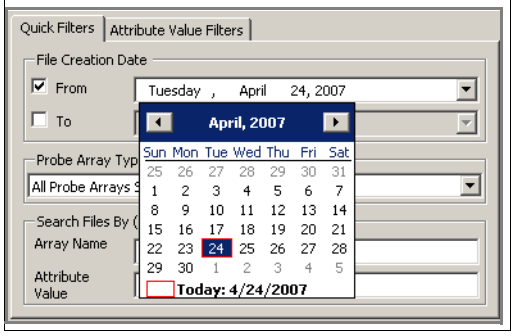
Figure 327 Quick Filters



4. Select a date or range of dates for file creation:
   a. Select the **From** check box.
   b. Click the arrow at the date (displays the current date).

      A calendar for the current month appears (Figure 328).

Figure 328 From Calendar



c. Select a date for the start of the range. You can move from month to month by clicking the < and > buttons.

   If you only select one date, the filter will display only the files created on that date.

To select a range of dates:

d. Select the **To** check box.

e. Select a date for the end of the range.

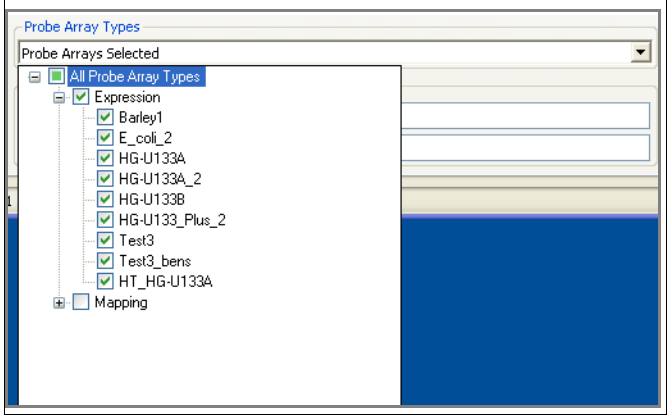
5. Select Probe Array Types:

   a. Click on the down arrow in the Selected Probe Array Types list.

      A list of the available probe array types is displayed (Figure 329).

      In some cases there may be multiple array models under the same header. in these cases you can click the + button to display the additional probe arrays.

Figure 329 Displaying array types



   b. Select the check boxes next to the probe array types you want displayed in the filtered list.

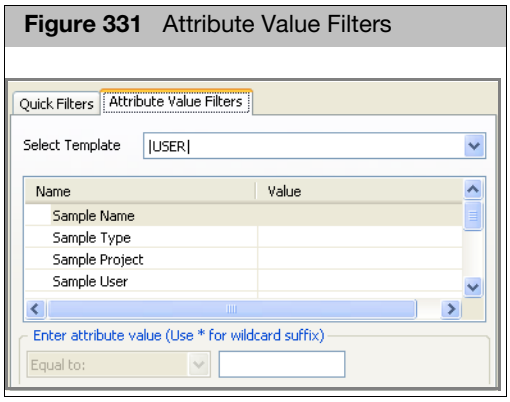
6. Enter text strings for Array Name and Attribute Value (Figure 330).

Figure 330 Selecting an attribute

You can use the "*" symbol as a wildcard in the Array Name and Attribute.

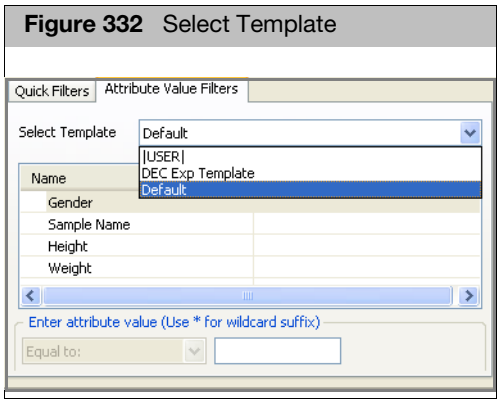
The Attribute Value filters (Figure 331) enable you to enter values for specific sample attributes.

Figure 331 Attribute Value Filters



7. To enter values for specific attributes:
   a. Click the Attribute Value Filters tab (Figure 331).
   b. Select a template with the attribute you want to search on from the Select Template list (Figure 332).

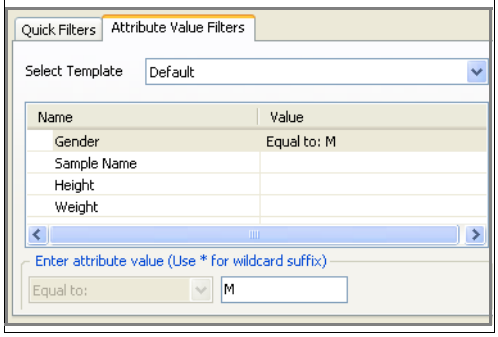
Figure 332 Select Template



The list displays only the templates with attributes that are being used in the data. |User| attributes are the attributes created specifically for a particular Sample (ARR) file and are not included in any template list.

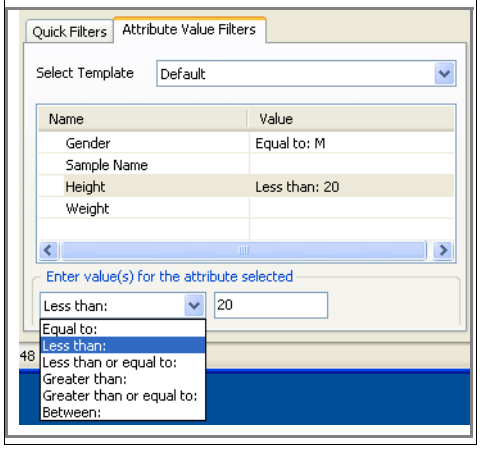
The attributes in that template appear in the Name list (Figure 333).

Figure 333 Selecting attribute and entering value



c. Select the attribute and enter a value for it in the Attribute box.

Figure 334 Selecting Limits



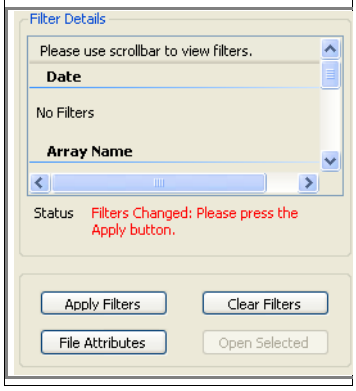
You can perform special searches by using the "*" and "," symbols.

"*" Serves as a wild card function. Using `searchstring*` will return all arrays that contain an attribute that starts with the search string. Using `*searchstring` will return all arrays that contain an attribute that ends with the search string.

If you select a numerical attribute, you can select from the following limits:

- Equal to
- Less than
- Less than or equal to
- Greater than
- Between (use comma-separated values to set the ends of the range).

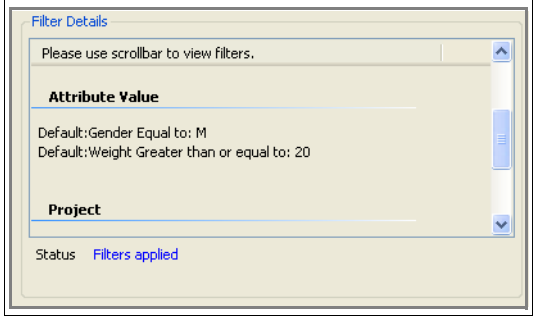
Figure 335 Filter details with Status notice



Whenever you change a setting in these filter boxes, you need to apply the changes. A notice appears to that effect in the Filter Details area (Figure 335).

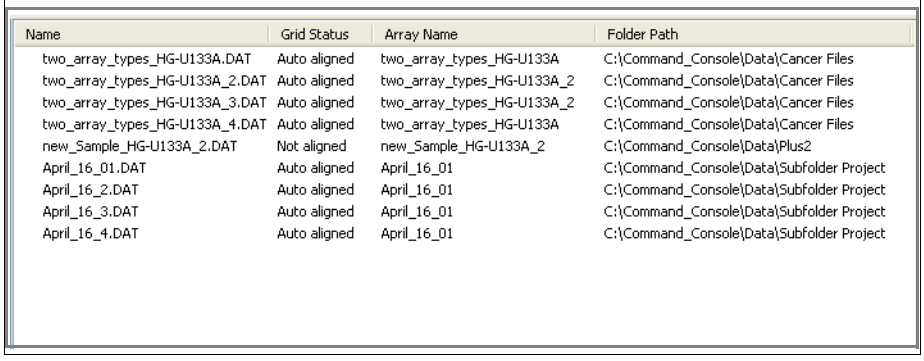
8. Click **Apply Filters** after making changes.
9. The changes are displayed in the Filter Details section (Figure 336).

Figure 336 Filter Details with attributes displayed



The filtered file list is displayed in the File List (Figure 337).

Figure 337 Filtered file list



Name	Grid Status	Array Name	Folder Path
two_array_types_HG-U133A.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_2.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_3.DAT	Auto aligned	two_array_types_HG-U133A_2	C:\Command_Console\Data\Cancer Files
two_array_types_HG-U133A_4.DAT	Auto aligned	two_array_types_HG-U133A	C:\Command_Console\Data\Cancer Files
new_Sample_HG-U133A_2.DAT	Not aligned	new_Sample_HG-U133A_2	C:\Command_Console\Data\Plus2
April_16_01.DAT	Auto aligned	April_16_01	C:\Command_Console\Data\Subfolder Project
April_16_2.DAT	Auto aligned	April_16_01	C:\Command_Console\Data\Subfolder Project
April_16_3.DAT	Auto aligned	April_16_01	C:\Command_Console\Data\Subfolder Project
April_16_4.DAT	Auto aligned	April_16_01	C:\Command_Console\Data\Subfolder Project

10. Select the file(s) you want to open from the File list and click the Open Selected button.

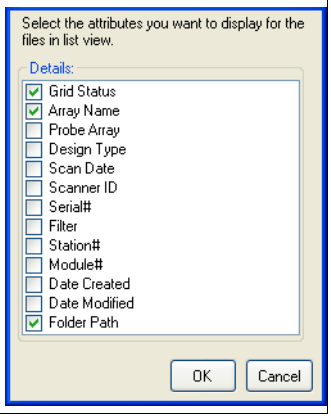
    The selected file is displayed in the Viewer.

Displaying different file attributes in the File list

1. Click the File Attributes button.

   The Choose Column Details dialog box appears (Figure 338).

Figure 338 Choose Column Details dialog box



   The dialog box displays a lit of the different characteristics that can be selected for display, with a check box next to each characteristic.

2. Select the check box for the characteristics you want to display.
3. Click **OK**.

The selected characteristics are displayed in the File list.

Using the open dialog box

The Open dialog box displays a list of all the available image files in the system.

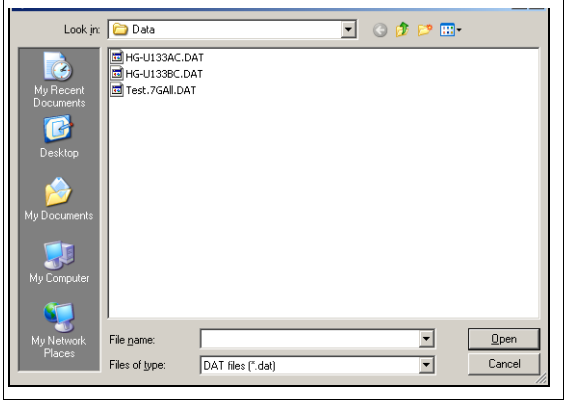
Opening a file using the Open dialog box

4. From the File menu, select **Open File**; or

   Click the **Open File** button in the GCC Viewer tool bar.

   The Open dialog box opens (Figure 339).

Figure 339 Open dialog box



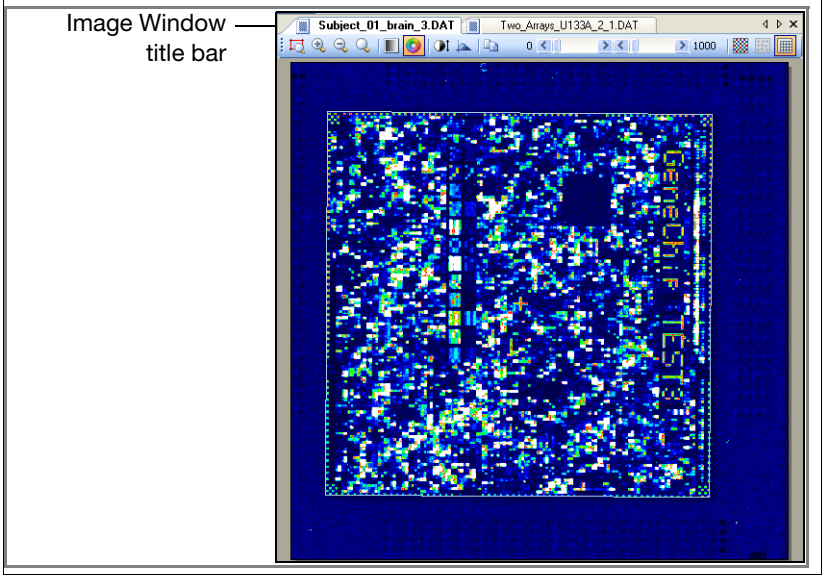
5. If necessary, use the dialog box tool bar to navigate to the directory with the file.
6. Select the file you want to view.
7. Click **Open**.

   The selected image file is displayed in the GCC Viewer.

Displaying multiple files

You can open more than one file in the GCC Viewer (Figure 340).

Figure 340 Displaying multiple image files

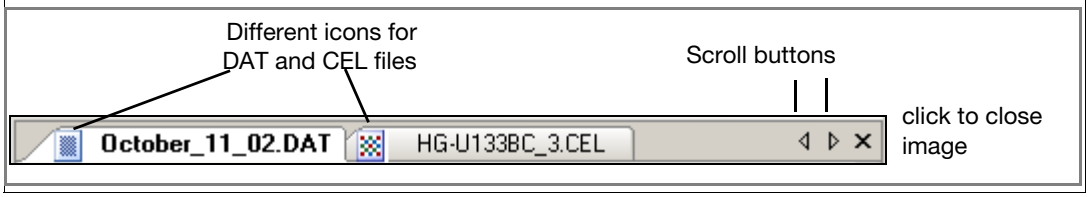


Displaying a particular image when you have more than one open

1. Click the tab at the top of the Image Window.

   Use the **<** and **>** scroll buttons in the Image title bar to scroll through the tabs if necessary (Figure 341).

Figure 341 Image window title bar

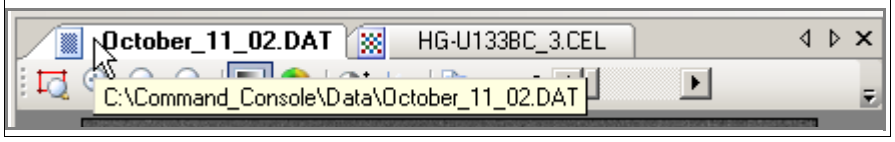


Different icons are used for DAT and CEL files.

Displaying the full path to a displayed file

1. Place your cursor on the file's title bar tab.
   The full path is displayed below the title bar (Figure 342).

Figure 342 Displaying the path to a file

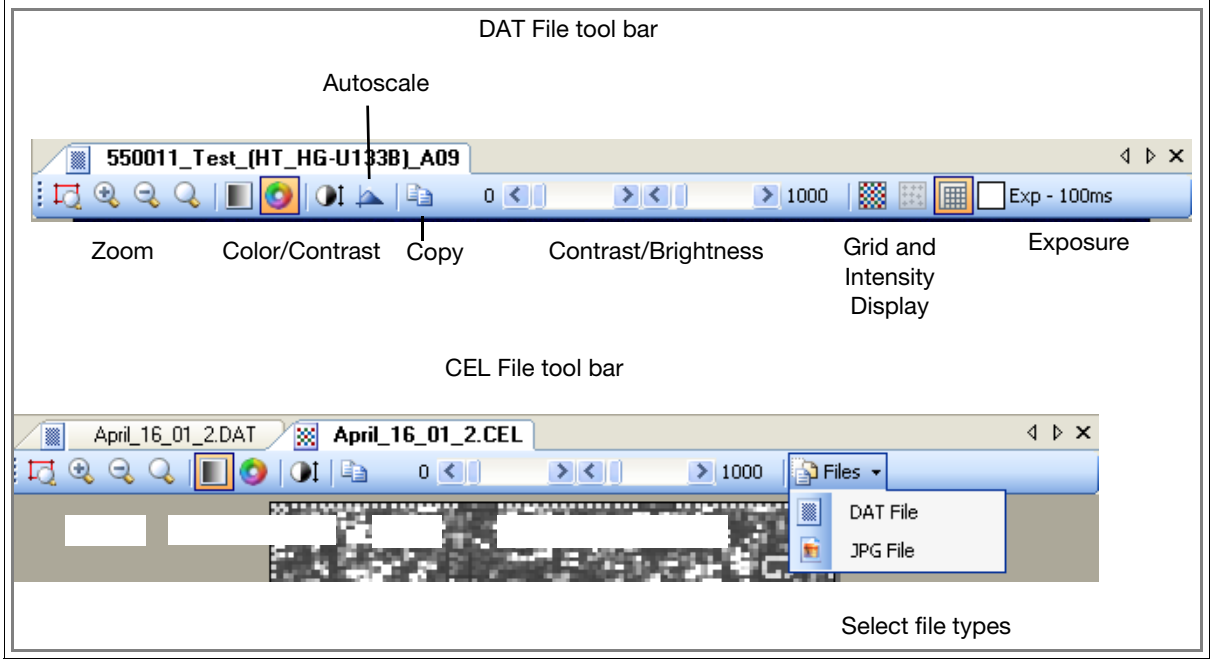


Changing the display of the image

This section explains how to use the Image tool bar controls (Figure 343) for:

- "Examining different parts of the image" on page 300
- "Adjusting the colors and contrast" on page 301
- "Changing the grid and intensity display" on page 302

Figure 343 Image window tool bar for DAT and CEL file

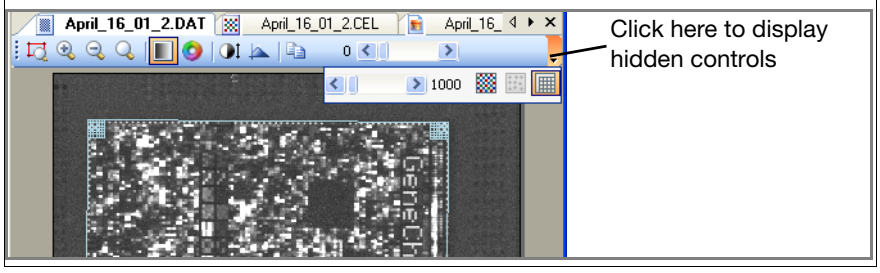


Part of the tool bar may be hidden if the GCC Viewer is too small.

Displaying the hidden controls

1. Click on the **Hidden Tool Bar** button at the right of the toolbar (Figure 344).

Figure 344 Displaying hidden controls



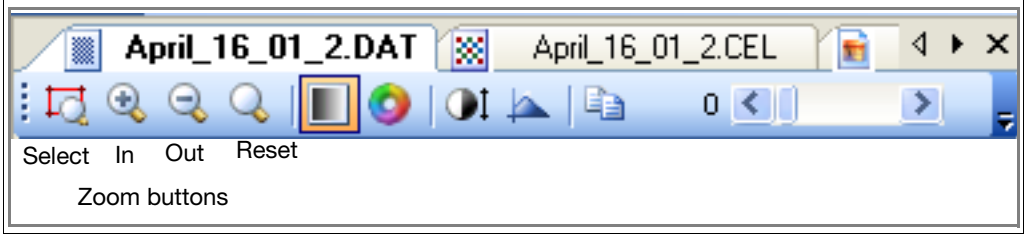
The hidden controls are displayed below the tool bar (Figure 344).

Examining different parts of the image

These functions work on DAT, CEL, and JPG files.

The Zoom controls are at the left end of the tool bar.

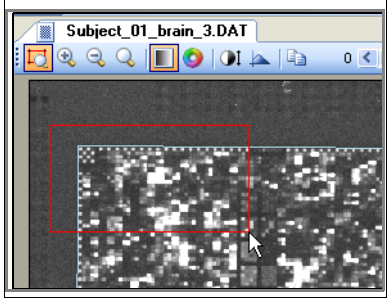
Figure 345 Zoom controls



Zooming in on a selected area of the image

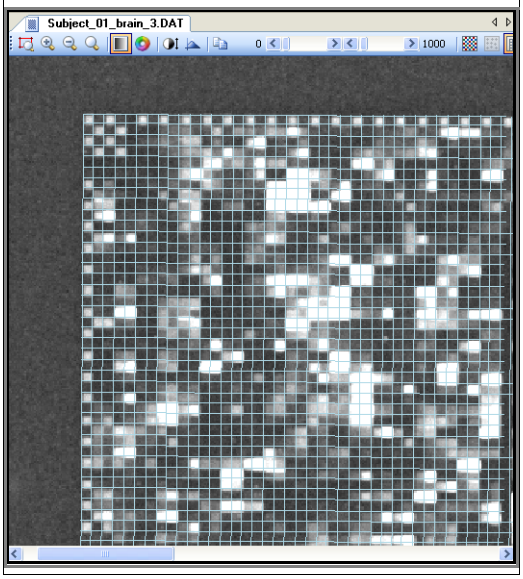
1. Click on the **Zoom Select** button .
2. Click and drag around the area you want to examine in more detail (Figure 346).

Figure 346 Click and drag



3. Release the mouse button.
4. The selected area is displayed in the GCC Viewer (Figure 346).

Figure 347 Zoomed-in view (with grid displayed)



Zooming in or out on the whole image

5. Click on the Zoom In button or the Zoom Out button .

Viewing a different area in magnified zoom

1. Click and drag the image to view the area of interest.

Zooming out

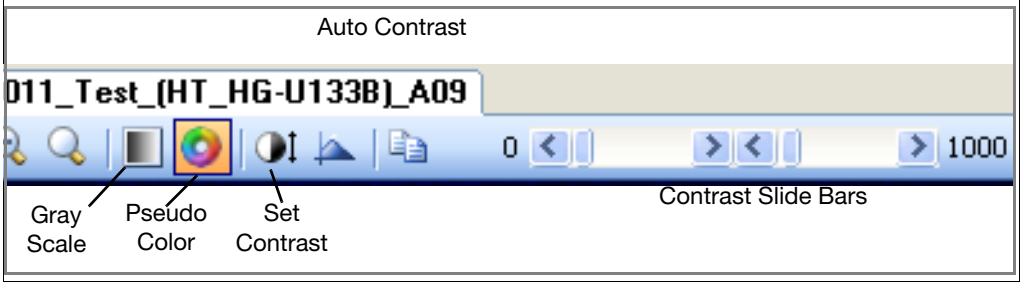
1. Click the **Zoom Reset** button .

   Note: You can also use the Grid box controls to select a particular corner or sub-grid for examination (see "Checking the grid alignment" on page 310).

Adjusting the colors and contrast

These functions work on DAT, CEL, and JPG files.

Figure 348 Color and Contrast controls



Switching between Gray Scale or Pseudo Color display

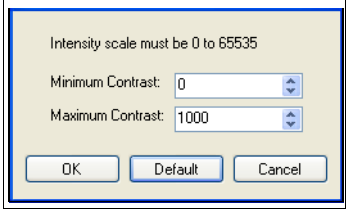
1. Click the **Gray Scale** or **Pseudo Color** buttons.

Adjusting the contrast range for the image

1. Click the **Set Contrast** button .

   The Set Contrast dialog box opens (Figure 349).

Figure 349 Set contrast dialog box



2. Set the minimum and maximum contrast range.
3. Click **OK** to use the settings; or

   Click **Default** to return to the default settings; or

   Click **Cancel** to close the dialog box without changing the settings.

You can also use the slide bars in the tool bar (Figure 348) to set the contrast without opening the Set Contrast dialog box.

Using the Autoscale Function

The autoscale function takes the image area you are currently viewing and calculates the intensity to find a better minimum and maximum contrast.

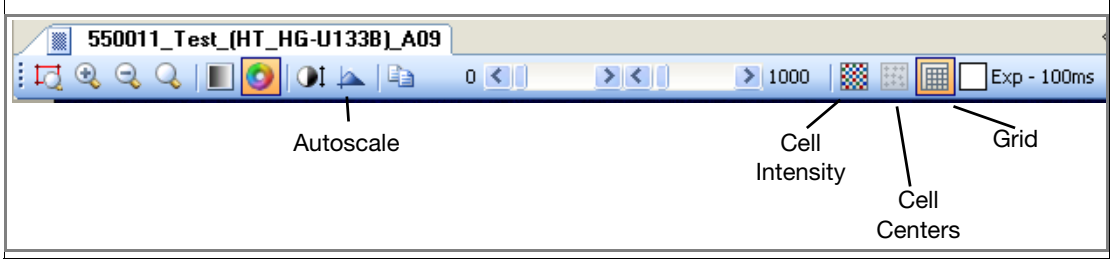
1. Click the **Autoscale** button .

   The contrast and brightness are automatically adjusted.

Changing the grid and intensity display

These functions only work when DAT files are displayed (Figure 350).

Figure 350 Image window tool bar, grid and intensity controls (for DAT files only)



Displaying cell intensity data

If you have a DAT file open with the associated cell intensity data (CEL) file available, you can view the intensity data in the DAT file Image window.

Display or hide the cell intensity data

1. Click the **Cell Intensity** button .

   The cell intensity data for the array is displayed.

   Note: When displaying cell intensity data for certain types of probe arrays, control feature cells that failed the cell summary analysis may be masked. See "Viewing failed control features" on page 277.

Displaying different exposures (GeneTitan expression array plate DAT files only)

Each GeneTitan array is scanned twice, with different exposure times. The image data from both exposures are in the GeneTitan DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Exposure button.

The Exposure button displays the currently displayed exposure time.

Switching between views of the different exposures

1. Click the **Exposure** button.

Figure 351 Exposure button

   The other DAT Exposure is displayed.

Displaying different wavelengths (Axiom array plate DAT files only)

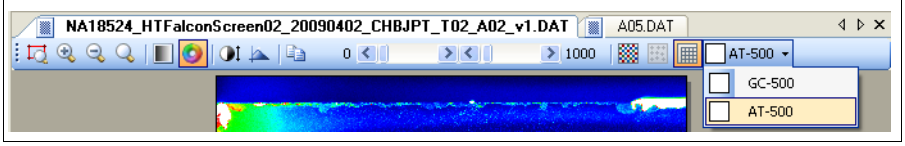
Each genotyping array is scanned twice, at different wavelengths. The image data from both exposures are in the genotyping DAT file. You can switch between the different exposures for checking the gridding, etc., by using the Wavelength button.

The Exposure button displays the currently displayed exposure time.

Switching between views of the different exposures

1. Click the Color button.

Figure 352 Wavelength button



   The other genotyping DAT Exposure is displayed.

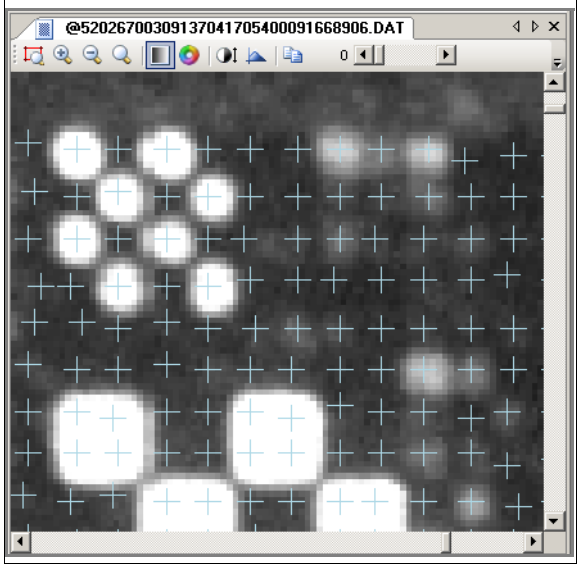
Displaying cell centers

The center of each cell on the array can be displayed for certain array types. The centers are visible only when viewing DAT files for probe arrays with sub-grids at a

sufficiently zoomed-in level. The cell center display can be used in evaluating gridding problems.

- Click the **Cell Centers** button  .
  The cell centers are displayed. (Figure 353)

Figure 353 Cell centers displayed for a sub-grid

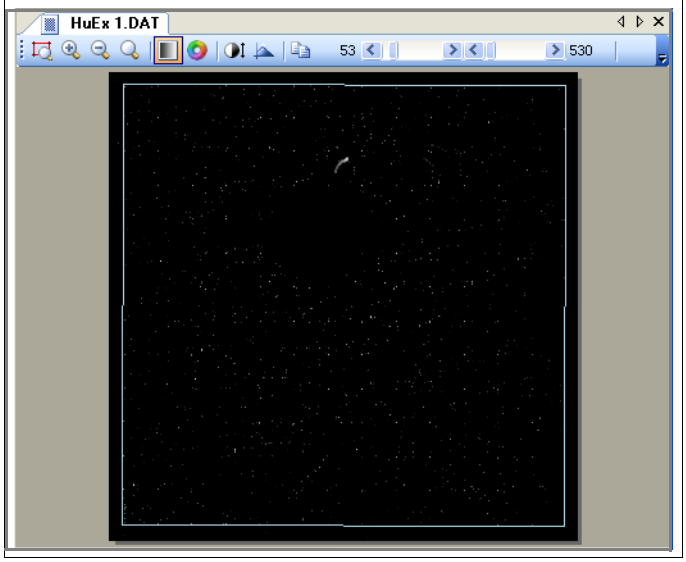


Displaying the grid corners

The grid can be displayed to evaluate gridding problems and perform manual gridding.

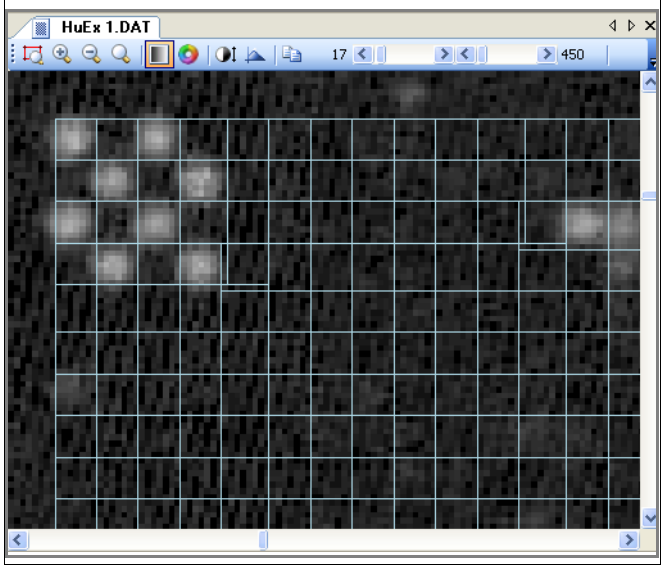
1. Click the **Grid Corners** button  .
   The outline of the grid is displayed on the image.

Figure 354 Outside edges of main grid displayed



The grid cells are not displayed until you have magnified the DAT file so that they are visible. (Figure 355)

Figure 355 Corner grid displayed for a sub-grid



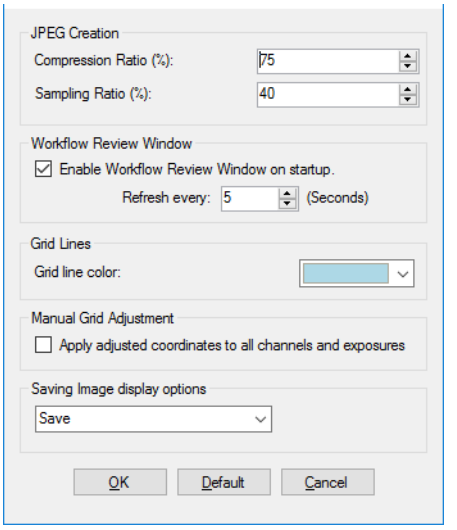
See "Checking the grid alignment" on page 310 of this manual for more information about manual gridding.

Changing settings for the grid display

1. From the **View** menu, select **Options...**

   The Options dialog box opens (Figure 356).

Figure 356 Options dialog box.



2. Select a new color for the grids from the Grid line color drop-down box.
3. Click **OK** to close the dialog box and enable the changes.

Saving image display options

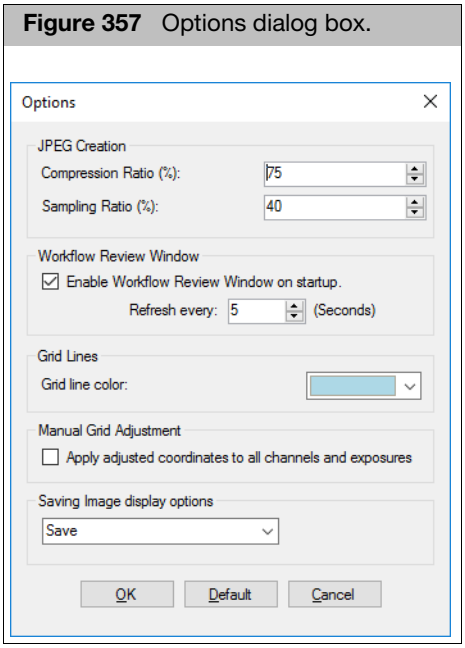
You can change the save options for the image display settings. These allow you to apply the same contrast and other settings to different image files.

Changing the Save Options for the image display options

1. From the **View** menu, select **Options...**

   The Options dialog box opens. (Figure 356)

Figure 357 Options dialog box.



2. Select an option from the Saving Image Display options drop-down box:
   - Do Not Save
   - Save: Save settings from one program session to the next.
   - During the program session: Save settings only until the Viewer is shut down.
3. Click **OK** to close the dialog box and enable the changes.

Learning about the image file

The Properties box displays information about the image file displayed in the window. The information can be displayed in alphabetical order, or ordered by different categories, depending upon the type of file displayed:

For a DAT file:

- Array Information
- Fluidics
- Grid Alignment
- Image
- Scanner

For a CEL file:

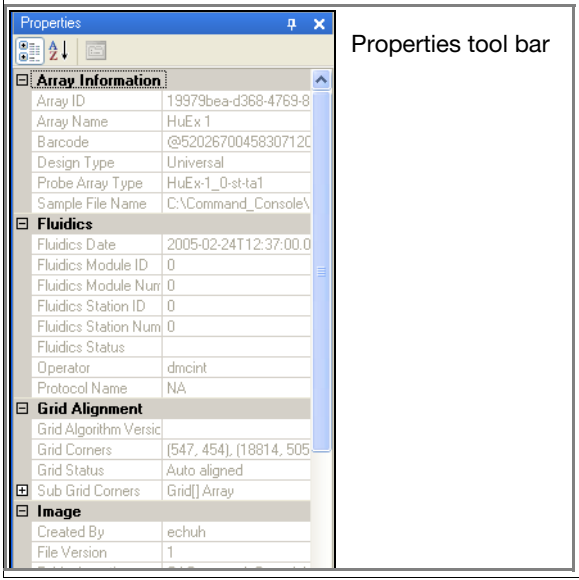
- Array Information
- Cel
- CEL Summary Report (only for files with CEL Summary Reports)
  - You can click on the Report row first, and then click on the button that appears to open a text display of the CEL Summary report (Figure 358).

Figure 358 Cel Summary Report Section

See Appendix C, "Cell summary report" on page 353 for more information.

- Fluidics
- Scanner

Figure 359 Properties box



Expand or collapse a component

1. Click on the +/- button to the left of the component.

Sorting the data in a different way

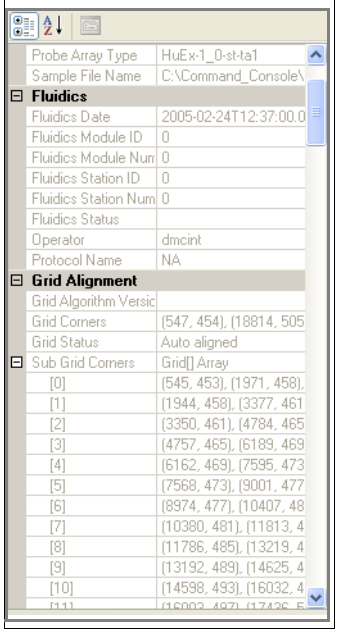
1. Click the **Category Sort** or the **Alphabetical Sort** button.

Grid information

The Grid information category displays information about the main grid and sub-grids:

- Global Grid: Displays the pixel coordinates for the corners of the main grid.
- sub-grids (when available): Displays the pixel coordinates for the corners of each sub-grid. (Figure 360)

Figure 360 sub-grids displayed



Checking the grid alignment

This chapter describes the use of the GCC Viewer for aligning failed grids:

- "Aligning the main grid" on page 310
- "Aligning sub-grids" on page 314
- "Aligning sub-grids on GeneTitan arrays" on page 320
- "Regenerating intensity values" on page 322

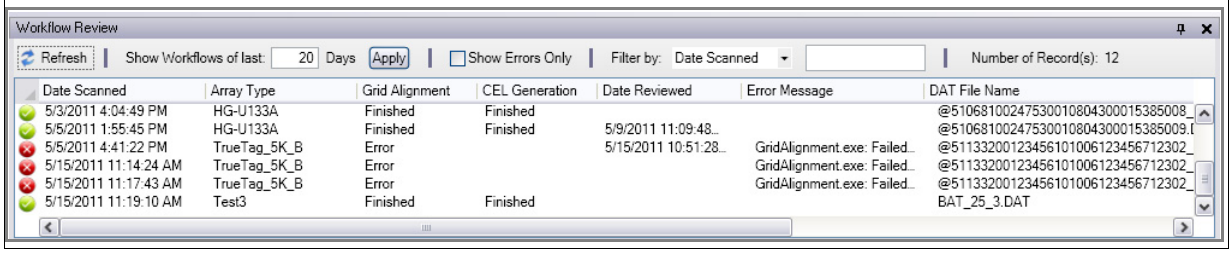
For general information about grid alignment, see "Array and grid types" on page 268.

Aligning the main grid

If the array has sub-grids, the main grid has to be aligned before aligning the sub-grids.

If the main grid is misaligned, you will see a notice in the Review list (Figure 361).

Figure 361 Notice of failed grid alignment



Viewing the main grid

1. Click the **Full Image** button Full Image in the Grids tool bar (Figure 362).

   The main grid is displayed for single-grid and multi-grid files.

You have two options for fixing an alignment problem:

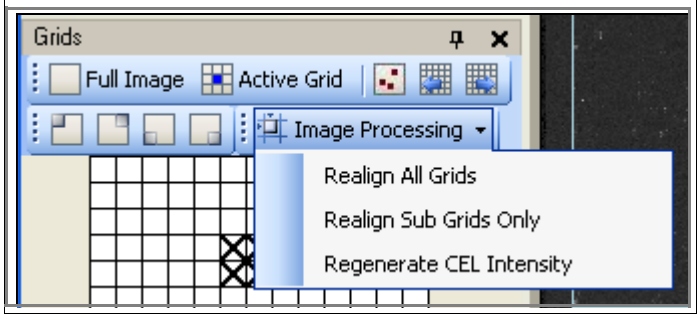
- You can run the gridding algorithm again.
- You can align the grid manually.

  Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

Running the gridding algorithm

In some cases you can realign the grid by running the alignment algorithm again.

Figure 362 Grid box tool bar



Running the alignment algorithm on an array that uses a single grid

2. In the Grids tool bar, click on the **Image Processing** button 

and select **Realign All Grids** from the shortcut menu. (Figure 362)

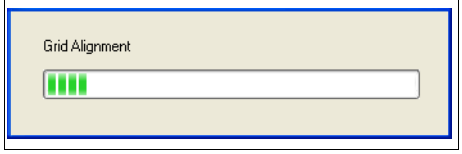
   A notice informs you that a new cell intensity data file (CEL) will be generated.

Figure 363 Notice of regridding

3. Click **Yes** to proceed with the alignment.

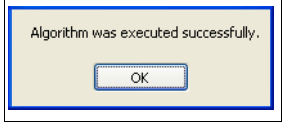
   Progress bars display the progress of the alignment and cell generation.

Figure 364 Progress bar



When the process is finished, a notice appears. (Figure 365)

Figure 365 Notice



New gridding information and a new CEL file are generated.

Aligning the grid manually

If the algorithm alignment fails, an error message appears. (Figure 366)

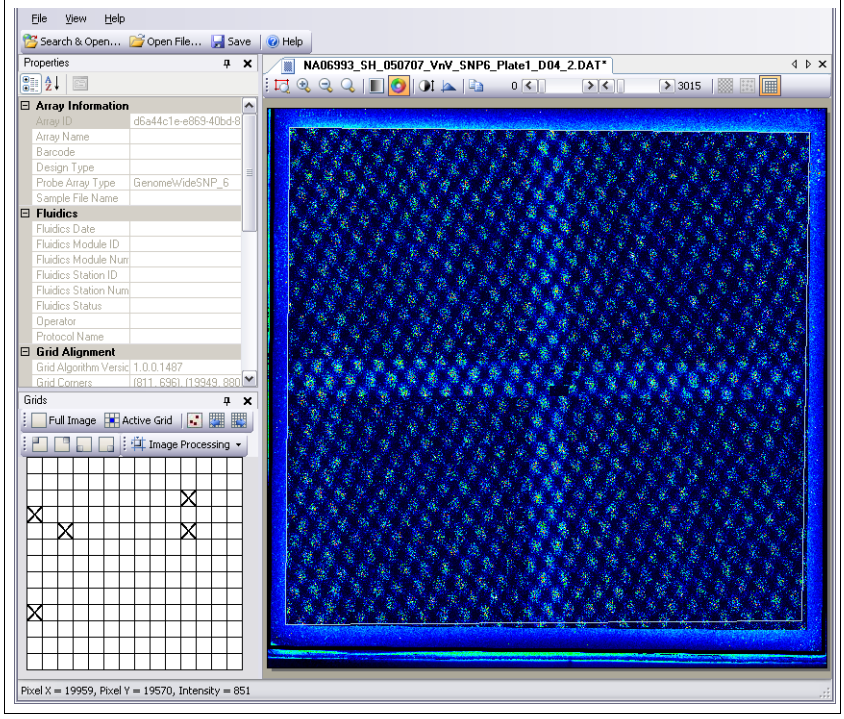
Figure 366 Notice of main grid misalignment

If you see the error message, you can manually adjust the main grid by using the following procedure:

1. Click on the failed DAT file in the Review window.

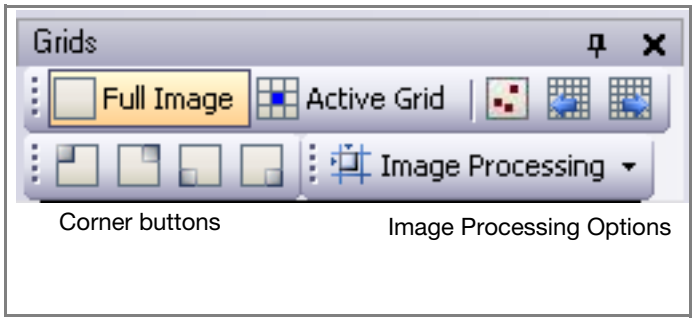
   The main grid is displayed in the Image window. (Figure 367)

Figure 367 Misaligned main grid



2. Align the grid at each corner of the image:

Figure 368 Grid box toolbar

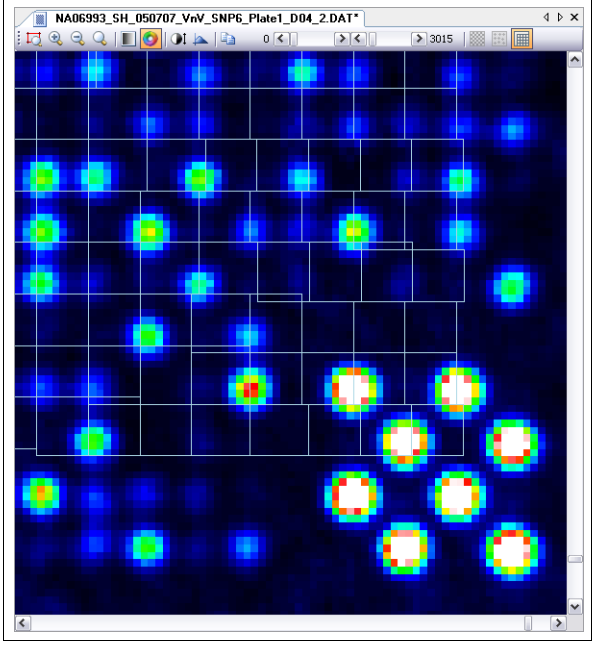


a. Click a Corner button in the Grid box toolbar (Figure 368) to choose a corner.

   The selected corner is displayed in the Image window. (Figure 369)

   The software displays a box around each feature of the corner grid.

Figure 369 Lower right corner displayed in the image window



b. Place the mouse arrow over the grid perimeter (the arrow becomes a double arrow, ↕ ⤢ ↔).

   The diagonal orientation of the double arrow along the perimeter of a corner probe cell indicates horizontal and vertical adjustments can be made simultaneously using the click-and-drag method or by using the keyboard arrow keys.

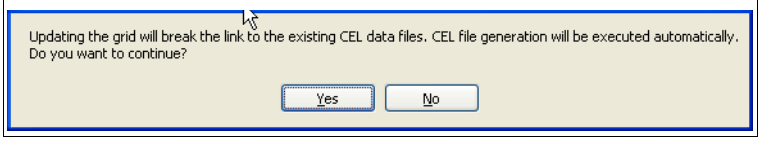
c. Use the click-and-drag method or the keyboard arrow keys to adjust the horizontal or vertical position of the grid so that it is aligned over the corner of the outermost corner checkerboard.

d. Repeat the above steps for the other corners of the main grid.

3. After you align the grid, click the **Save** button Save or select **File** → **Save** from the menu bar.

   A notice opens, informing you that a new cell intensity data file will be generated automatically. (Figure 370)

Figure 370 Notice



4. Click **Yes** to save the DAT file and generate a new CEL file.

   The cell intensity data file will be generated automatically.

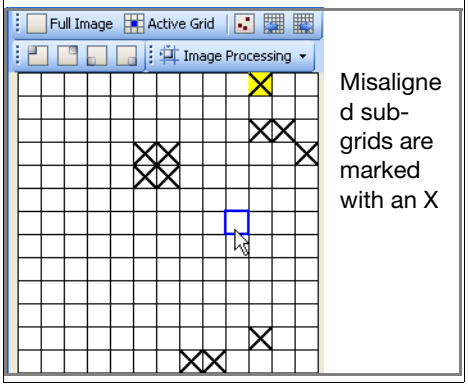
   For arrays with a single grid, you can now proceed to generate the CEL file (see "Regenerating intensity values" on page 322).

   For arrays with sub-grids, you can now check the alignment of the sub-grids (see "Regenerating intensity values", below).

Aligning sub-grids

Sometimes one or more sub-grids may require alignment. The failed sub-grids are marked with an X in the Grids box (Figure 371).

Figure 371 Grid box



If the sub-grid alignment fails you can:

- Run the sub-grid alignment algorithm.
- Perform a manual alignment on the failed sub-grids.

  Note: Realigning the grids will update DAT headers and break the parent-child relationship between DAT files and existing CEL files until the CEL files are regenerated.

Running the sub-grid alignment algorithm

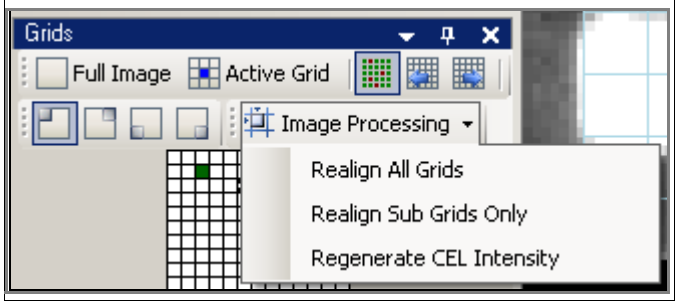
You can run the sub-grid alignment algorithm if some of the sub-grids are misaligned or if you have manually aligned the main grid.

Running the alignment algorithm again on an array that uses sub-grids

1. In the Grids toolbar, click on the **Image Processing** button 

and select **Realign All Grids** from the shortcut menu. (Figure 372)

Figure 372 Grids tool bar for array with sub-grids



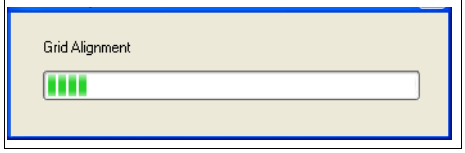
A notice informs you that a new cell intensity data file (CEL) will be generated. (Figure 373)

Figure 373 Regridding notice

2. Click **Yes** to proceed with the alignment.

   Progress bars display the progress of the alignment and cell generation. (Figure 374)

Figure 374 Progress bars



When the process is finished, new gridding information and a new CEL file are generated and will align the main grid and all sub-grids.

Running the sub-grid alignment algorithm only

1. In the Grids toolbar, click on the **Image Processing** button 

and select **Realign sub-grids Only** from the menu. (Figure 372)

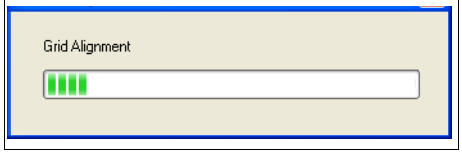
   A notice informs you that a new cell intensity data file (CEL) will be generated. (Figure 375)

Figure 375 CEL generation notice

2. Click **Yes** to proceed with the alignment.

   Progress bars display the progress of the alignment and cell generation. (Figure 376)

Figure 376 Progress bars

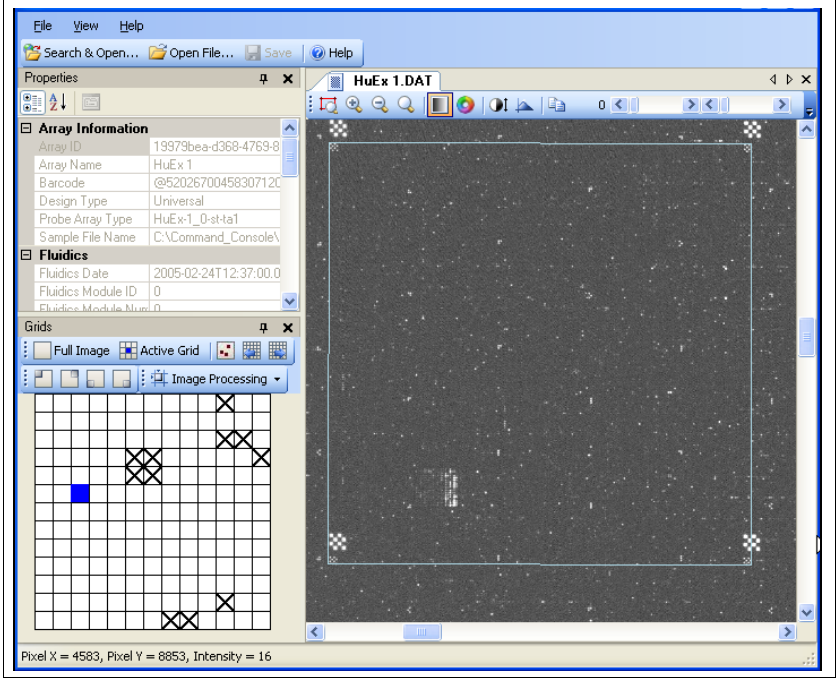


When the process is finished, new gridding information and a new CEL file are generated.

Manually aligning the sub-grids

The boundaries of a sub-grid are indicated by the alignment patterns at the four corners of the sub-grid. A small checkerboard may mark the corner of two or more sub-grids, depending upon its position in the main grid. (Figure 377)

Figure 377 sub-grid borders



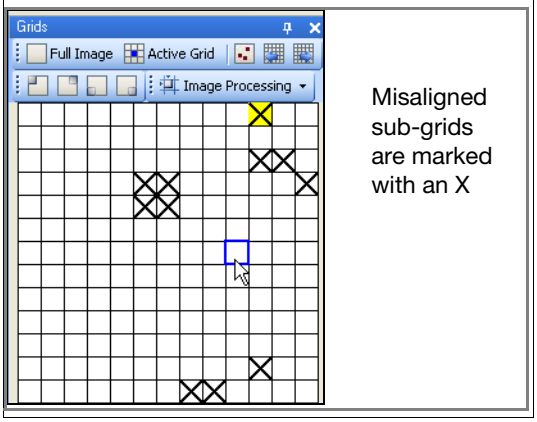
If the sub-grids are not aligned correctly, the following error message appears after imaging an array or opening a DAT file: (Figure 378)

Figure 378 Notice of sub-grid misalignment(s)

Navigating from sub-grid to sub-grid

The failed sub-grids are marked with an X in the Grids box. (Figure 379)

Figure 379 Misaligned sub-grids in the Grids box

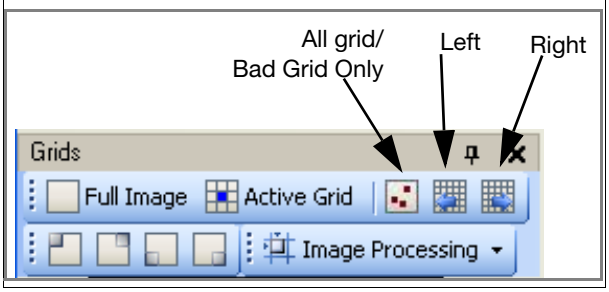


Highlighting

- Selected sub-grids are highlighted in blue
- Selected misaligned sub-grids are highlighted in yellow
- Modified sub-grids are highlighted in green.

  Note: You can step through sub-grids using the right and left buttons. (Figure 380)

Figure 380 Grid box toolbar, sub-grid step buttons



Stepping through all sub-grids

1. Toggle the Step button  to the all position
2. Click the left  and right  buttons to step through the sub-grids.

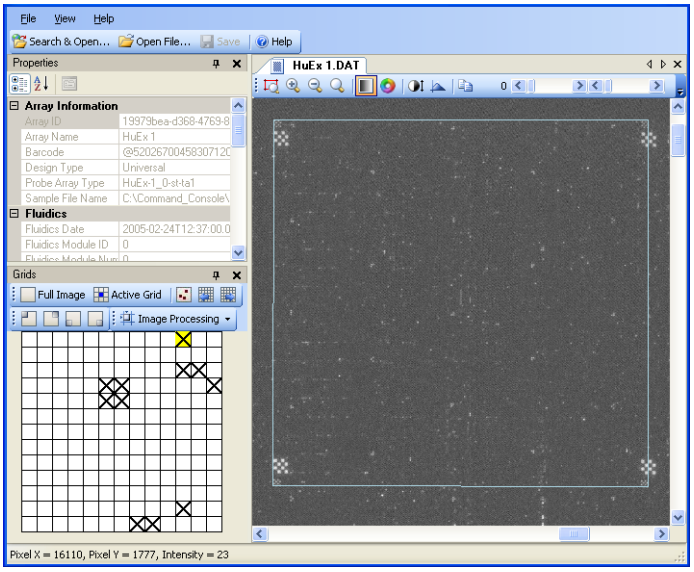
Stepping only through the misaligned grids

1. Toggle the Step button to the misaligned position.
2. Click the left  and right  buttons to step through the sub-grids.

Manually align a failed sub-grid

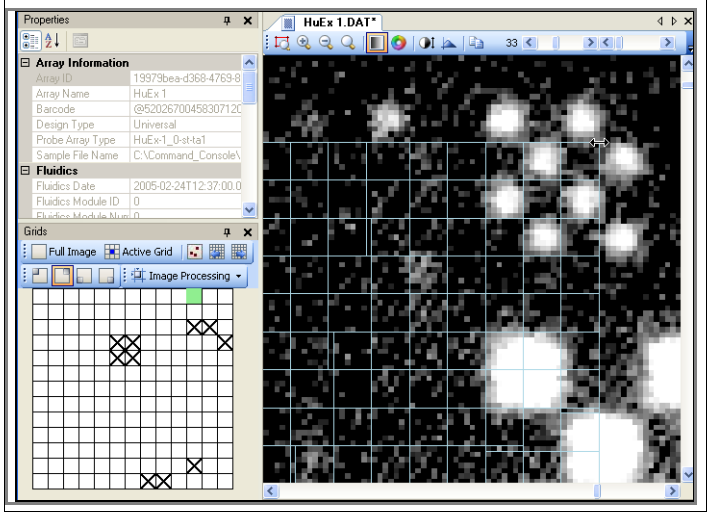
1. Click **OK** in the sub-grid Alignment Failure dialog box. (Figure 378)
2. Click on the sub-grid you want to align in the Grid box.
3. A zoomed-in view of the sub-grid appears in the Image window. (Figure 381)

Figure 381 Selected sub-grid



4. Align the sub-grid at each corner:
   a. Click the **Go To Corner** button for the corner you want to align.
      A zoomed-in view of the corner of the sub-grid appears. (Figure 382)

Figure 382 The upper right sub-grid corner

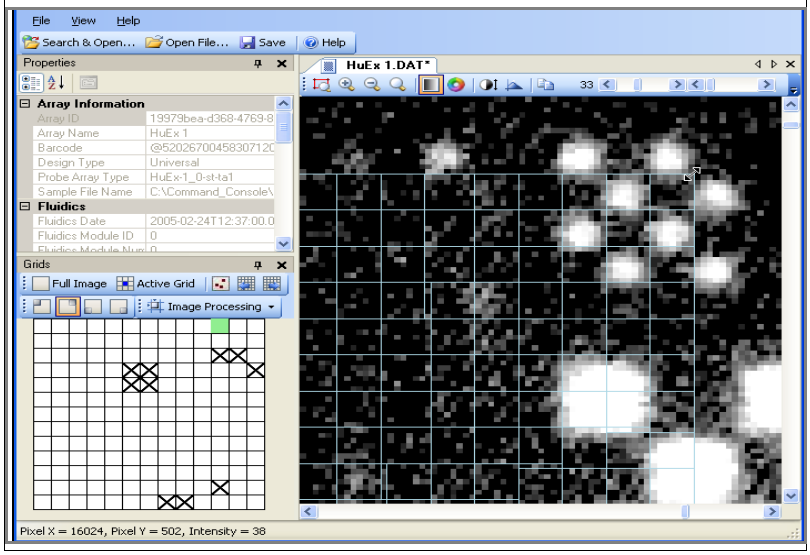


   b. Place the mouse arrow over the grid perimeter (the arrow becomes a double arrow, ↕ ⤢ ↔).

The diagonal orientation of the double arrow along the perimeter of a corner probe cell indicates horizontal and vertical adjustments can be made simultaneously using the click-and-drag method or by using the keyboard arrow keys.

c. Use the click-and-drag method or the keyboard arrow keys to adjust the horizontal or vertical position of the sub-grid so that it is aligned over the outside corner of the small checkerboard pattern. (Figure 383)

Figure 383 Dragging the sub-grid boundary

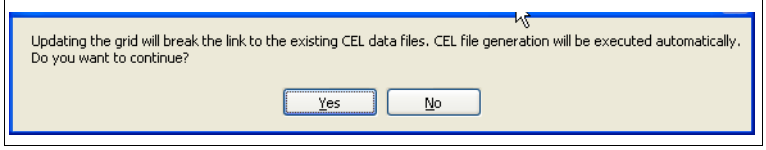


d. Repeat steps A through C for the other corners of the sub-grid.

5. Continue manually aligning all misaligned sub-grids.
6. After you align the grid, click the **Save** button Save or select **File** → **Save** from the menu bar.

   The Save Notice appears. (Figure 384)

Figure 384 Save notice



7. Click **Yes** to save the file.

   The file is saved and CEL file generation is done.

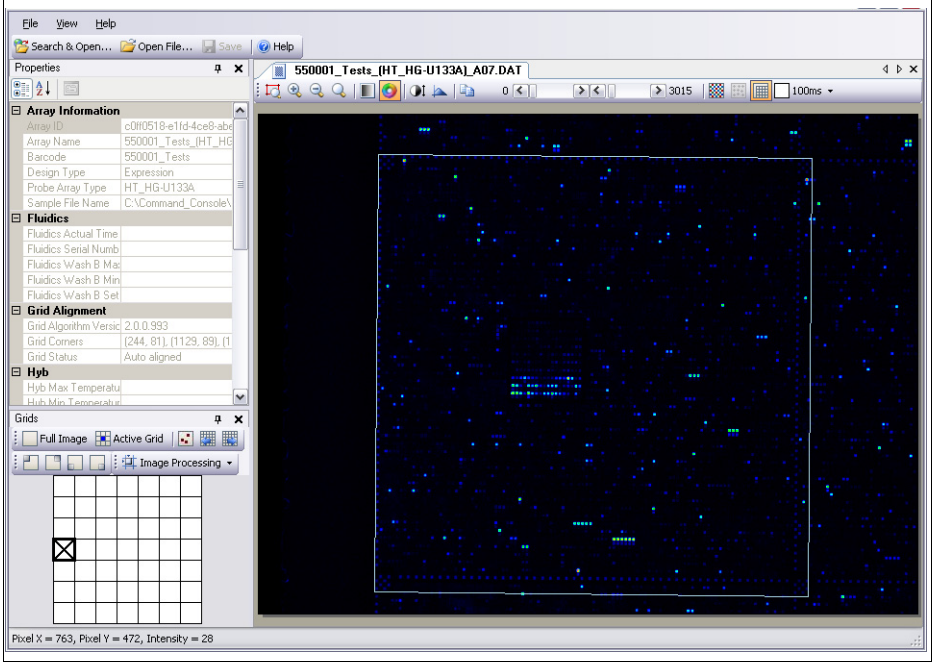
Aligning sub-grids on GeneTitan arrays

You use the same controls and steps to align sub-grids for GeneTitan arrays as you do for cartridge arrays, with the following exceptions:

- You do not need to perform a main grid alignment

- You may have to check the grid alignment for both exposures (see "Displaying different exposures (GeneTitan expression array plate DAT files only)" on page 303) or both wavelengths (see "Displaying different wavelengths (Axiom array plate DAT files only)" on page 303.
- You can select an option to apply adjusted coordinates to all channels and exposures (see "Changing the manual grid adjustment setting" on page 321

Figure 385 GeneTitan Array DAT file, grid selected



Changing the manual grid adjustment setting

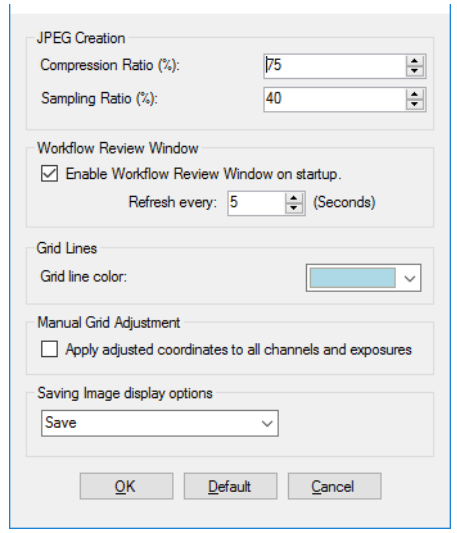
You can apply the coordinate adjustments made to one exposure time or channel to the other exposure time or channel.

Changing settings for the manual grid adjustment

1. From the **View** menu, select **Options...**

   The Options dialog box opens. (Figure 386)

Figure 386 Options dialog box.



2. Select or deselect the Manual Grid Adjustment check box.
3. Click **OK** to close the dialog box and enable the changes.

Regenerating intensity values

Cell intensity values are generated automatically after:

- Running any grid alignment algorithm.
- Saving a DAT file after manual gridding.

You can also regenerate the intensity values without performing one of these other steps.

Regenerating the intensity values

1. In the Grids toolbar, click the **Image Processing** button 

.
2. Select **Regenerate CEL Intensity** from the list.

   A new CEL intensity data file will be generated. It will automatically have an underscore and number appended to the name to distinguish it from a previously generated file.

Exporting images in other formats

You have two options for exporting a copy of the image:

- "Copying images to the computer clipboard"
- "Creating a JPG file" on page 323

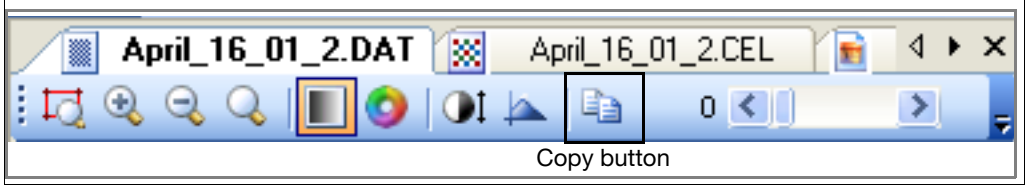
Copying images to the computer clipboard

1. Display the image you want to copy in the Image window.

   Note: You can zoom in on a specific region of the image if you desire before copying.

2. Click the Copy button in the image window tool bar (Figure 387) or press Ctrl c.

Figure 387 Copy button



The image is now copied to the clipboard.

You can then paste the image into a graphics program such as MS Paint, then save the file as you normally would.

Creating a JPG file

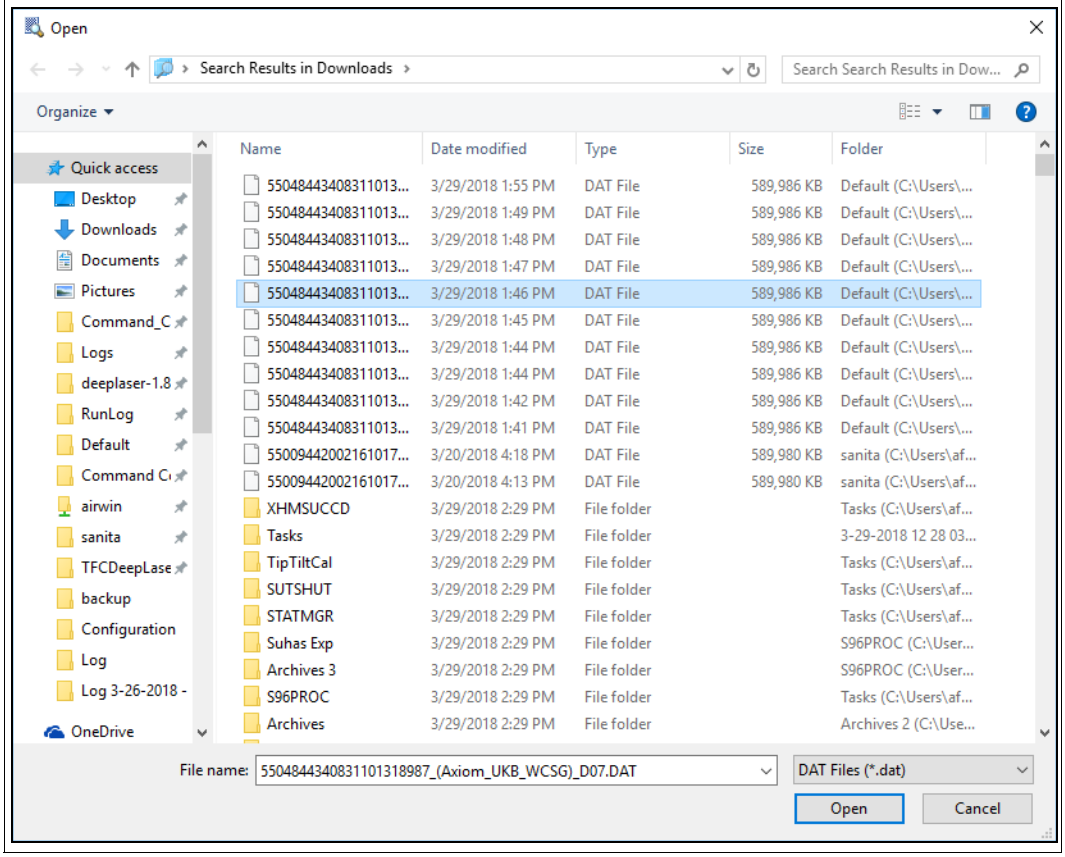
You can create a JPG copy of a DAT file for archive purposes.

Creating a JPG copy of a DAT file

1. From the File menu, select **Create JPG from DAT...**.

   The Open dialog box opens. (Figure 388)

Figure 388 Open dialog box for JPG creation



2. Select the DAT file you want to copy.
3. Click **Open**.

   The JPG file is created.

Viewing the JPG file

1. Click **File** → **Open File**.

   An Open window appears.
2. Navigate to the file's location as you normally would.
3. Click to highlight it, then click **Open**.

   The selected image file is now displayed in the Viewer.

1. Opening the JPG in the Windows Picture and Fax Viewer

- In the Folder View, click the Explore link next to the JPG file.

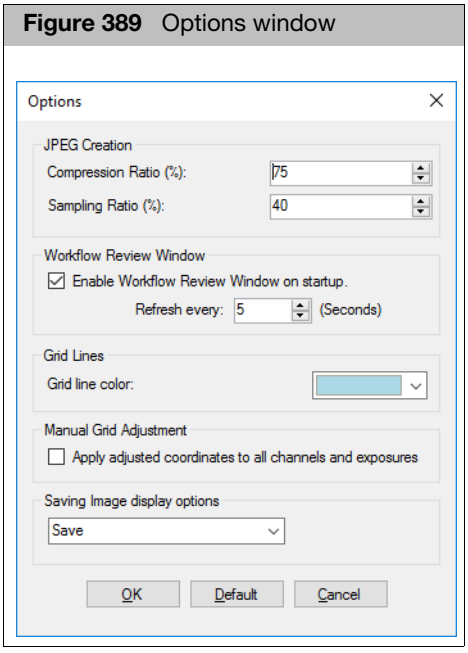
  The selected JPG file is displayed in the Windows Picture and Fax Viewer.

Changing settings for the JPG conversion

1. From the **View** menu, select **Options...**

   The Options window appears. (Figure 389)

Figure 389 Options window



2. Change the values for Compression Ratio and Sampling Ratio.

   Increasing either of these values increases the resolution of the JPG image, but also increases the size of the JPG file.
3. Click **OK** to close the dialog box and enable the changes.

10 Probe array types

Changing probe array types

GCC enables you to change the probe array type for any or all of a group of files.

The Change Probe Array Type function enables you to:

- Change the probe array type for the selected Sample and data files, regrid the associated DAT files, and regenerate the associated CEL files
- Change the probe array type field for selected CEL files

You might want to use this function:

- If you are working with probe arrays that can be used for more than one type of analysis.
- If you have analyzed a set of prototype arrays using a preliminary set of library files, and you now have the correct library file set.

  Note: The Change Probe Array Type function cannot be used for GeneTitan Array Plates.

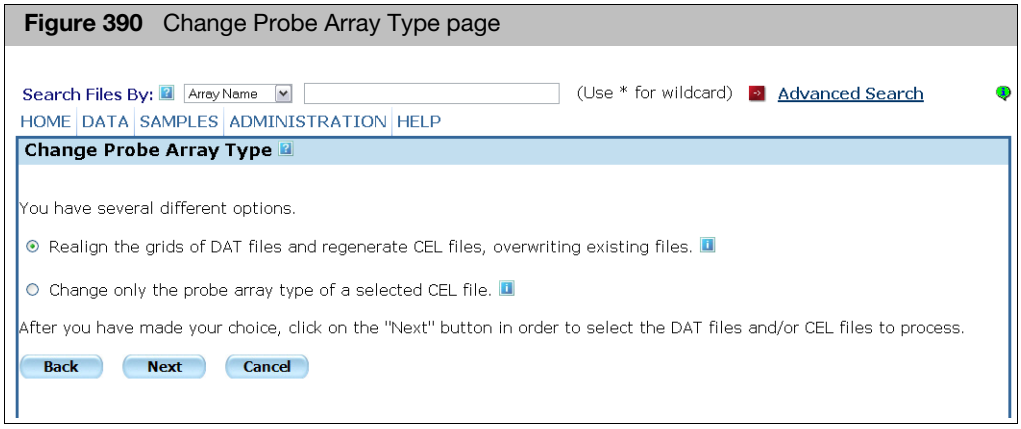
1. Select the files for which you which to change the probe array type.

   You can select files to change from:

   - The Folder View (see "Selecting files" on page 57).
   - The Project View (see "Selecting files" on page 65).
   - The Search Results page (see "Selecting files" on page 75).
2. Select **Change Probe Array Type** from the Command to Run drop-down list.

   The Change Probe Array Type page opens. (Figure 390)

Figure 390 Change Probe Array Type page



3. Select the option you want to use:

- Realign the grids of DAT files and regenerate CEL files, overwriting existing files.
- This option will:
  - Change the probe array type for the selected Sample and data files
  - Re-grid the associated DAT files
  - Regenerate the associated CEL files and the cell summary report file

IMPORTANT! Realigning the grids will break the parent-child relationships between DAT files and CEL files and between CEL files and CHP files until the CEL files are regenerated (Any CHP files are not automatically regenerated; you must regenerate them manually). Choosing this action will not delete any vital information because you can change the probe array type back to its original value if you change your mind.

- Change only the probe array type of a selected CEL file.

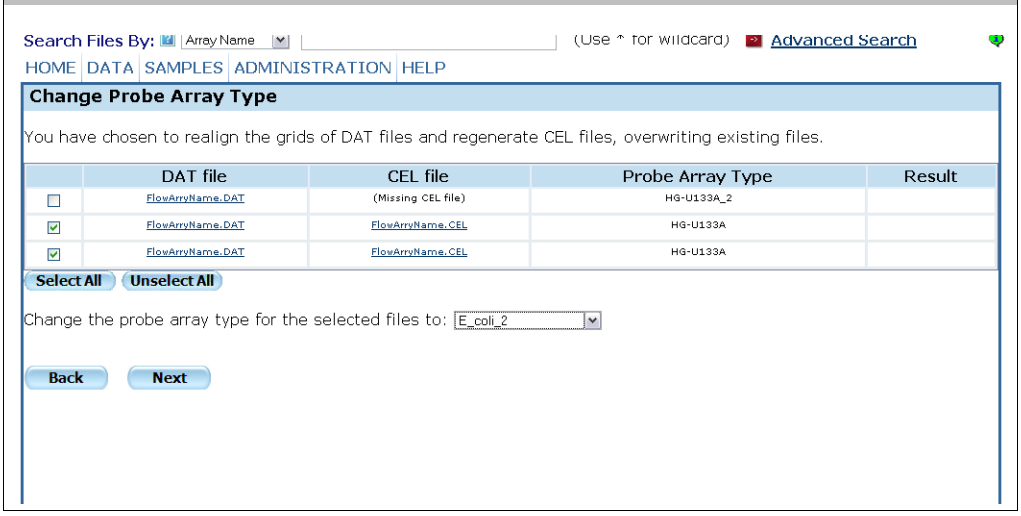
  This option will only change the probe array type information in the selected CEL file(s). It does not modify the Sample probe array type information in the Sample file or the DAT file.

  This option is for use when using a CEL file that belongs to a multi-use array. These arrays that can be analyzed in multiple ways, as an Expression array or a Genotyping array.

4. Click **Next**.

   The page displays the data files. (Figure 391)

Figure 391 Change Probe Array Type page, step 2

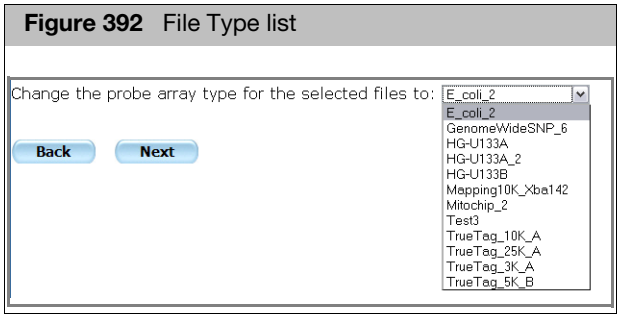


5. Select the files to be changed by selecting the check boxes in the left-hand column.

   You can use the **Select All** and **Deselect All** buttons to select all or deselect all files.

6. Select the probe array type you want to change the selected files to from the drop-down list. (Figure 392)

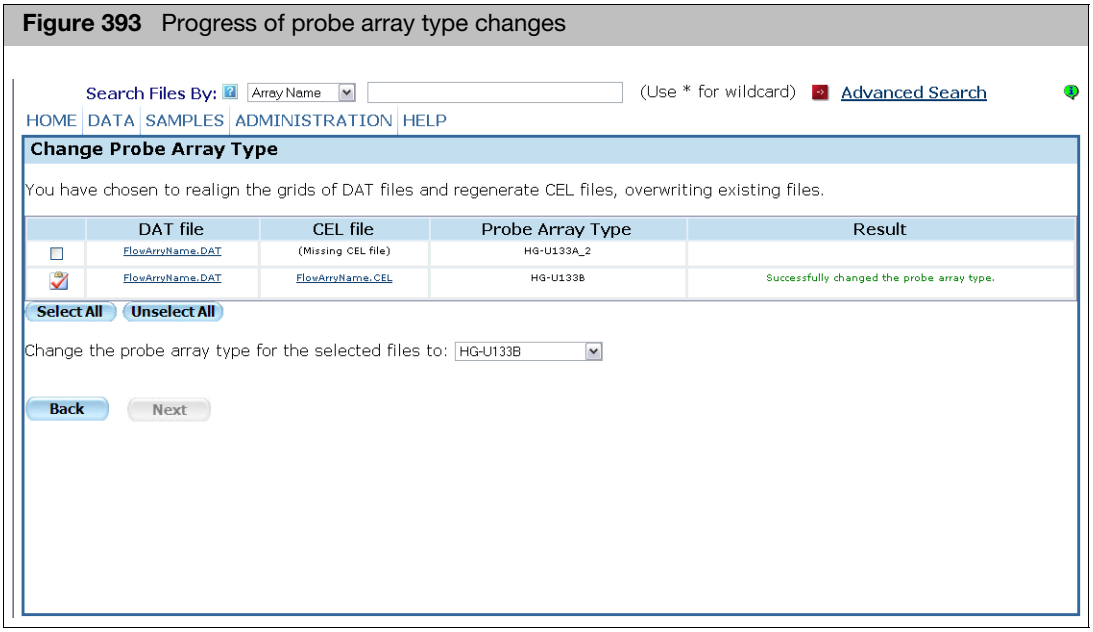
Figure 392 File Type list



7. Click **Next**.

   The page displays the progress of the transformations. (Figure 393)

Figure 393 Progress of probe array type changes



Administration functions

The Administration functions provide additional options for organizing and tracking your data:

- "Working with templates"
- "Tracking the workflow" on page 336

Working with templates

Templates are used to organize a set of attributes that you can use to create a new Sample file.

Attributes are properties used to describe a sample and its associated array(s). Attributes include:

- Sample Name
- Gender
- Date
- Array Type
- Array Barcode

When you create a template, you specify:

- the attributes included in the template
- the data type for each attribute:
  - Text: text string
  - Number: Floating point or Integer
  - Date: Calendar data
  - SingleSelect: enables the user to select a single item from a controlled vocabulary list
- whether the attribute is required
- value options for SingleSelect attributes

Templates allow you to organize attributes and collect consistent data for your experiments and samples.

The following templates are included in the GCC install:

- MIAME sample information
- Pedigree template

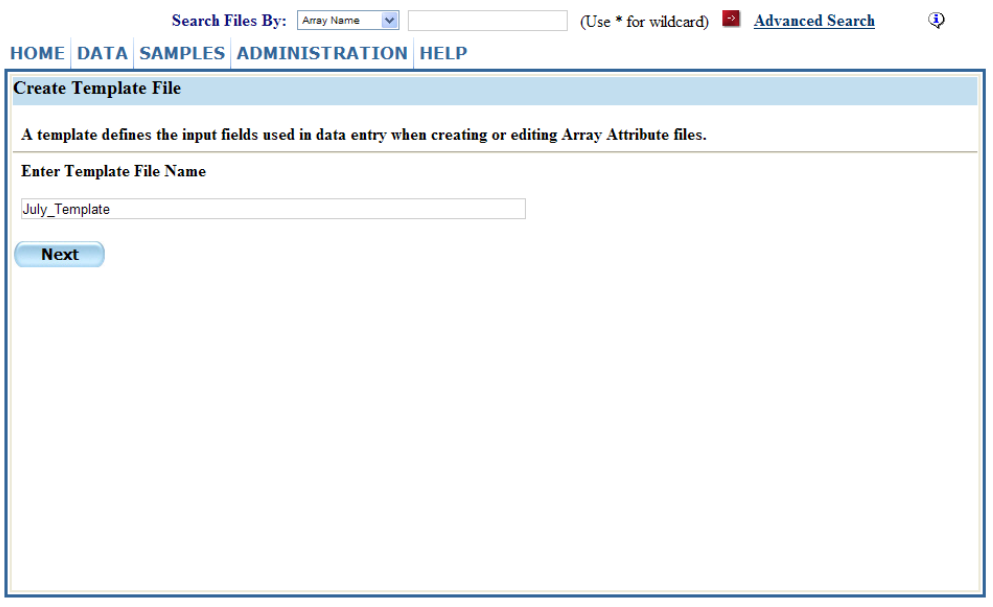
This section describes the following functions:

- "Creating a template", below
- "Editing a template" on page 331
- "Deleting templates" on page 333
- "Managing default templates" on page 335

Creating a template

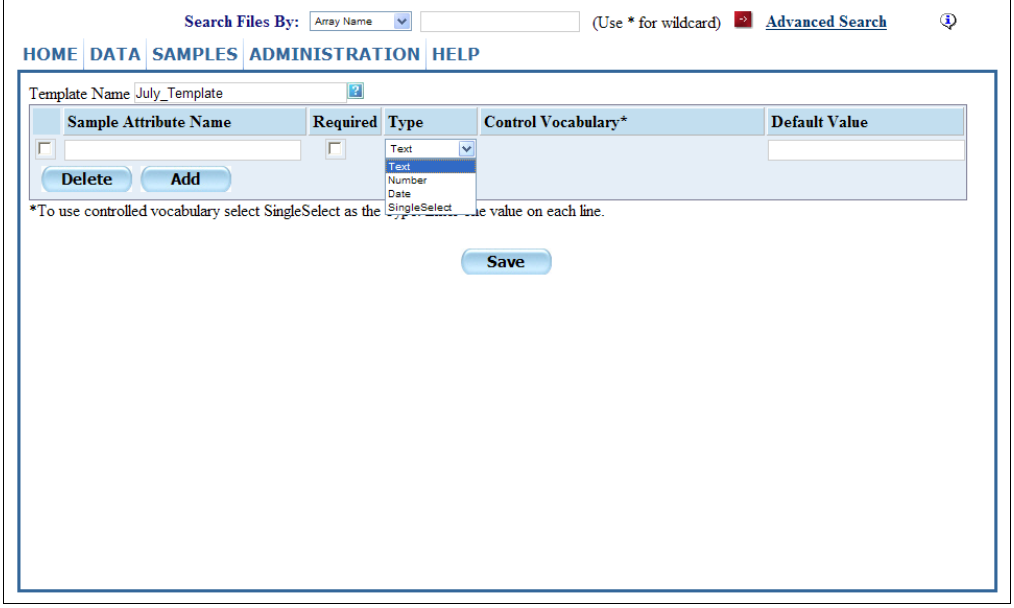
1. From the Templates menu, select **New Template**.
   The Create Template File page appears. (Figure 394)

Figure 394 Create Template File page



2. Enter a name for the template and click **Next**.
   The Add Attributes page opens. (Figure 395)

Figure 395 Edit Templates page



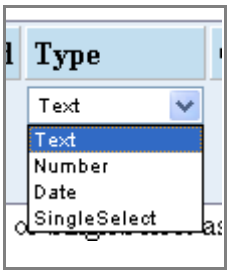
The page displays a list of the attributes for the template.

Adding a field to the list

1. Click **Add**.

   A new row appears in the list, with the following boxes for entering information or links:

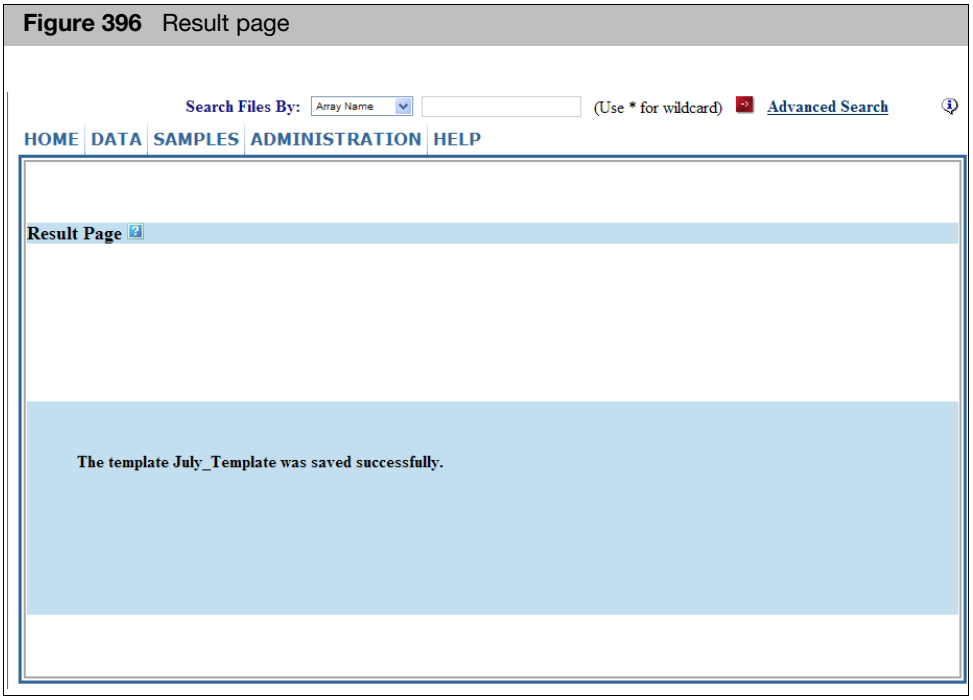
Sample Attribute Name	Enter a name for the attribute.
Required	Click if the attribute is required.
Type	Select from drop-down list: • Text: Text string • Number: Integer or floating point number • Date: Calendar data • SingleSelect: Presents a list of items for the user to choose
Control Vocabulary	Enter values for the controlled vocabulary, placing multiple values on separate lines.
Default Value	Enter a default value to be displayed for the field in a new Sample file.



2. Enter or select values for the field characteristics.
3. Repeat Step 1 and Step 2 for the other attribute fields you want to add.
4. After creating the attribute fields, click **Save** to save the template.

   The Results Page displays the name of the created template (Figure 396).

Figure 396 Result page



Editing a template

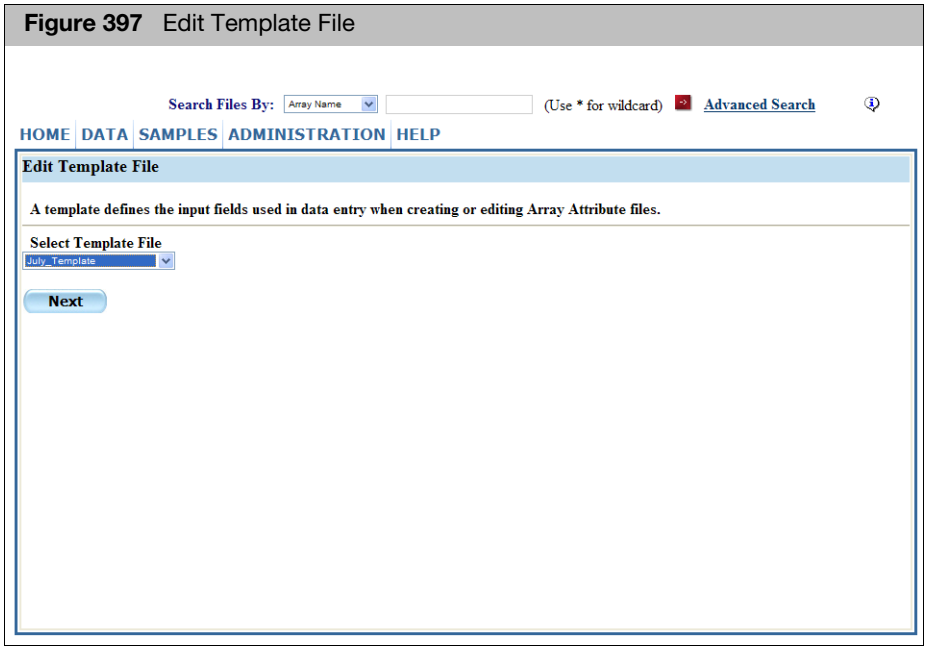
You can edit an existing template.

Note: Deleting an attribute from a template or changing data type will cause attribute discrepancies if you have already used the template to create Sample files. For more information, see "Sample attributes conversion" on page 115.

1. From the Templates menu, select **Edit**.

   The Edit Template File page appears. (Figure 397)

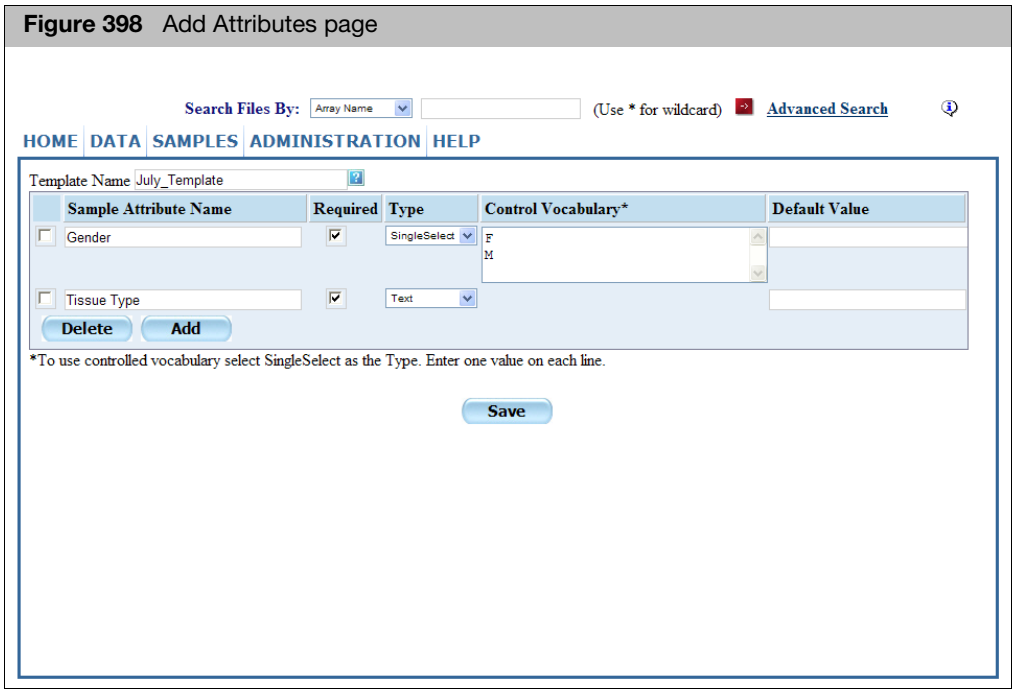
Figure 397 Edit Template File



2. Select the template you want to edit and click **Next**.

   The Add Attributes page opens. (Figure 398)

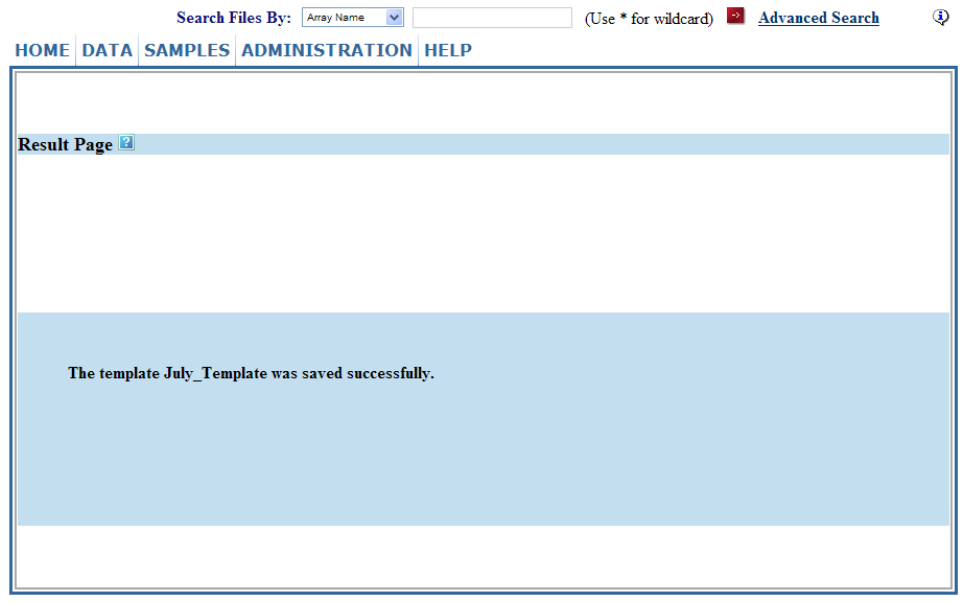
Figure 398 Add Attributes page



You can add, edit, or delete fields with the same functions used to create a new template. For more information see "Creating a template" on page 329.

3. After editing the attribute fields, click **Save** to save the template.
   The Results Page displays the name of the created template.

Figure 399 Results page



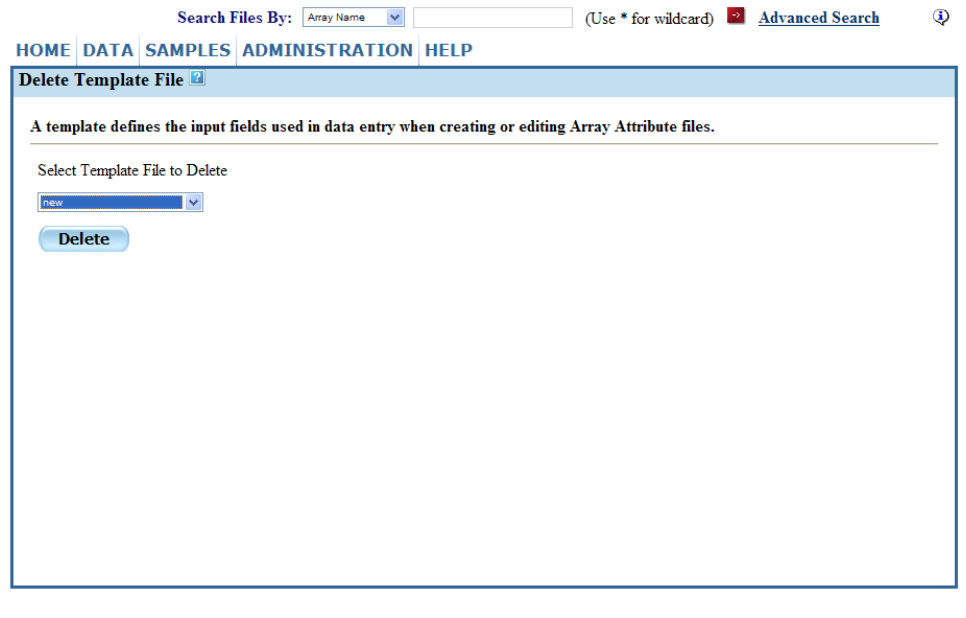
Deleting templates

You can delete a template from the list.

Note: Deleting a template will cause attribute discrepancies if you have already used the template to create Sample files.

1. From the Administration menu, select **Templates** → **Delete**.
   The Delete Template File page appears. (Figure 400)

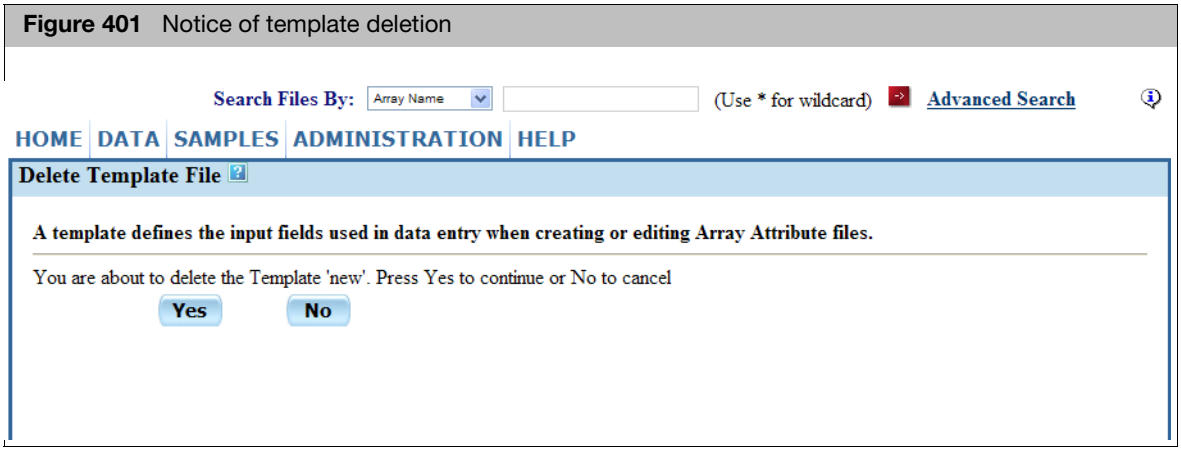
Figure 400 Delete Template File page



2. Select the template to be deleted from the drop-down list.
3. Click **Delete**.

   The template is deleted. (Figure 401)

Figure 401 Notice of template deletion



Managing default templates

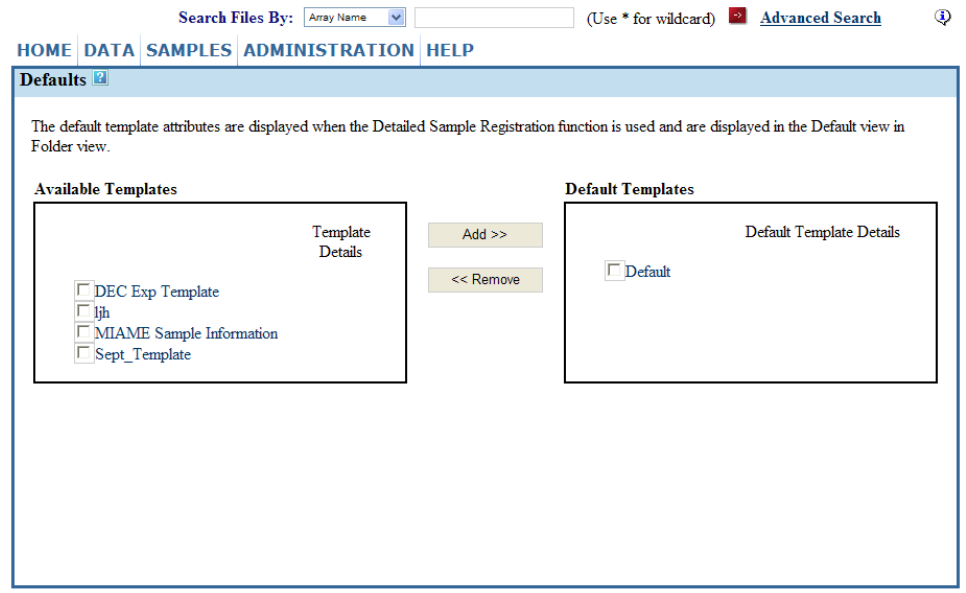
The default template attributes are displayed when the Detailed Sample Registration function is used and are displayed in the Default view in Folder view.

Changing the default templates

1. From the Administration menu, select **Templates** → **Default**.

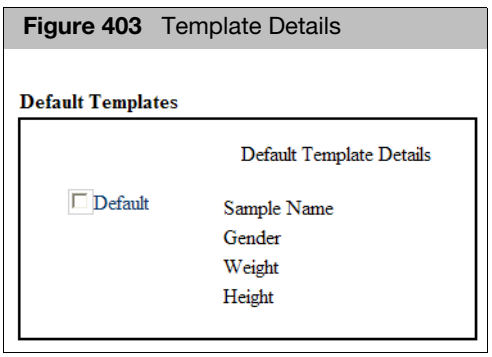
   The Default Template File page appears. (Figure 402)

Figure 402 Manage Default Templates page



   Click on a template name to see a list of the attributes in that template. (Figure 403)

Figure 403 Template Details



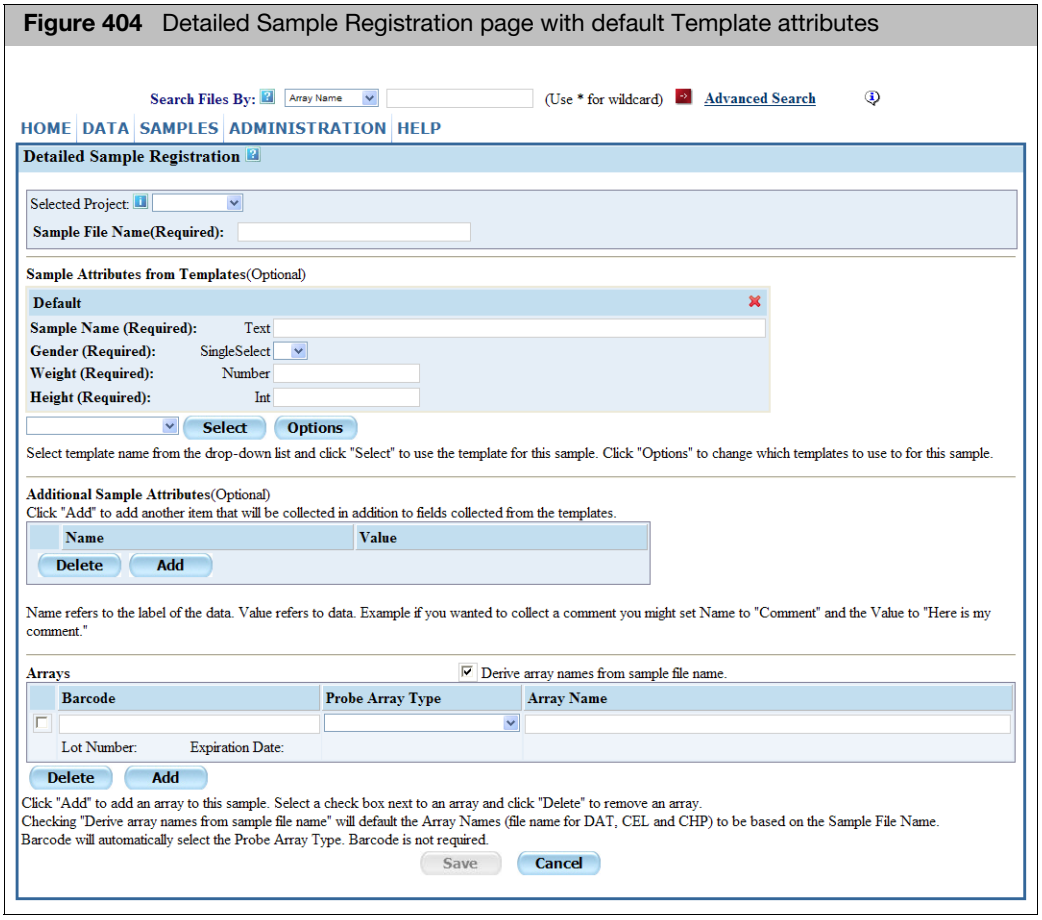
2. Select the template(s) to be defined as default templates from the Available Templates list.
3. Click **Add**.

   The template is moved to the Default Templates list.

   You can also click the **Remove** button to remove templates in the Default Templates list.

The template attributes will be available in the Detailed Sample Registration page. (Figure 404)

Figure 404 Detailed Sample Registration page with default Template attributes



Tracking the workflow

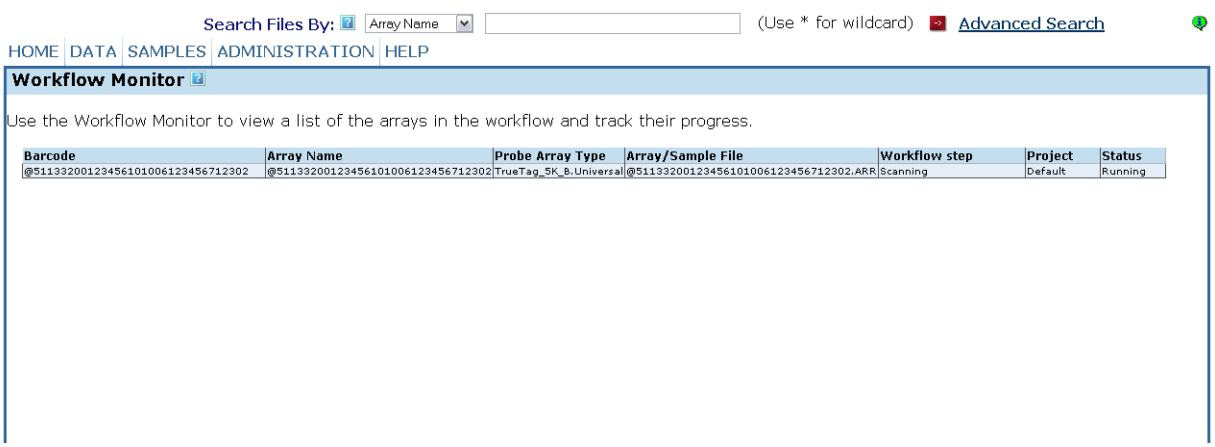
The Workflow Monitor page enables users to view a list of the arrays in the workflow and see what their status is.

Viewing the Workflow Monitor page

1. Click **Administration** → **Workflow**.

   The Workflow Monitor page opens (Figure 405).

Figure 405 Workflow Monitor page



The Workflow Monitor page displays a list of the files waiting to finish workflow steps. It displays an item for each file and each unfinished step in the workflow; a file may have multiple entries, depending upon what step in the workflow has been completed.

For each file, the following information becomes available:

Barcode	Barcode of array.
Array Name	Name assigned to the array by the user.
Probe Array Type	Model of probe array.
Sample file	Name of Sample file.
Workflow Step	The uncompleted step in the workflow.
Project	Project folder the Sample file is assigned to.
Status	• Running. • Not Ready. • Error.

Sorting the file list by any column

1. Click on the column's header.

A Networking

Network functionality

A computer running, GCC can be connected to a Windows network to provide the following functions:

- **Using network data storage**

  If the Windows network has a network data root, you can consolidate data from multiple computers running GCC Instrument Control in a single location. GCC Portal provides convenient ways to keep Sample (ARR) files and data files (DAT and CEL) in the same folder on the network data storage.

- **Running different parts of the workflow on different IC workstations**

  In some cases the Fluidics Station and Scanner used to process an array are controlled by different workstations. GCC software enables you to perform different workflow tasks on different workstations while consolidating the Sample (ARR), Data (DAT and CEL) and Audit files at a single storage location (during processing the files may be on different machines).

Examples of different configurations for GCC with Windows network are given in "Sample configurations for GCC with network functionality" on page 339. Contact your IT/CIS support for help with configuring network functionality.

After installing the GCC components, to use the network functionality you need to:

1. Connect the computer to a Windows network with necessary permissions and have permissions set for using network data storage.

   See "Setting up Windows networking" on page 343 for more information.

2. Configure GCC Services with the proper domain and user account with password to access the network assets.

   See "Configuring GCC services" on page 344 for more information.

3. Add network data storage as a data root in GCC Portal

   "Adding the network data storage as a data root" on page 347.

Sample configurations for GCC with network functionality

This section describes some sample configurations using GCC network functionality:

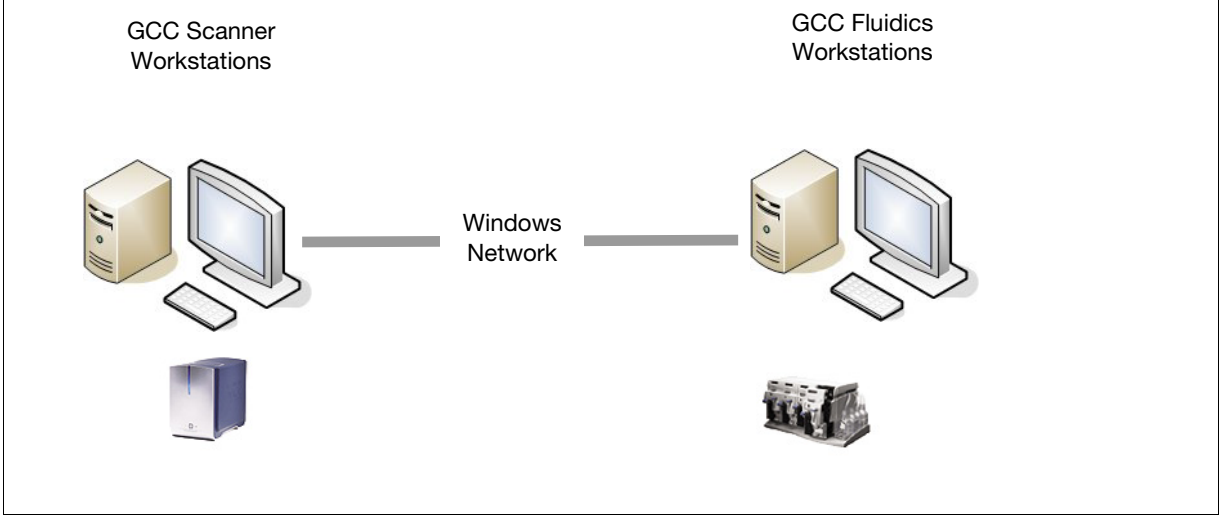
- "Linked instrument control systems"
- "Network storage" on page 341

The sample configurations show some of the ways you can connect computers with different roles in order to consolidate data, perform different parts of the workflow, and provide data access to other users.

Linked instrument control systems

This configuration (Figure 406) enables you to perform different instrument control tasks on different workstations while consolidating the data files on the Scanner workstation.

Figure 406 Linked instrument control system



In the linked IC Workstation configuration, the Scanner Workstation and the GCC Fluidics Workstation are linked with Windows Network.

Computer roles in linked control systems

Scanner system

The scanner workstation can be considered the 'main' system, in that the Sample files will be generated and stored there and all related DAT, CEL, and CHP files can be consolidated at the same location.

The dataroot of the scanner workstation is shared so that the fluidics workstation can access the Sample files and log AUDIT information for the arrays that are run through the fluidics station, without needing to copy the files locally.

Requirements for the scanner system:

- Has the following software installed
  - Windows 10 Enterprise 2016 LTSB
  - GCC Portal with GCC Portal Web Server
  - GCC Viewer
  - GCC Scanner Control

Tasks that can be performed using the IC Scanner Workstation:

- Create and edit Sample (ARR) file and Register Array
- Run Scan on array to create DAT file
- Grid and get CEL Data (and perform manual grid alignment check if necessary)
- Index and search the workstation data.

Fluidics system

In the linked system, the fluidics workstation does not store any Sample files, or generate DAT, CEL or CHP files. It uses the Sample files on the scanner system, and writes back AUDIT information about the fluidics processing. If necessary, the fluidics workstation can also register arrays/samples that will be stored on the scanner workstation.

The IC workstation has GCC Portal and GCC Instrument Control installed. A Fluidics workstation can control up to eight fluidics stations.

Requirements:

- Has the following software installed
  - Windows 10 Enterprise 2016 LTSB
  - GCC Portal with GCC Portal Web Server.
  - GCC Fluidics Control
- Connected through Windows Network to the Scanner System.
- Have necessary Domain and User Permissions settings to enable Read/write to the Scanner System.
- GCC Services configured to work with Scanner System.
- Have Scanner System set up as a data root for GCC Portal

Tasks that can be performed using the IC Fluidics Workstation:

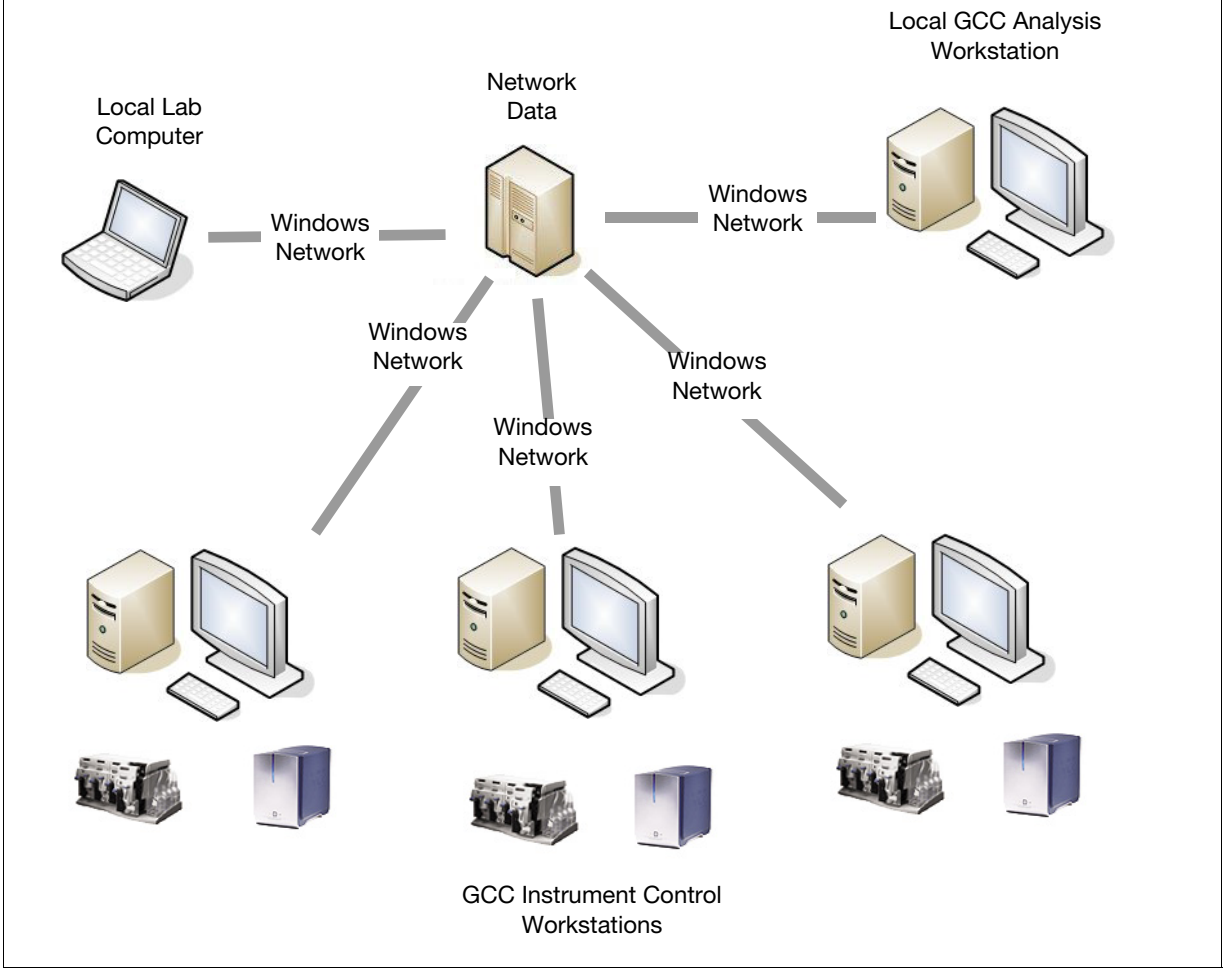
- Run Fluidics station and update the Audit file for the array.
- Index and search the Fluidics workstation data and the Scanner workstation data.
- Edit Sample (ARR) files on the Scanner and Fluidics workstation data.

The Fluidics system can also move data to and from Scanner System using Windows Explorer.

Network storage

This configuration (Figure 407) provides storage and tools to consolidate the data produced by a set of IC workstations. It also enables other users linked through the Windows Network system to access the data.

Figure 407 Network Data Storage configuration



Computer roles for network storage

The network data storage configuration supports the following computer roles:

- "Network data storage"
- "GCC IC workstations"
- "Local analysis workstation"
- "Local lab computer"

Network data storage

Network data storage serves as the central data repository for the networked computers. Sample (ARR) files are created on it and the DAT and CEL data are pushed out to it from the IC workstations. The network data storage computer does not need to have any GCC software installed.

GCC IC workstations

The IC workstation has GCC Portal and GCC Instrument Control installed. An IC workstation can control one scanner and up to eight fluidics stations.

GCC IC Workstations have the following requirements:

- Has the following software installed
  - Windows 10 Enterprise 2016 LTSB
  - GCC Portal with GCC Portal Web Server
  - GCC Viewer
  - GCC Instrument Control
- Connected through Windows Network to the network data storage.
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.
- GCC Services configured to work with network data storage.
- Have network data storage set up as a data root for GCC Portal.

Tasks that can be performed using the IC Workstation:

- Create Sample (ARR) file and Register Array on network data storage and the workstation.
- Run Fluidics and Scan array to create DAT file.
- Grid DAT files, perform manual grid alignment check if necessary, and generate CEL file data.
- Use GCC Portal data management functions to upload DAT and CEL files to network data storage in same folder as Sample (ARR) file.
- Index and search the network data storage and the workstation data.
- Edit Sample (ARR) files on the network data storage and the workstation.

  Note: The local IC workstation can also move data to and from network data storage using Windows Explorer.

Local analysis workstation

The IC workstation has GCC Portal and GCC Viewer installed.

A local Analysis Workstation has the following requirements:

- Windows 10 Enterprise 2016 LTSB
- GCC Portal with GCC Portal Web Server.
- GCC Viewer
- Connected through Windows Network to the network data storage
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.
- GCC Services configured to work with network data storage.
- Have network data storage set up as a data root for the GCC Portal

It can perform the following tasks:

- Create and edit Sample (ARR) files on the network data storage and the workstation.
- Index and search the network data storage and the workstation data.
- Manual Gridding of DAT files on the workstation.
- Re-calculating CEL file data after gridding.

The local Analysis Workstation can also move data to and from network data storage using Windows Explorer.

Local lab computer

Lab Computers do not have any GCC software installed. Lab Computers are commonly used to perform higher-level analysis on the data.

Requirements:

- Connected through Windows Network
- Have necessary Domain and User Permissions settings to enable Read/Write access to the network data storage.

The local Lab computer can move data to and from network data storage using Windows Explorer.

Setting up Windows networking

A computer running GCC can be connected to a Windows network to provide different options for data consolidation and sharing.

Computers connected to the network are organized into domains. A domain is a group of computers that share common security and user account information.

Each user is assigned to a domain and given a user account with a name and password.

Any computer on the proper domain with necessary user permissions can get on the system using Windows Explorer and move data files on and off the network data storage.

If on a Windows domain these need to be domain accounts. If not on a Windows domain the share and the machine need matching account names and passwords.

Work with your IT department for help in setting up the necessary domain and user accounts.

If the domain, user account, and permissions are correct, when the computer running GCC is connected to the network you should be able to see the network data storage using Windows Explorer. You will not be able to add network data storage as an GCC data root or use GCC Portal to search the network data storage until you have configured the GCC Services with the proper domain and account information.

Sharing and security

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly.

Work with your IT department for help in setting the permissions.

Examples

Let's take two different examples of how you might configure your file permissions for a network folder.

In the first example, you have a folder that is shared by your department. This folder enables read and write access to a Windows domain group called “Liver Cancer Group”, and grants no other permissions to anyone else. In order for GCC to be able to access this network folder, you must change your GCC Services to run as one of the users who is a member of the Liver Cancer Group.

In the second example, you have a folder on a computer in a lab that you want access to, but you don't want anyone else to access that folder. If you create a local user account on that computer called LocalUser, with the password “LocalPassword”, then, you can share that folder on the network, but grant access only to LocalUser. If you have a computer outside of that lab that has GCC installed, then you can also create LocalUser as a local user on this second computer, with the same password, and then change the GCC services on that second computer to run as LocalUser. Now, if you add your network folder as a Data Root, then you should be able to have complete access to that network folder in GCC.

Configuring GCC services

GCC services are tools that perform the functions of the software. To add a network data share as a data root, these services need to be configured as a domain user account, instead of a local system account.

The GCC services that need configuring include:

- GCCAuditLogger
- GCCIndexer
- GCCTaskManager
- GCCWebServer
- GCC96FS_WorkflowSvc

If on a Windows domain these need to be domain accounts. If not on a Windows domain the share and the machine need matching account names and passwords.

Note: You can use matching local accounts on a domain, but you need to be logged in using an account with Administrator privileges to perform this configuration.

Configuring the GCC portal services

1. From the Start menu, click **Control Panel** → **Administrator Tools**.
   The Control panel opens.
2. Double-click the **Services** icon.
   The Services window opens.

   There are five GCC Services:
   - GCCAuditLogger
   - GCCIndexer
   - GCCTaskManager
   - GCCWebServer
   - GCC96FS_WorkflowSvc

   You will need to perform steps 3 through 6 for all services.
3. Right click **GCCAuditLogger** (**or another service you are configuring**) and select Properties.
   The Properties dialog box opens.
4. Click the **Log On** tab.
5. Change the log on information for the service.
   a. Change the service to Log on as "This account".

- Supply a domain user and password if on a domain.
- Supply a local account with matching username and password as the network storage device if not.

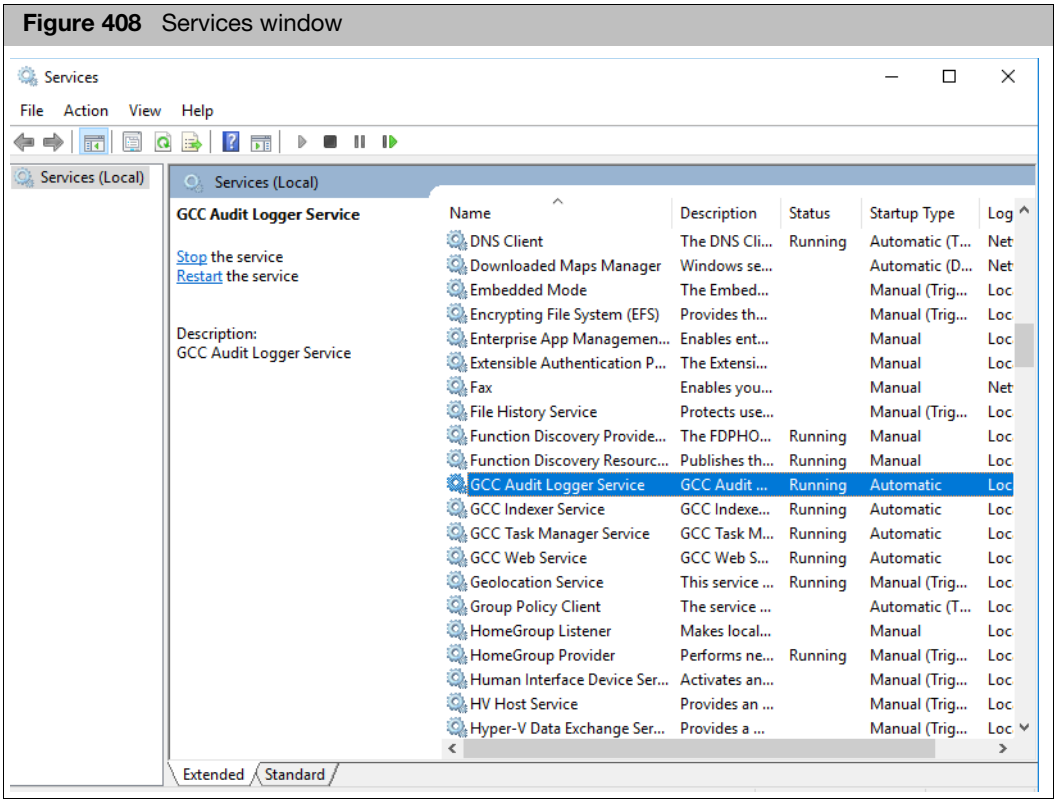
b. Click **OK**.

6. Stop and start the service from the services dialog.
7. Repeat steps 3 through 6 for the other GCC services.

Configuring the GCC portal services

1. From the Windows Start menu, click **Windows System** → **Control Panel**.
   The All Control Panel Items window opens.
2. Make sure the **View by** (upper right) is set to **Small icons**, then click on **Administrative Tools**.
   The Administrative Tools window appears.
3. Locate, then double-click **Services**.
   The Services window opens (Figure 408).

Figure 408 Services window



- **GCC Services:**
  - GCCAuditLogger
  - GCCIndexer.
  - GCCTaskManager
  - GCCWebServer
- **GCC WorkflowBroadcastService**: This service enables the instrument to notify analysis applications that data is available for analysis.

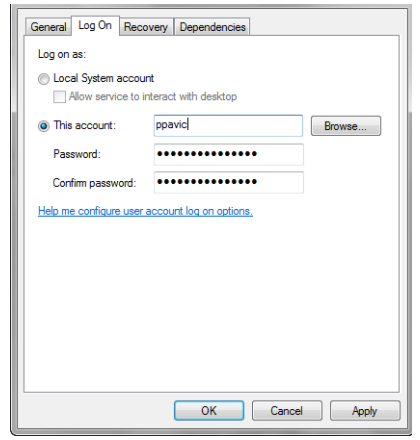
- **GCC DeepLaserService**: This service enables the instrument to send notifications and upload data to the Thermo Fisher Scientific Cloud.

4. Right-click **GCC Audit Logger** (**or another service you are configuring**) and select **Properties**.

   The Properties dialog box appears. (Figure 409)

5. Click the **Log On** tab.

Figure 409 GCC AuditLogger Properties dialog box, Log On tab



6. Change the log on information for the service.
   a. Change the service to Log on as "This account".
   b. Supply a domain user and password if on a domain.
   c. Supply a local account with matching username and password as the network storage device if not.
7. Click **OK**.

   A message window appears stating you have been granted Log On As privileges.

8. Click **OK**.

   A message window appears stating you must stop and restart the service to initiate your new login appears.

9. Click **OK**.

   The Services window appears.

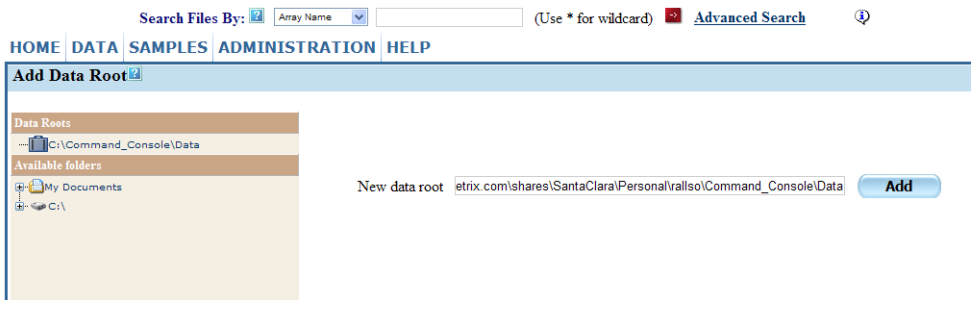
10. Click to highlight the service you just modified. then **Stop** and **Start** the service from the services dialog.
11. Repeat steps 4 through 10 for each remaining GCC service.

Adding the network data storage as a data root

Adding the network data storage as a data root in GCC Portal

1. Start GCC Portal.
2. Navigate to **Data** → **Data Roots** → **Add**.
3. Paste the UNC path to the share into the dialog box. UNC paths follow this format: \\servername\share. Mapped network drives should not be used (mapped network drives are network folders that a user has mapped to a drive letter, for example, “H:”.)

Figure 410 Adding network data root

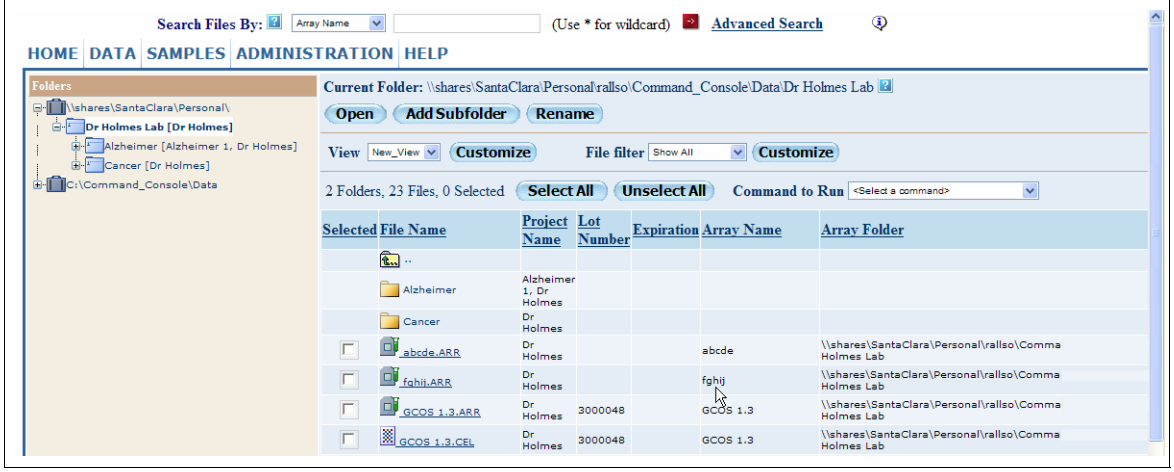


4. Click **Add.**

   Note: If you have not configured the GCC Services correctly, you will see a warning message in the Add Data Root window. For more information on, see "Configuring GCC services" on page 344

   If you configured this correctly you should be able to view the share in the Folder Viewer.

Figure 411 Network data root



B Windows sharing and security issues

You can use the Windows Sharing and Security settings to control access to your data when using network functionality. GCC supports setting permissions at the folder level, not the file level, even though the Windows settings can be set at the file level. You can change the settings for Sharing, permissions, and security for a selected file, but you need to be very careful about setting permissions when using GCC; you could lock yourself out of your own data or deny access to other people if the permissions are set incorrectly.

Note: Contact your IT/CIS support for help in setting the permissions for folders and files.

The Windows file sharing and security issues are described in further detail in:

General principles of security in the Command Console software

Security within Command Console can be separated into two different functional areas:

- Viewing file lists in the web UI, either from folders or from search results.
- File operations, such as editing or creating.

Security for viewing file lists is implemented at the folder level. If a user has read permissions on a particular folder, Command Console will not display files within that folder if the user does not have read permissions for those files. In addition, if the user tries to perform various operations on those files, the operating system will not allow it. Conversely, if the user has read permissions to several files in a folder, but does not have read permissions on the parent folder, the files will not be displayed in the Command Console software. In order to maintain consistent permissions on files within the system, individual files should not have permissions set differently from their parent folder. If this occurs due to other applications or operating system functions, the permissions on all the files in a folder can be reset by an administrator.

When performing file operations, including editing the Sample (ARR) file, re-gridding the Image (DAT) file, or regenerating an Intensity (CEL) file, a user may be prohibited by the operating system if the user does not have appropriate permissions for that file. The Command Console UI attempts to indicate when an operation fails due to permissions, but there are times when the operating system does not indicate why an operation failed. If the user e10ects to be able to modify a file but cannot, and can modify other files within the same folder, it is possible that individual files have permissions that limit access. If this occurs, the file permissions should be checked by an administrator and reset as necessary.

How do files get permissions that do not match the folder?

Under most operating conditions, the files in a folder will have the same permissions as the folder in which they reside. However, there are particular cases when a file is moved that may cause the file to retain certain permissions that were applied to the file in its previous location. In this case, the file will not have the same permissions as the new folder or the other files in the folder.

This happens to files that are moved to a new folder on the same NTFS partition on a local hard disk. It is important to note - this is a function of the Operating System, not Command Console.

As an example, a data folder has two subfolders, Project1 and Project2, and the Project1 and Project2 folders have different permissions. If a user with appropriate permissions moves a file from Project1 to Project2, the files moved to the Project2 folder may retain some of the permissions applied in the Project1 folder. If another user who has permissions to the Project2 folder but not to the Project1 folder tries to perform operations on these moved files, the operations may fail.

There are many conditions where this does not occur:

- Moving a file from a local hard disk to network storage (C:\data to \\storage\data)
- Moving a file from one folder to another on network storage (\\storage\data to \\storage\backup)
- Moving a file from one local hard disk to another local hard disk (C:\data to D:\data)
- Copying files from one location to another

How does Command Console show this error?

The files or folders to which the user does not have access are not visible in the GCC Portal pages. For example, if the user has read permission for a folder, but is denied access to specific files in the folder, then the following files are not displayed on the following pages:

- Folder View
- Search Results
- Project View

How to avoid this issue

There are ways to avoid this issue that will not impact normal operations. These include:

- Not setting overly restrictive permissions on shared systems, especially Instrument Control Workstations
- Using network storage for the bulk of data, and applying permissions on the network folders
- Only applying permissions on the network folders that are truly necessary
- Access data through UNC paths whenever possible

Security recommendations

- Set permissions for groups, as opposed to individuals, for greater simplicity.
- Only restrict permissions to the degree needed, again for greater simplicity.
- Set permissions at the folder level when creating data roots and projects.
- Don't use Deny permissions unless absolutely necessary, as these are more likely. to cause a situation with conflicting entries.
- Don't restrict (deny) the "Read permissions" permission. This is needed in order for the software to properly determine the rights the user has for a given object.
- Take care when moving files that the consistency is not broken. If possible, move files by using the WebUI Copy Project and Upload Data functions.
- When permissions do get out of sync, they can be easily restored by an admin, who can remove the conflicting ACL entries and allow the file to get its permissions by pure inheritance.

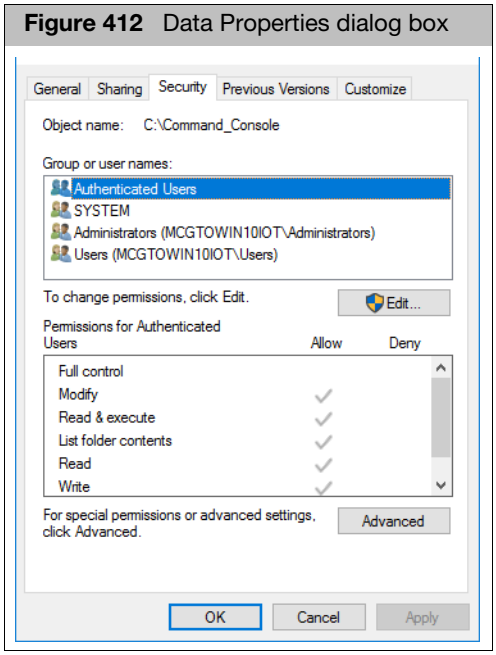
How to adjust permissions for files in a folder

To reset the permissions for all files and sub-folders in a folder:

1. Right-click on the folder in question and select **Properties.**

   The folder's Properties dialog box appears.
2. Click the Security tab. (Figure 412)

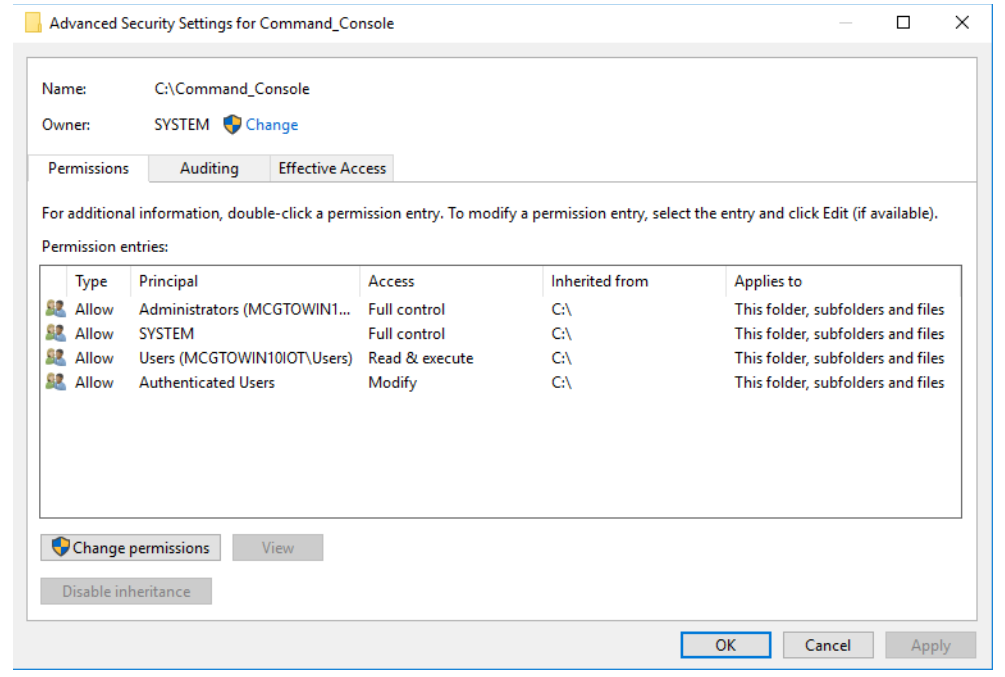
Figure 412 Data Properties dialog box



3. Click the **Advanced** button.

   The Advanced Security Settings dialog box opens. (Figure 413)

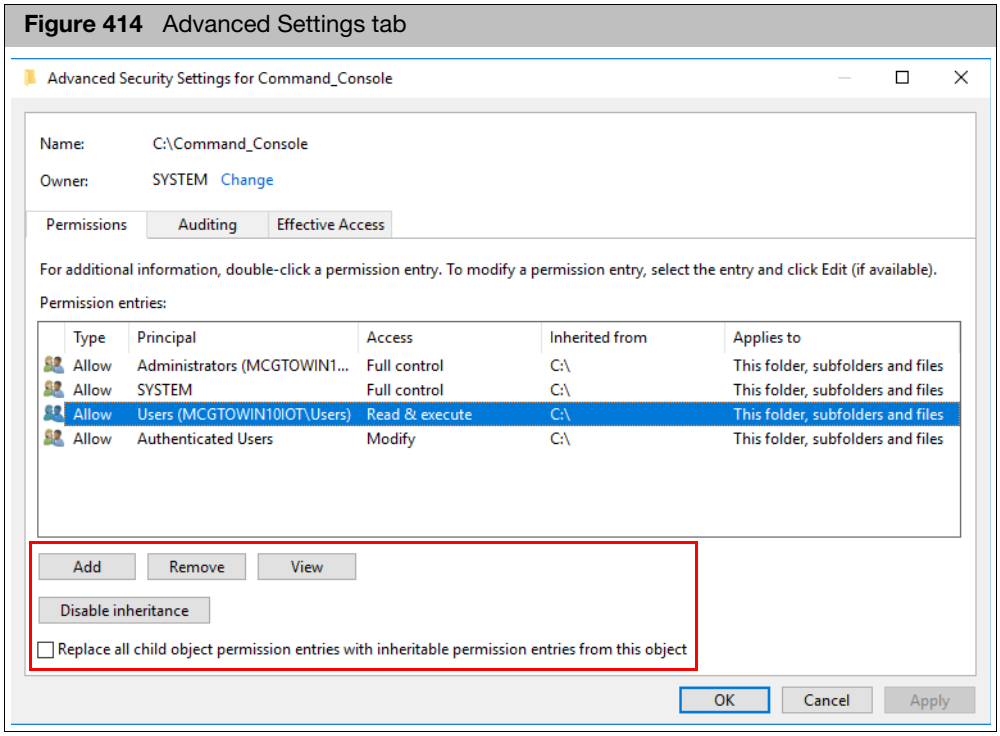
Figure 413 Advanced Settings tab



4. Verify that the security settings are appropriate.
5. Click to select (highlight) the permission entry you want to modify, then click **Change permissions**.

   The following permission options appear. (Figure 414)

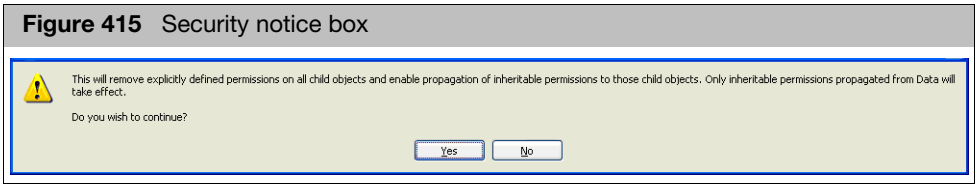
Figure 414 Advanced Settings tab



6. Click the appropriate button and click the **Replace all child object permission entries...** check box (if applicable), then click **OK**.

   The following notice may appear. (Figure 415)

Figure 415 Security notice box



   To replace the permission you just modified, click **Yes**.

   Note: This will reset the permissions for all files and sub-folders of the selected folder.

Cell summary report

Report description

The Cell Summary Report is a tool for monitoring the performance of the hybridization and grid alignment of arrays. The report enables you to detect problems in these steps and compare the performance of different chips.

The Cell Summary Report uses the control features on the array. Control features are cells with special probes; the corresponding targets are spiked into the sample cocktail. The resulting patterns of bright and dark cells are used in grid alignment and other processes.

In GCC the Cell Summary Report is automatically generated when CEL files are generated for certain types of arrays. These arrays require a GRC file in the library file set. If you generate a CEL file for one of these arrays and the GRC file is not available, you will see an error notice.

You can learn more about the Cell Summary reports in the following sections:

- "Report description"
- "Using the cell summary report" on page 358
- "Cell summary report algorithm" on page 359

The cells that failed the analysis can be seen in the GCC Viewer when looking at the DAT or CEL file (see "File display differences" on page 276).

The reports are placed in the data root and subfolder with the CEL file.

The cell summary report components are described in "Cell summary report Components for non-re-sequencing chips".

Cell summary report Components for non-re-sequencing chips

The Cell Summary Reports for all types of chips except Resequencing (Expression, Mapping, and others) provides information on the following features:

- Non-synthesized features
- OligoB1 features
- OligoB2 features

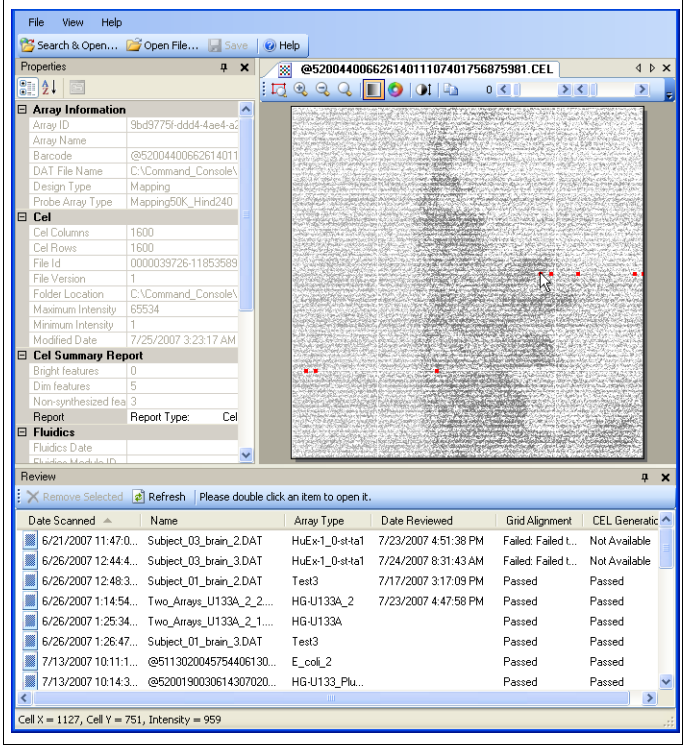
Refer to the relevant manual for the GeneChip array for more information about these features.

Opening the Cell Summary Report

1. Open the CEL file in the GCC Viewer.
2. In the Properties box, click on the Report row.

   A button appears in the Report Row. (Figure 416)
3. Click on the button to open a text display of the CELL Summary report.

Figure 416 Cel Summary Report Section



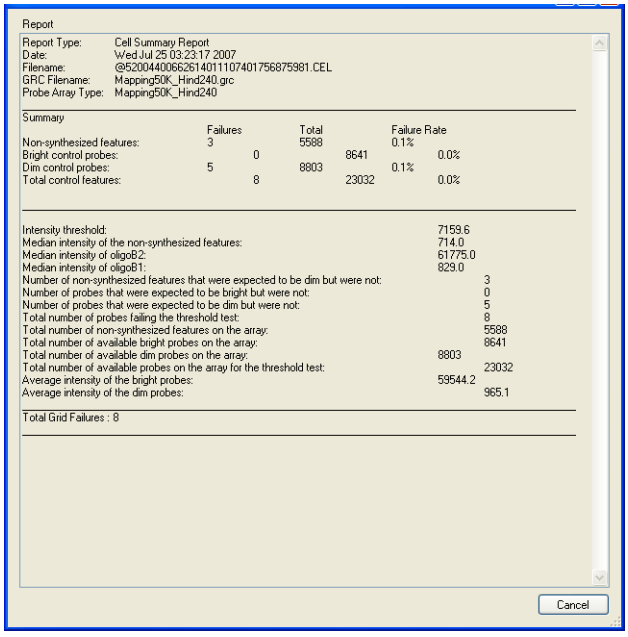
The Text Editor opens with the Cell Summary Report displayed. (Figure 417)

Figure 417 Cell Summary report for Non-resequencing array

Report Header

Report Summary

Metrics

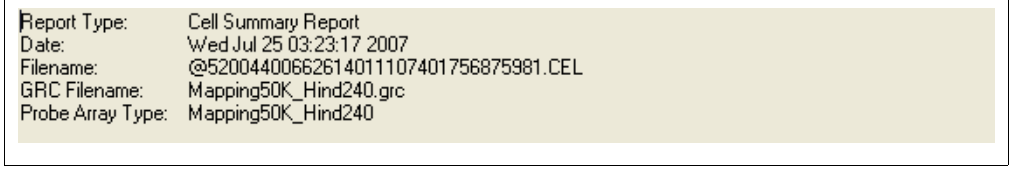


This report contains the following sections:

- "Report header"
- "Summary" on page 355
- "Metrics" on page 356

Report header

Figure 418 Expression Cell Summary report: header



The report header (Figure 418) lists basic information about the Cell Summary report:

Report Type Used to distinguish types of reports (Cell Summary Report, Algorithm Report, etc.).

Date Time and date report was generated.

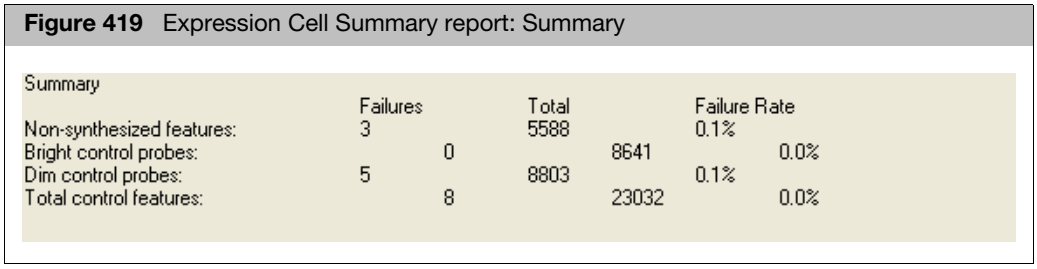
Filename Input CEL data file name that was used to generate the report.

GRC Filename Name of the GRC file used to generate the report.

Probe Array Type Array type used for the CEL file.

Summary

Figure 419 Expression Cell Summary report: Summary



The Summary (Figure 419) displays information:

For the following types of features:

Non-synthesized features

Bright control probes

Dim control probes

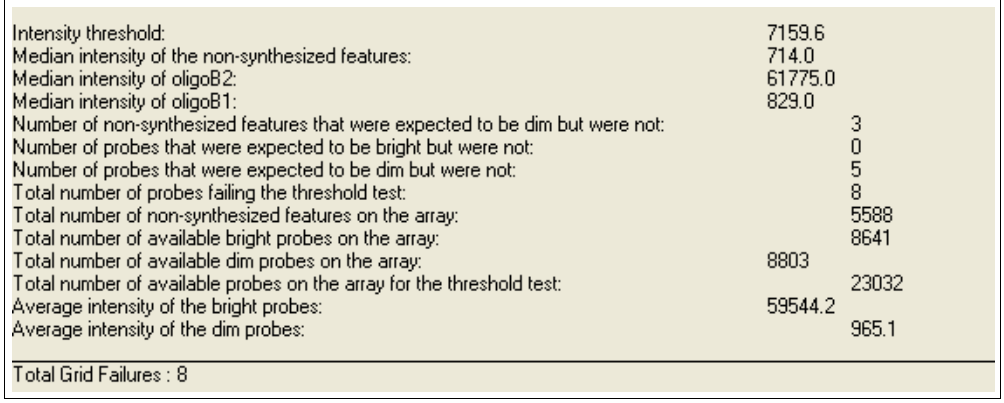
Total control features

The summary lists the following values:

Failures	The number of features in the category that failed.
Total	The total number of features in the category.
Failure Rate	The percentage of features in the category that failed.

Metrics

Figure 420 Expression Cell Summary report: metrics



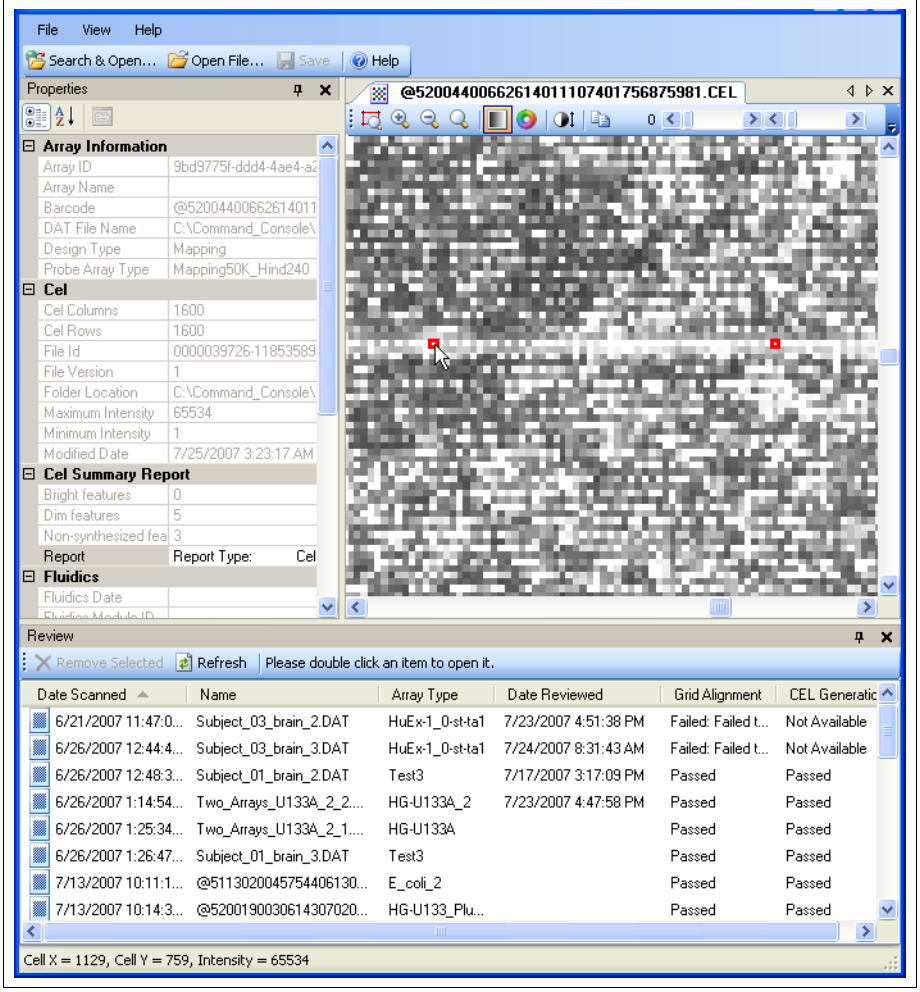
Intensity threshold:	7159.6
Median intensity of the non-synthesized features:	714.0
Median intensity of oligoB2:	61775.0
Median intensity of oligoB1:	829.0
Number of non-synthesized features that were expected to be dim but were not:	3
Number of probes that were expected to be bright but were not:	0
Number of probes that were expected to be dim but were not:	5
Total number of probes failing the threshold test:	8
Total number of non-synthesized features on the array:	5588
Total number of available bright probes on the array:	8641
Total number of available dim probes on the array:	8803
Total number of available probes on the array for the threshold test:	23032
Average intensity of the bright probes:	59544.2
Average intensity of the dim probes:	965.1

Total Grid Failures : 8

The metrics section (Figure 420) displays additional data about the B1 and B2 oligos.

Failed cell locations

Figure 421 Cell intensity data with failed control features masked



Note: To view these probes on a DAT file, view the cell intensity display. For more information about this option, see "Viewing failed control features" on page 277.

Using the cell summary report

The Cell Summary report provides clues to problems in the fluidics, grid alignment, and other issues with the cell file.

It can be used to establish a baseline for performance, which can then be used for quality control for subsequent experiments.

Features can fail the evaluation due to sample and system issues such as:

- Incorrect gridding
- Incorrect concentration of control oligo in sample (too high or too low)
- Incorrect scanner arc correction
- Incorrect recording of the scanner pixel size
- Incorrect parameters for cell file generation
- Debris in the sample or on the array glass
- Array defects

Rules of thumb

When processing a group of samples, identify the cell files that have the largest number of evaluation failures. This would be about ten percent of the cell files in the group. Use the graphic display described below to examine those cell files to identify any sample or system issues.

When processing one or two samples use the graphic display to examine those cell files with evaluation failures greater than ten.

In the event of substantial (greater than one hundred) evaluation failures the following guidelines may be helpful:

- Failures limited to mostly bright or mostly dim control probes usually indicate debris or array defects.
- Failures limited to mostly non-synthesized features often indicate non-specific binding and usually do not compromise any biological measurements.
- Failures spanning both bright and dim probes often indicate gridding, scanning or other systematic issues.

The relationship between Cell Summary Report results and biological results varies depending on the application. It is best to track these and determine trends for your laboratory and application.

Cell summary report algorithm

The algorithm's goal is to use the probe design information to identify all probes that should have high intensities and make sure they in fact have high intensities. Similarly with the probes that should be dim. The features that fail the evaluation are totaled and flagged to enable their graphic display.

Depending on the array/assay type, it is the target for the B1 probes that is spiked in and in others the target for the B2 probes is used.

Thus, the first step of the algorithm is to determine which of the two probe types is brighter overall. The median for each of the B1 and the B2 probes is determined and if there is sufficient contrast (difference in median intensities) the probe type with the larger median is taken to be the bright probe type.

If the contrast is insufficient an algorithm failure is reported. This kind of failure is typically only seen in the case of gross errors—such as use of the wrong library file, improper use of control reagents (spiking in both or neither of B1 and B2 control reagents) or rotation of the DAT image. The threshold is the calculated midpoint (or log midpoint) of the B1 and B2 medians.

The algorithm examines each feature. If the feature is either B1, B2, or non-synthesized, then the intensity is compared against the threshold; otherwise, the feature is ignored. If the feature fails the threshold, then the feature is added to the total and the feature flagged to enable graphic display.

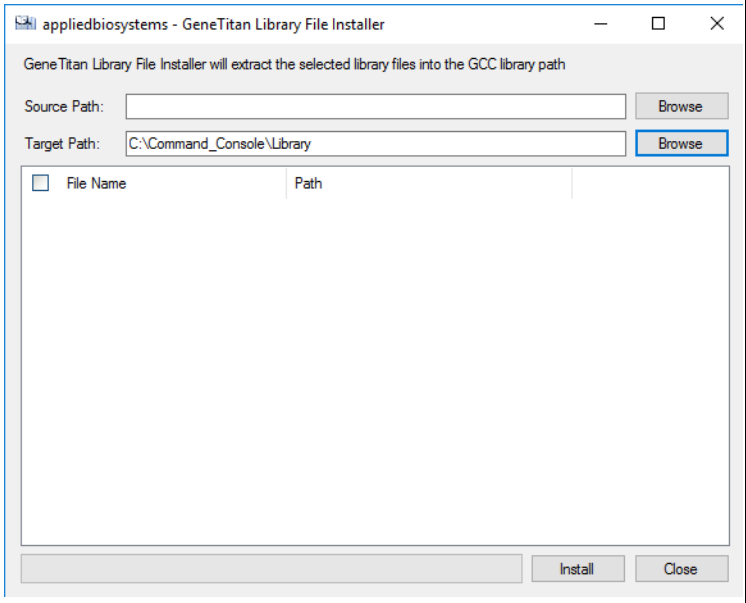
D Installing library files and scripts

GeneTitan library file installer

1. From the Launcher, double-click on **GeneTitan Library File Installer**.

   The GeneTitan Library File Installer window appears. (Figure 422)

Figure 422 GeneTitan Library File Installer



2. Click the Source Path's **Browse** button.

   A Browse For Folder window appears.

3. Navigate (as you normally would) to the source location of the library files you want to install.

4. Click **Select Folder**.

   The available library file packages appear in the File Name and Path pane.

   Note: Use the default Target path. Changing the target path is not recommended.

5. Click the check box(es) adjacent to the library filename you want to install, then click **Install**.

   A progress bar appears.

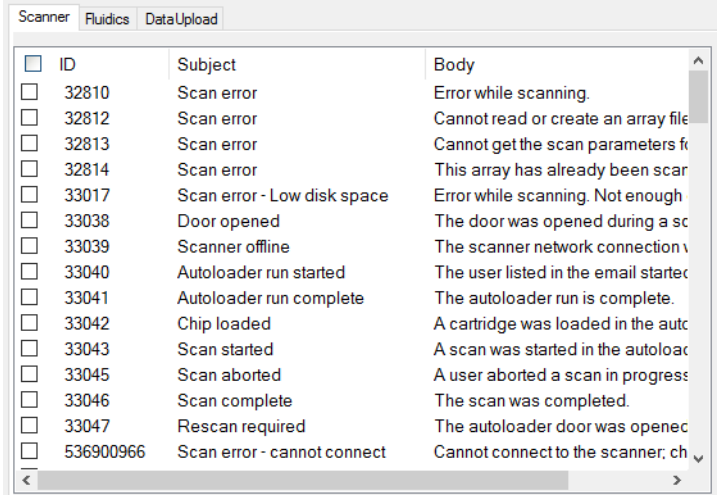
   After the installation is complete, an Installed successfully message appears.

6. Click **OK** to acknowledge the message, then close then the GeneTitan Library File Installer window.

7. Enter the email account the messages will be sent from in the From box.
8. Enter the email account(s) to receive the message in the To... Box
9. Enter the SMTP Server and Port information in the appropriate boxes.
10. You can click the Test button to send a test e-mail.
11. Select the Scanner or Fluidics tab, depending upon which instrument you want to select messages for (Scanner or Fluidics).

    The message list displays the messages you can select from. The messages correspond to different types of failures or other conditions in the instrument, as shown in Figure 423.

Figure 423 Message List for Scanners



12. Select and edit messages:
    a. Select the check box next to the message ID.
    b. Click in the subject or body column for the message and edit the text.

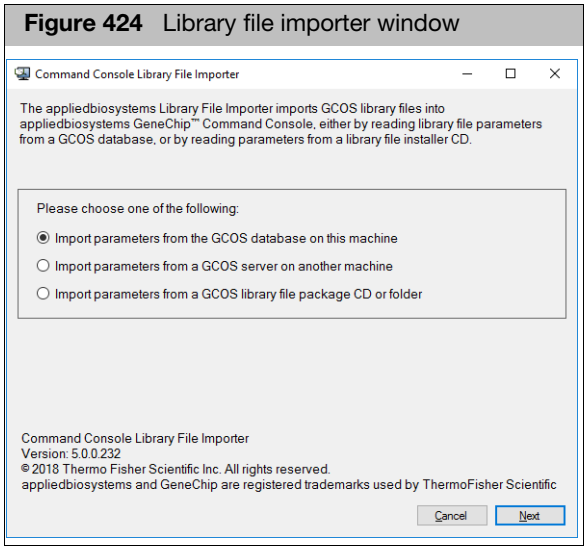
       You can click the Default button to return to the original configuration.
13. Click **Save** to save the configuration changes.

Library file importer

Importing from CD or folders

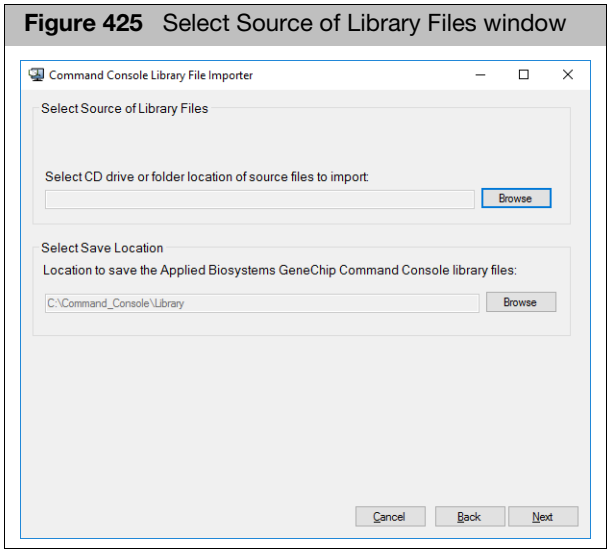
1. From the Launcher, double-click on **Library File Importer**.
   The Library File Importer window appears. (Figure 422)

Figure 424 Library file importer window



2. Click on the Import parameters from a GCOS library file package CD or folder radio button, then click **Next**.
   The Select Source of Library Files window appears. (Figure 425)

Figure 425 Select Source of Library Files window

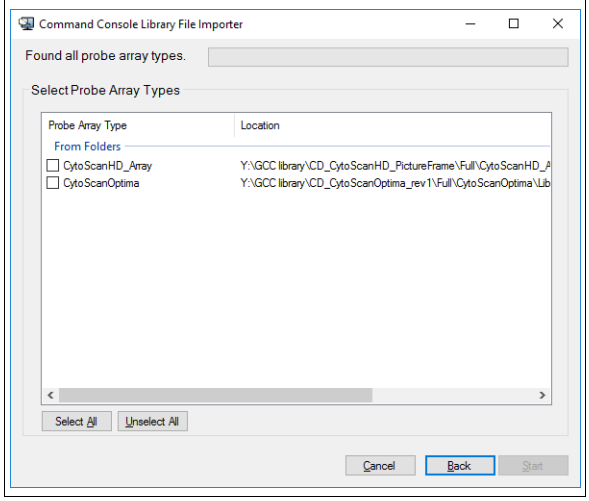


3. Click the **Browse** button to select the drive location for files you want to import. The Browse for Folder window appears.
4. Navigate to your source location as you normally would, then click **OK**.
5. Click the **Browse** button, to select a saving location for files you are importing. The Browse for Folder window appears.

6. Navigate to your save location as you normally would, then click **OK**.
7. At the Library File Importer window (after your source and save locations are set), click **Next**.

   The Select Probe Array Types window appears (Figure 426) and displays a list of the library files available in the selected folder or CD with their location. Duplicate probe arrays types are grouped at the top of the list.

Figure 426 Select Probe Array Type window

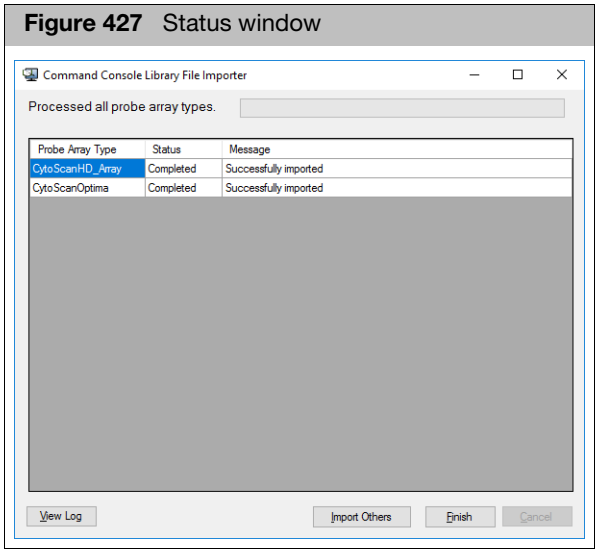


8. Click the appropriate check box or click **Select All**, then click **Start**. Click **Unselect All** to deselect your checked box(es).

   A Status window (Figure 427) with a progress bar appears.
9. After processing has been successfully completed, click **Finish**.

Note: If you have selected the same library file from two sources, a warning appears. Click **OK** to return to the Select Array window, then deselect the duplicate array package. If you have selected library files that are already installed, a Choose Library Version window appears. Click the radio buttons to choose the appropriate versions, then click **OK**.

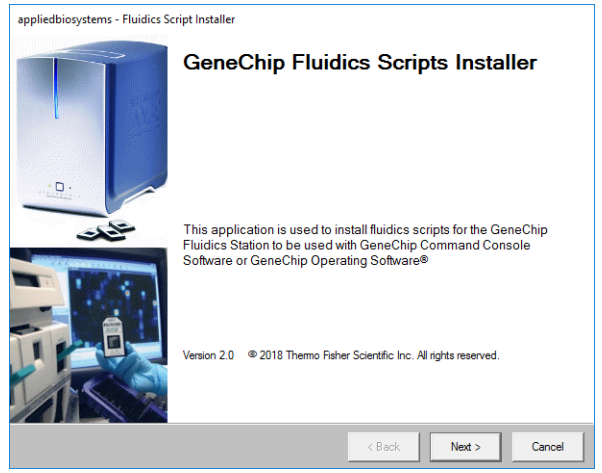
Figure 427 Status window



Fluidics script installer

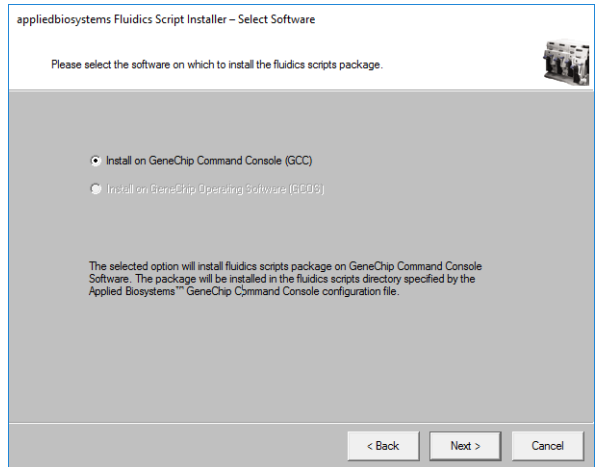
1. From the Launcher, double-click on **Fluidics Script Installer**.
   A Welcome window appears. (Figure 428)

Figure 428 Fluidics Scripts Installer



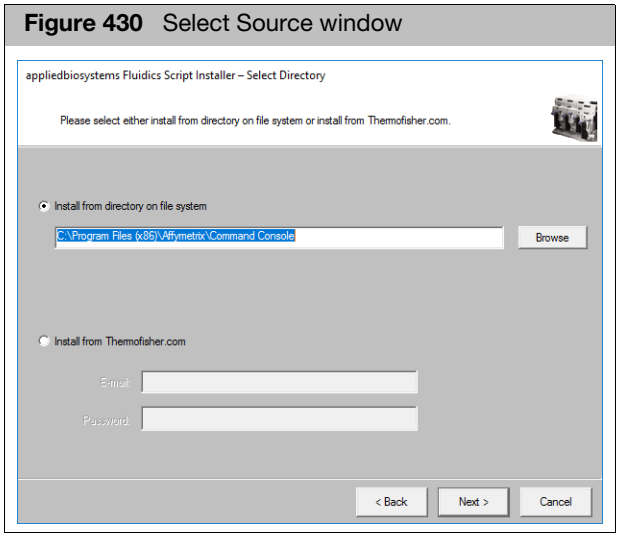
2. Click **Next**.
   The Select Software screen appears. (Figure 429)

Figure 429 Select Software



3. Click **Next**.
   The Select Directory window appears. (Figure 430)

Figure 430 Select Source window



Installing from a directory

1. Click the radio button.
2. Click **Browse**.
3. Navigate to the file location as you normally would.
4. Click to select the protocol, then click **OK**.
5. The file location is now displayed.
6. Click **Next**.

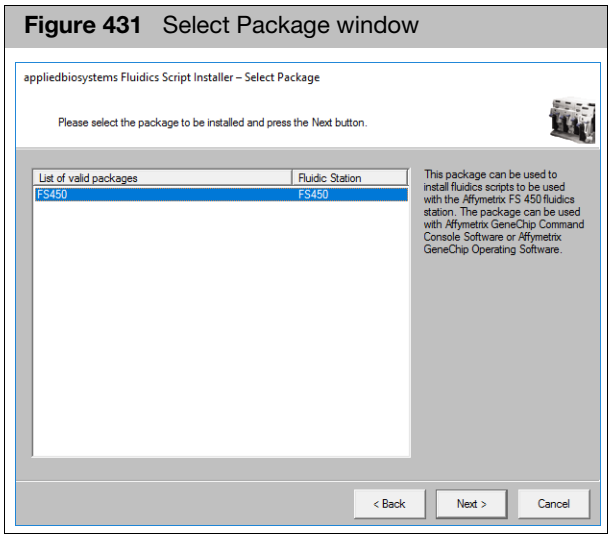
   The Select Package window appears. (Figure 431)

Installing from thermofisher.com

1. Click the radio button.
2. Enter your registered username (email) and password.
3. Click **Next**.

   The Select Package window appears. (Figure 431)

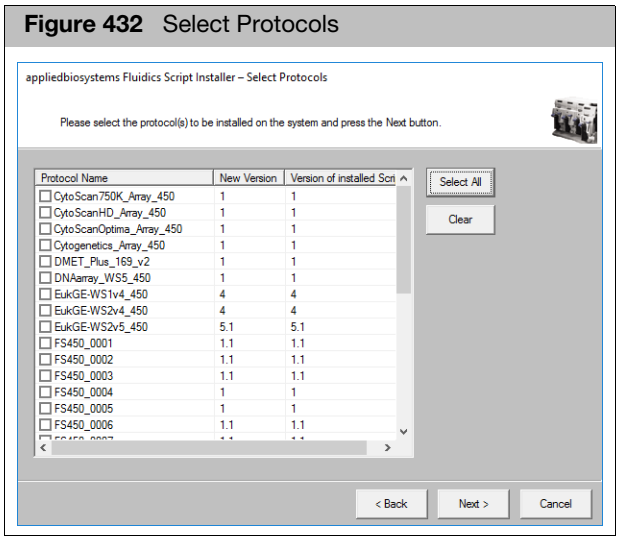
Figure 431 Select Package window



4. Select the package you want to install, then click **Next**.

   The Select Protocols window appears. (Figure 432)

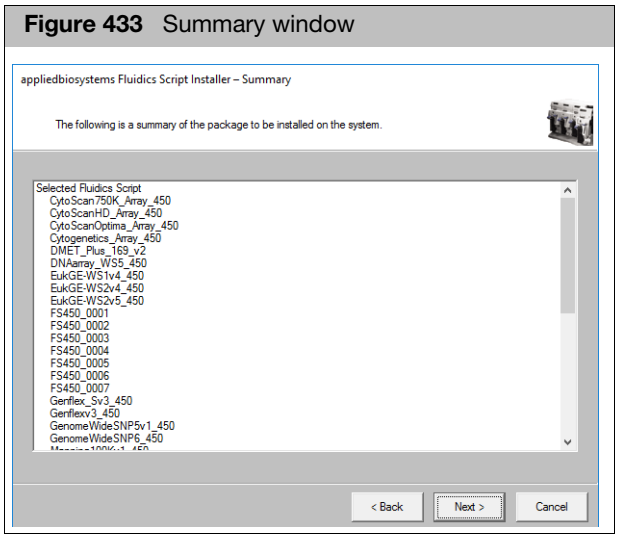
Figure 432 Select Protocols



5. Select the check box(es) of the protocols you want to install, then click **Next**.

   The Summary window appears. (Figure 433)

Figure 433 Summary window



6. Review the information and click **Next**.

   An Install window appears with a progress bar.

   When the install is completed, the Finish window appears.

7. Click **Close**.

Note: If you opened the Installer through the GCC Fluidics Control Software, you must close the software, then reopen it for the installed scripts to appear in the drop-down lists.

Notification e-mails

Configuring notification e-mails

GCC provides e-mail notification of problems when:

- Running the GCS 3000 with AutoLoader
- Running the FS-450 Fluidics Station
- Running the GeneTitan Instrument
- Running the Data Uploader

You will need to get information on the SMTPPort and SMTPServer from your IT department.

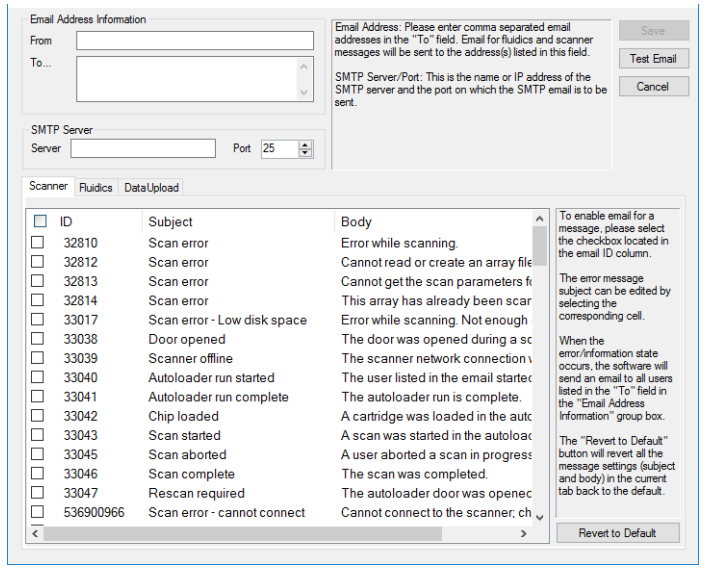
Configuring the notification for GCC Fluidics control or GCC Scan control

1. In the appropriate instrument control software, click the Email button; or

   From the Edit menu, select **Email Messages...**

   The GCC Email Configuration Editor opens (Figure 434).

Figure 434 GCC Email Configuration Editor

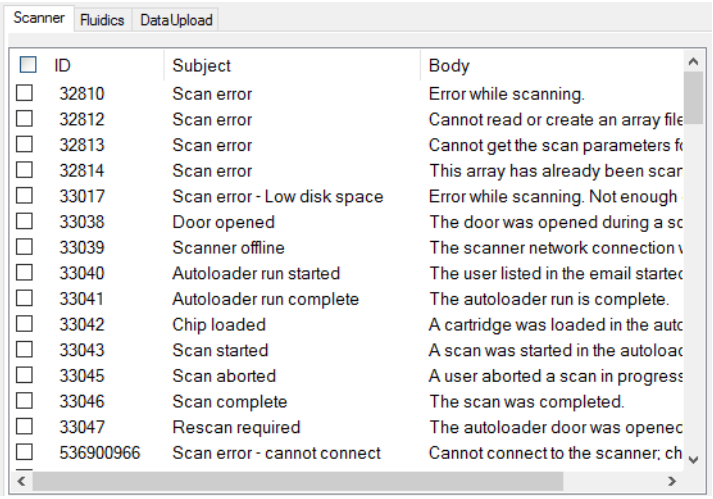


2. Enter the email account the messages will be sent from in the From box.
3. Enter the email account(s) to receive the message in the To... Box
4. Enter the SMTP Server and Port information in the appropriate boxes.
5. You can click the Test button to send a test e-mail.

6. Select the Scanner or Fluidics tab, depending upon which instrument you want to select messages for (Scanner or Fluidics).

   The message list displays the messages you can select from--they correspond to different types of failures or other conditions in the instrument.

Figure 435 Message List for Scanners



7. Select and edit messages:
   a. Select the check box next to the message ID.
   b. Click in the subject or body column for the message and edit the text.

      You can click the Default button to return to the original configuration.
8. Click **Save** to save the configuration changes.

Log files generated by GCC

GCC log files

The log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and installer.

These log files provide useful information for troubleshooting problems and may be requested by your support person. For details on how to collect and send log files, see "Error logs" on page 41

The following files apply to both Cartridge Systems and GeneTitan Instruments. All the GCC log files from C:\Command_Console\Logs

The different log files include:

Systemlog.XML	XML file with system information.
Workflow.log	Text file with information on workflow status and history.
GCC_LibFileImporter. log (with date and time code)	Text file with info on use of the Library File Importer.

Other GCC Files

Your support person may need the following files for troubleshooting:

1. Library files (*.PARAMS, *.MASTER, *.WORKFLOW, *.SMD, *.MEDIA) located in C:\Command_Console\Library, excluding the large analysis library files (CDF, PSI, GRC).
2. Provide a list of all sub folders and their contents under the library files folder located in C:\Command_Console\Library. Please ensure there are no duplicate library files, as these can cause problems.
3. GCC system configuration file located at C:\Command_Console\Configuration\Calvin.System.config
4. Pending job order files located in C:\Command_Console\Jobs
5. Other GCC related information, such as:
    a. The number of files under C:\Command_Console\Data, including sub directory.
    b. If the system is a networked system or a standalone system.
    c. Other applications installed on the system, such as antivirus application, MS Office, Internet Explorer versions.

GCC log files for cartridge systems

The following files are instrument-specific log files that apply to GCS 3000/FS 450 Instruments:

fluidics.log	Text file with info on Fluidics Station use
scanner.log	Text file with info on Scan Control use
FS.log (with date and time code)	Text file with information on the Fluidics Script installation.

GCC log files for GeneTitan systems

Log files for the GeneTitan Instrument control processes are placed in subdirectories of the Command Console\Logs\ folder.

Your support person may need the following files for troubleshooting:

GeneTitan Fluidics

1. C:\Command_Console\Logs\96F\
   a. subdirectories named by date (e.g. Log7-29-2009)
   – Collect all dated directories and contents since the GeneTitan app was started, not just the date of the event (some logging goes into files from the date the app started so this can be critical for us).
   – Absolutely required are all the log directories from the date the run was started to the date of the event.
2. C:\Command_Console\Logs\96F\FluidicErrorLog - all files in this directory
3. C:\Command_Console\RAP2

   The main user interface to this logging structure is file is C:\Command_Console\RAP2\RAP.html.
   - RAP.html contains historical information (since GCC 4.3 was installed) about what has been run on the system
   - RAP.html contains links to locations within the RAP2 folder and to some locations the standard logs found in C:\Command_Console\Logs\96F
   - The logging structure supplements the standard logs found in C:\Command_Console\Logs\96F. It does not replace it.
   - The RAP2 folder is not on the 30 day log file cleaner path.

GeneTitan MC Imaging Device

1. C:\Affymetrix\GeneChipHTScanControlMC\Log - collect all dated directories and contents since the GeneTitan app was started
2. C:\Affymetrix\GeneChipHTScanControlMC\RunLog - collect all dated directories and contents since the GeneTitan app was started.

Collecting GCS3000/FS450 log files

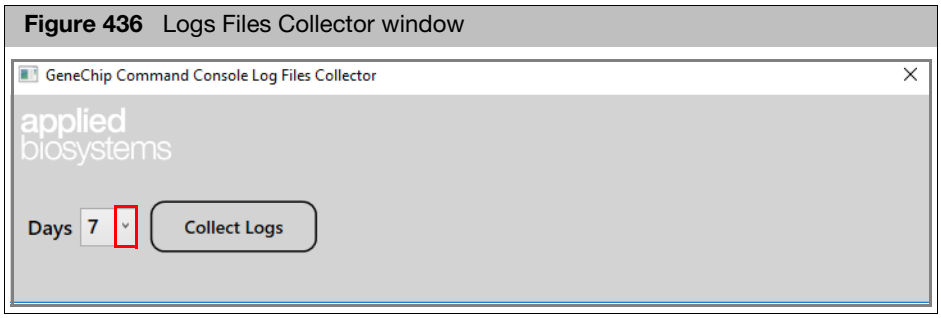
Log files are produced by different GCC components. The logs provide a record of the tasks performed by different components, such as the migration tools and installer.

These log files provide useful information for troubleshooting problems and may be requested by your support person.

1. From the GCC Launcher, click **Log Collector**.

   The Collect Logs window appears. (Figure 436)

Figure 436 Logs Files Collector window

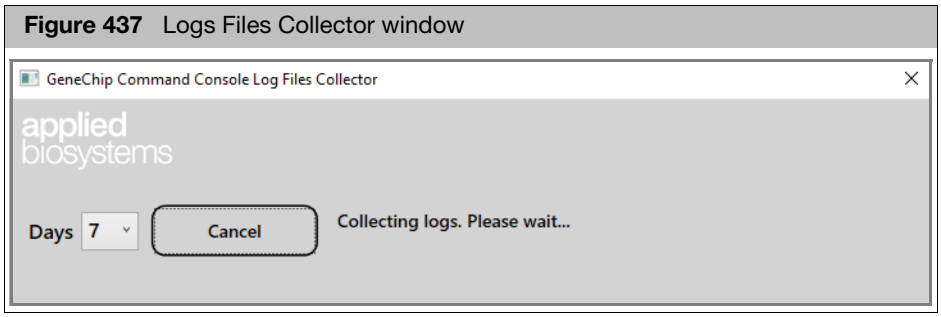


2. Click on the **Days** drop-down to select the number of days worth of log files you need to collect.
3. Click **Collect Logs**.

   A **Collecting logs. Please wait...** message appears. (Figure 437)

   To terminate a log collection in progress, click **Cancel**.

Figure 437 Logs Files Collector window



After a few moments, a zip file containing your collected logs is placed onto your Desktop for easy access.

TSV files

Using TSV files for batch editing

You can no longer download batch registration or batch editing files in TSV (Tab-Separated-Values) format in GCC, but you can use previously created TSV files. The format of TSV files is discussed here.

The header row in a TSV file includes special properties that define the file and the physical array:

Path The path to where the Sample file is created. Can be used to place Sample files in project folders.

Project The project that the Sample (ARR) file is assigned to.

> **Note:** Specify either the Path or the Project for the files. Specifying both will return an error message.

File Name Unique identifier for the Sample file.

Array Name Name assigned to the array during registration.

Probe Array Type Part number for the array(s).

Barcode Barcode on the array(s).

Attributes Additional information about the sample and experiment that you can use to interpret your results.

Path

The path needs to be associated with a data root. You can assign a set of sample files to a particular project if you select that project's folder in the Path field.

Note: Specify either the Path or the Project for the files. Specifying both will return an error message.

Project

Specifying a project for the Sample file will determine the folder the Sample file is created in.

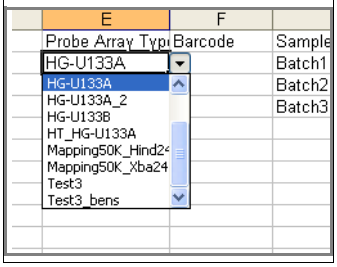
File Name

Enter the name assigned to the Sample file to be created.

Barcode, array name and array type

If you are using Excel, you can select the probe array type from a drop-down list (Figure 438). The drop-down list can be disabled in Excel if you want to enter multiple arrays for each sample.

Figure 438 List of probe arrays in Excel spreadsheet



You can also enter multiple array information into the file.

Note: You can use custom barcodes to register an array in Batch Registration.

Entering multiple arrays

1. Enter a comma-delimited list in the barcode column: FirstArrayBarcode, SecondArrayBarcode
2. Enter a comma-delimited list in the array name column: FirstArrayName, SecondArrayName
3. Enter a comma-delimited list in the Array Type column: FirstArrayType, SecondArrayType

Attributes

Enter the values for the attributes in the appropriate columns.

GCC uses two types of attributes for Batch Registration:

- Template Attributes: Attributes that have been defined in a template. When you select templates for the downloaded batch registration file, the array attributes in those templates are included as headings in the batch registration file.
- User Attributes: Attributes that you add in the Batch Register file.You create a user attribute by entering the attribute name and other characteristics in the column header, and then entering attribute values in the appropriate cells.

Attributes need to have the following characteristics defined:

- AttributeName
- TemplateName (if any; not used for User Attributes)
- DataType

Different methods are used for defining attribute characteristics in TSV and Excel format, as described below.

TSV format

In TSV format, all of the attribute characteristics are defined in the column header, as shown in the template below.

- Header format for Template Attribute:
  `AttributeName:TemplateName:DataType`
- Header format for User Attribute: `AttributeName:*:DataType`

Reconnector

Introduction

Use the Reconnector to restore file associations among Drop and Scan data files (DAT, CEL, and CHP) and a pre-registered Sample (ARR) file on the network.

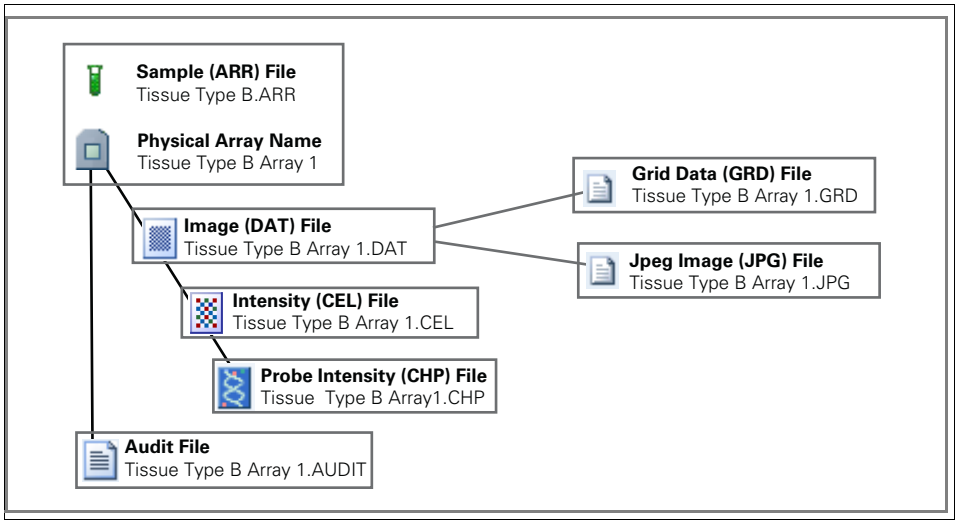
The types of data and files used in GCC, the methods used to track relationships between files, and the types of problems that can occur are described below.

The GCC software tracks:

- Information about the experiment, sample, and array(s)
- Probe array data
- Other information about probe array processing

GCC uses the file types to store array information and data, as shown in Figure 439.

Figure 439 File types used in GCC

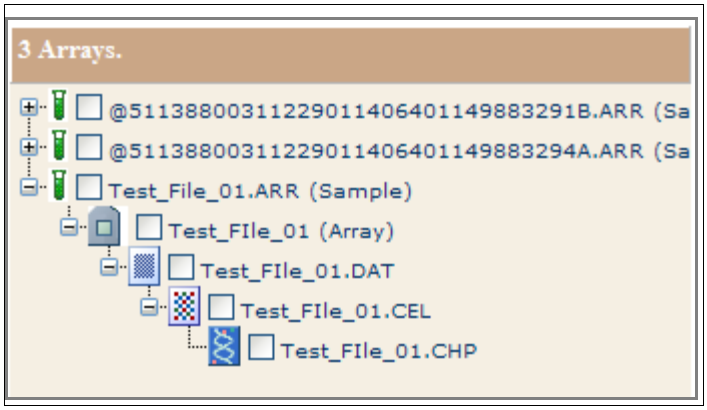


- Information about the sample, experiment, and physical array are collected in Sample (ARR) files.
- Probe array data generated during scanning and processing are collected in Data files of various types.
  - Image Data (DAT)
  - Cell Intensity Data (CEL)
  - Probe Intensity Data (CHP)

  Note: Array data files in GCC use the same file extensions as in GCOS, but they are in a different format; GCOS-format array data files cannot be viewed using GCC tools, such as the GCC Viewer. You can use DEC to convert GCOS-format files into GCC format.

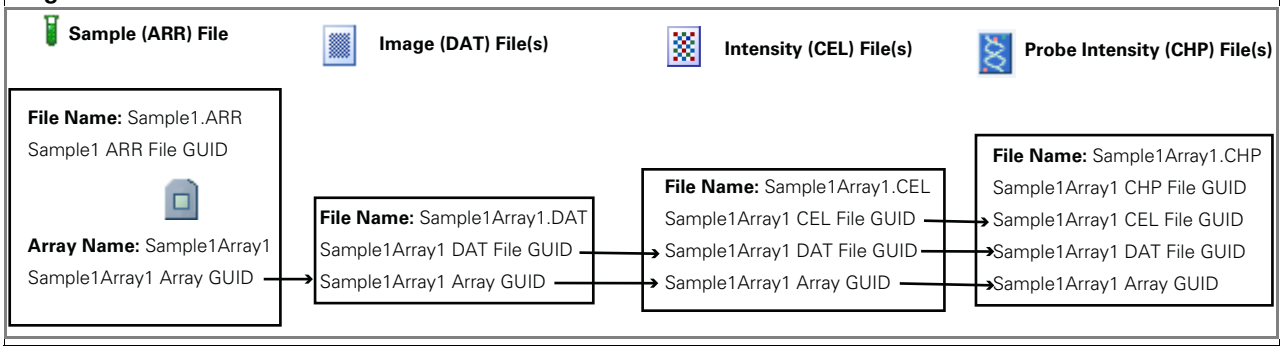
The DAT, CEL and CHP data files all have parent-child relationships, as shown in Figure 440.

Figure 440 File Hierarchy displayed in GCC



In GCC the lineage information for probe array data files is preserved using GUIDs, or Globally Unique Identifiers. A GUID is a number that is unique to that file. Each sample and data file is assigned a GUID for tracking file lineage information (Figure 441).

Figure 441



- Other files containing additional information about the probe array processing
  - Info about processing the array (AUDIT)
  - Sub-grid information (GRD) (only for arrays with sub-grids)
  - JPEG image (JPG) (only for arrays with sub-grids?)

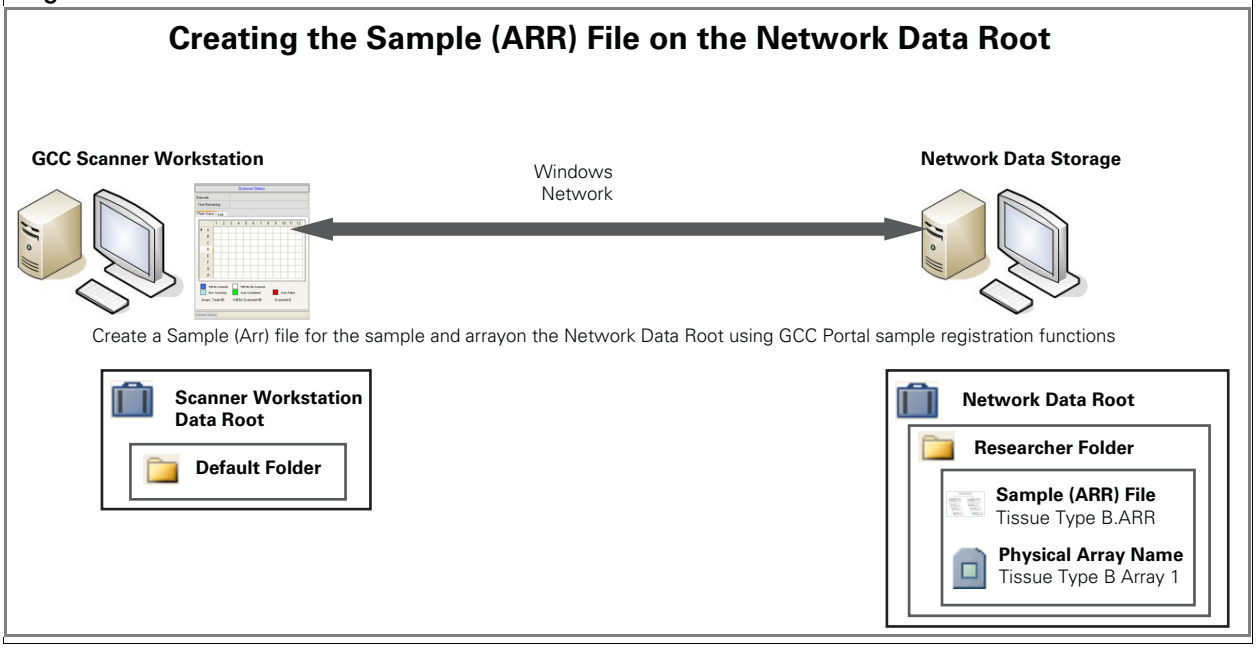
Connecting files

Drop and scan data files and pre-registered sample files

There are also circumstances where you can have multiple (commonly two) sample files for the same array, which is an error condition in GCC. This can happen when you perform scans on arrays with sample (ARR) files on a network data root and a problem arises with the network connection.

You can create Sample (ARR) files on any data root your GCC system has access to, including network data storage. (Figure 442)

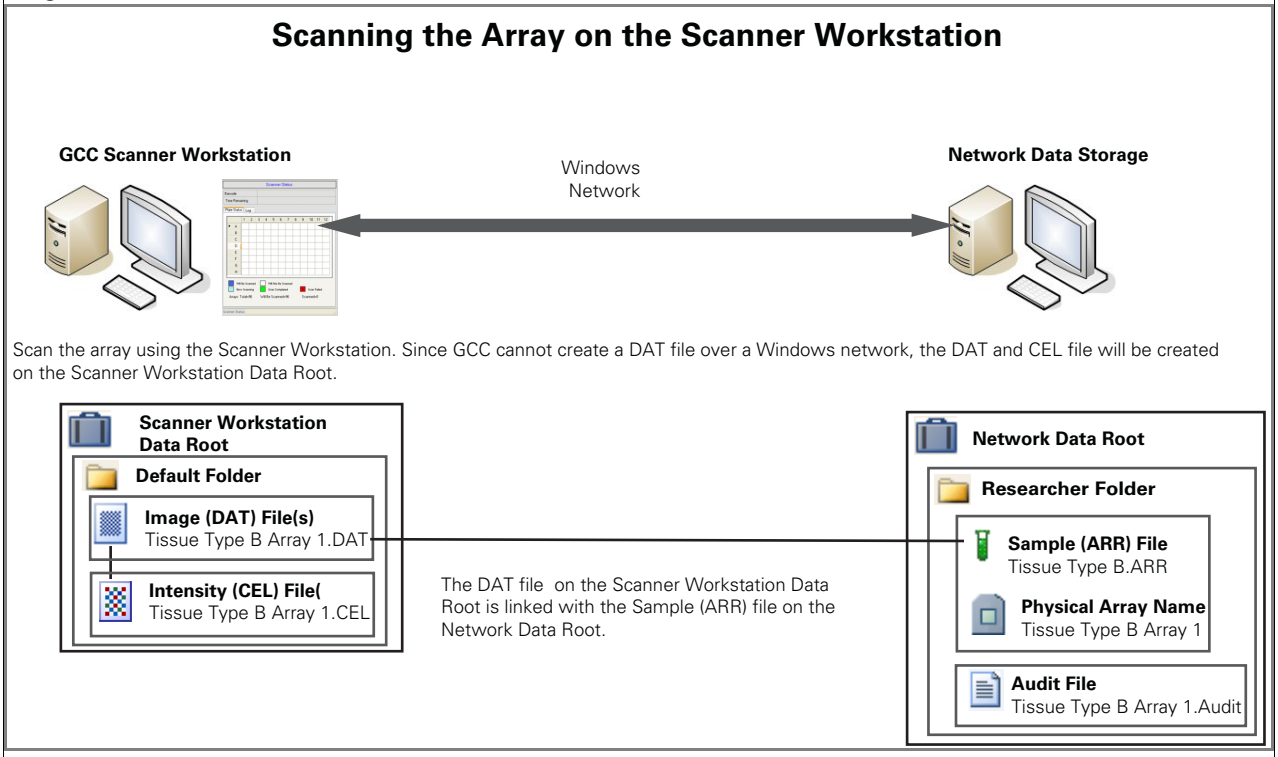
Figure 442



However, you cannot create DAT files over a network connection to network data storage; instead, the DAT files are created in the default folder on the Scanner Workstation computer. (Figure 443)

This is done to protect the DAT file from any problems related to the networks, so that an array can always be scanned successfully even when a network is unreliable.

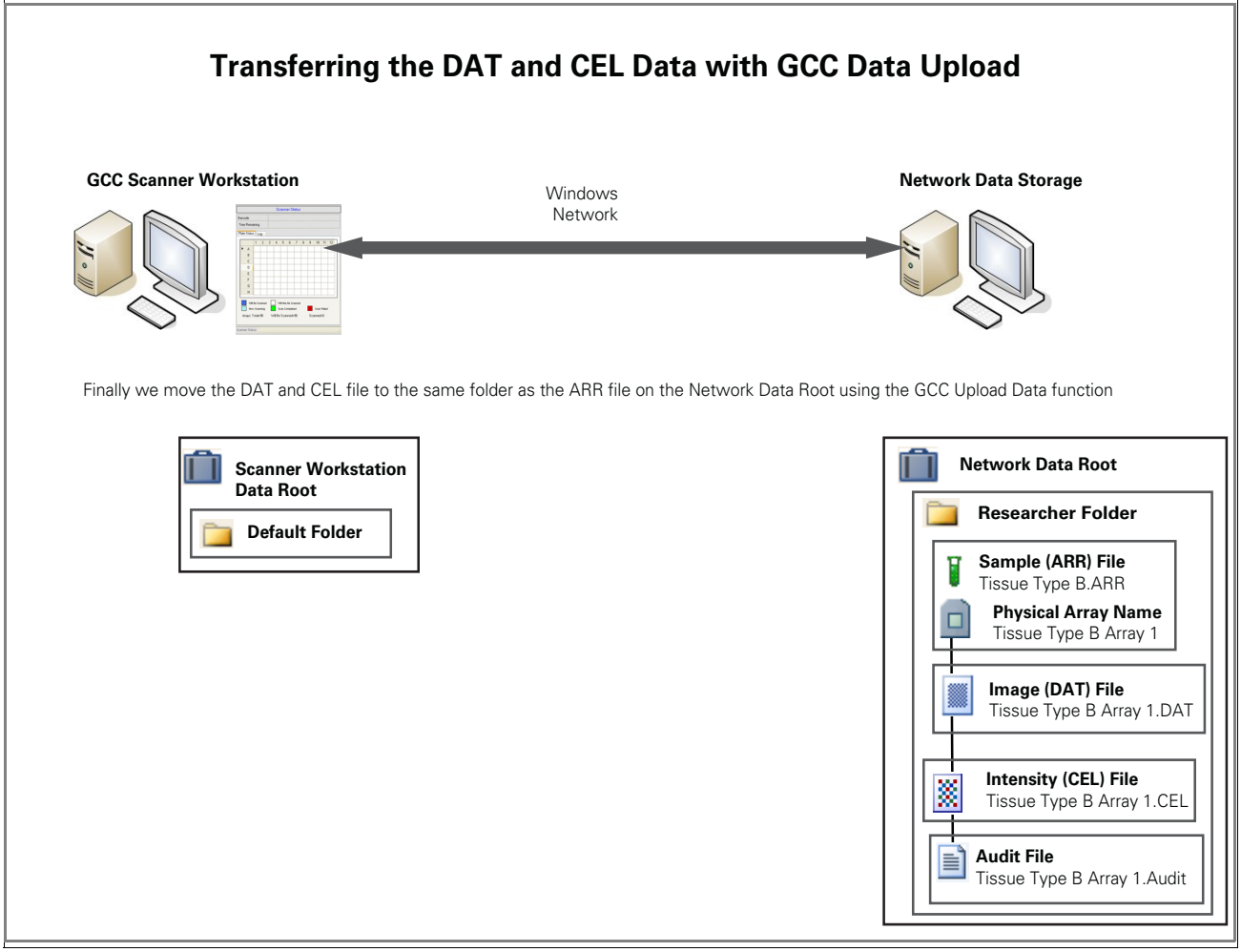
Figure 443



The Upload Data function can be used to automatically transfer DAT and CEL files from the Default folder to the network data storage where the Sample (.ARR) file is located. (Figure 444)

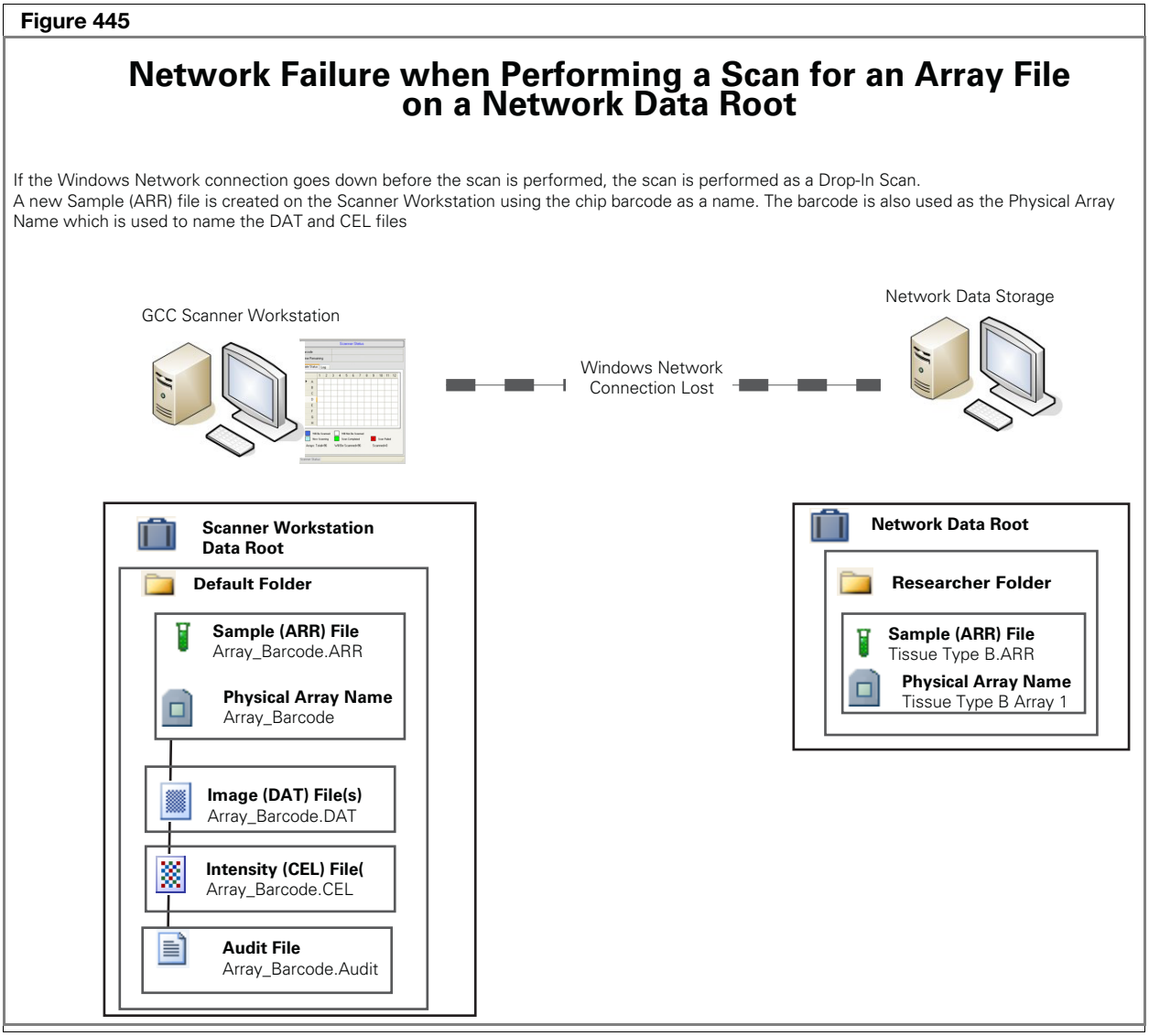
Upload Data is useful when you wish to consolidate data from different workstation computers onto one network data storage site.

Figure 444



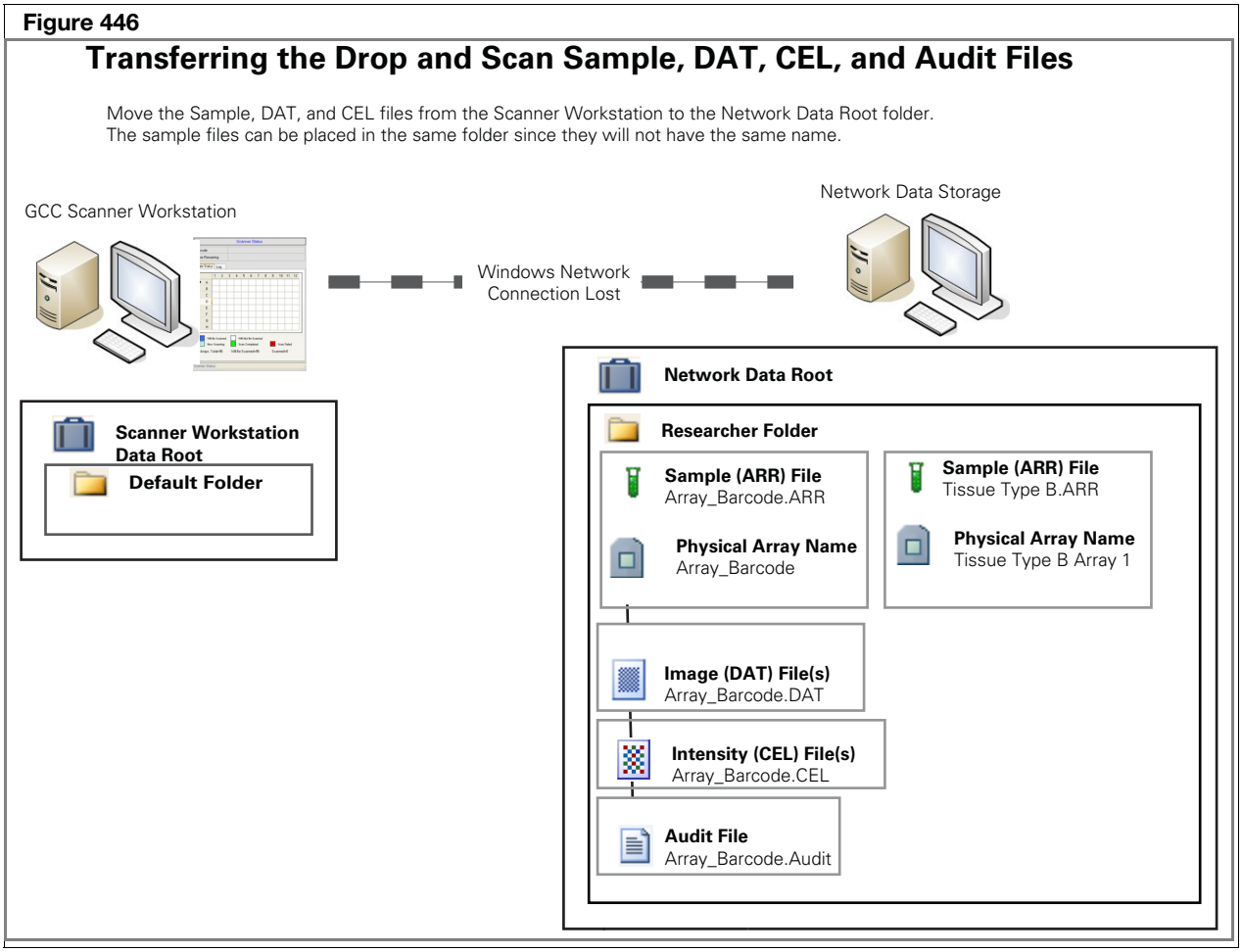
If the network connection between the network data root and the scanner workstation fails during the scan, the actual scan isn't affected. However, the links between the Sample file on the network data root and the DAT and CEL files on the Scanner workstation will be broken, and a a new Sample (ARR) file is created in the Scanner Workstation default folder (with the array barcode used as a name). (Figure 445)

Figure 445



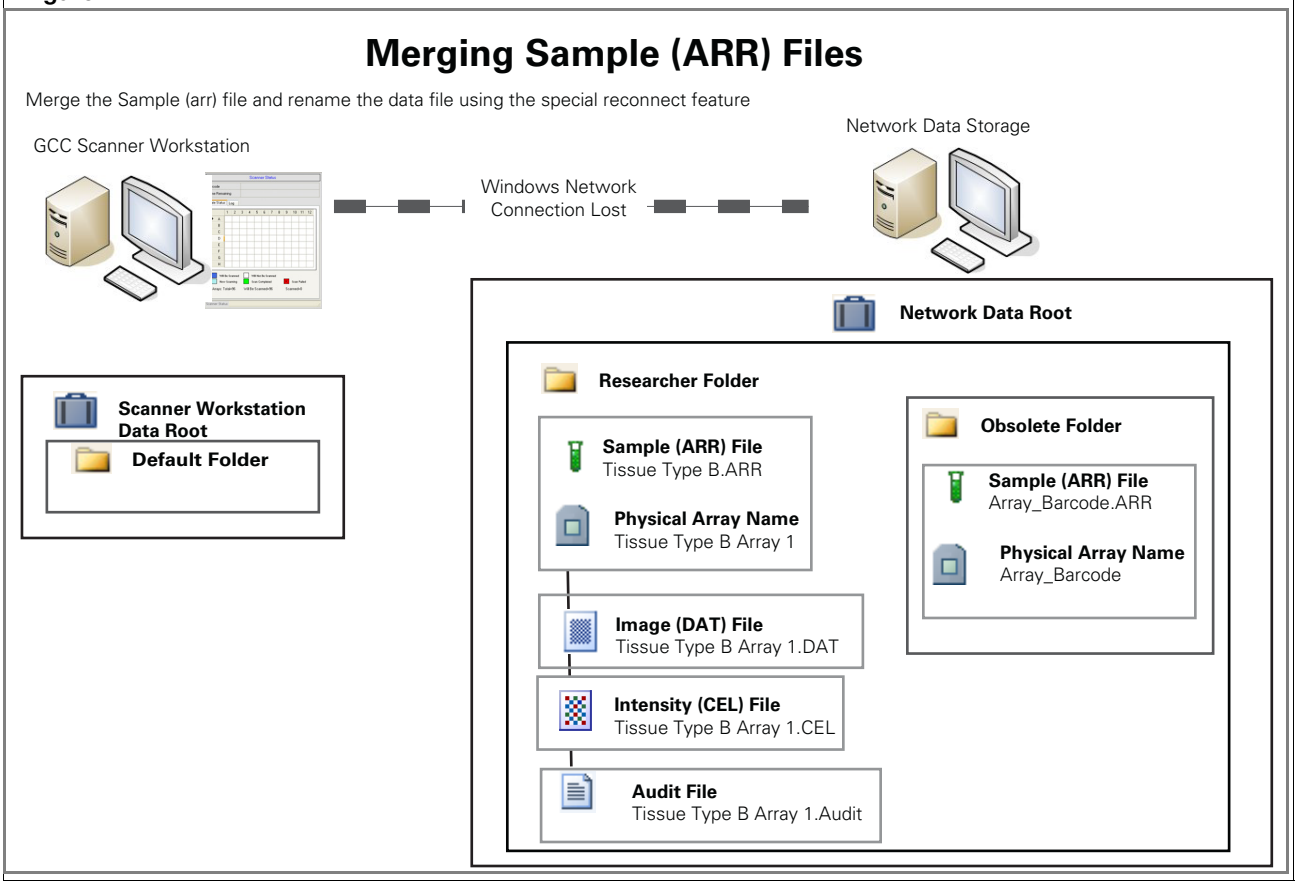
In this case, you cannot use the GCC Upload Data function to transfer the array data files to the Network Data Root. You can transfer the Sample and Data files manually, using Windows Explorer or another tool. (Figure 446)

Figure 446



After transferring the Sample and Data files to the network data root, you can use the Connect Drop and Scan Data Files and pre-registered ARR file function of the Reconnect tool to associate the DAT and CEL files with the preregistered Sample File, and to merge the sample file data from the drop and scan files. (Figure 447)

Figure 447


Merging Sample (ARR) Files
Merge the Sample (arr) file and rename the data file using the special reconnect feature
GCC Scanner Workstation
Windows Network
Connection Lost
Network Data Storage
Network Data Root
Researcher Folder
Scanner Workstation
Data Root
Default Folder
Sample (ARR) File
Tissue Type B.ARR
Physical Array Name
Tissue Type B Array 1
Image (DAT) File
Tissue Type B Array 1.DAT
Intensity (CEL) File
Tissue Type B Array 1.CEL
Audit File
Tissue Type B Array 1.Audit
Obsolete Folder
Sample (ARR) File
Array_Barcode.ARR
Physical Array Name
Array_Barcode

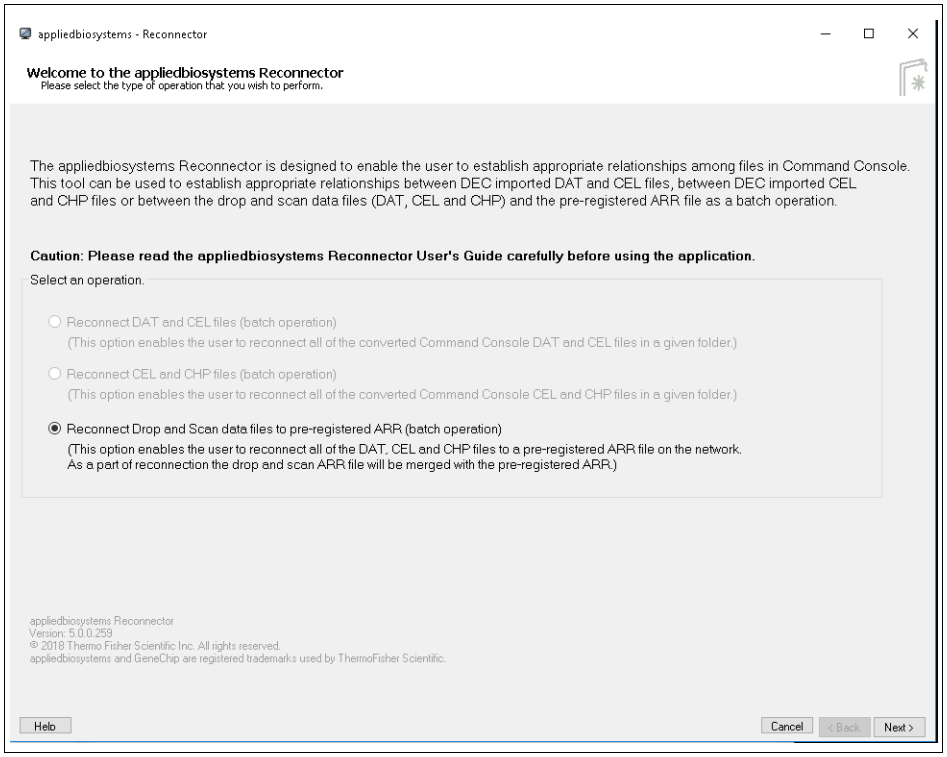
Starting Reconnector

IMPORTANT! All files to be reconnected in a particular operation must be in the same source folder and must be in GCC format before reconnecting.

1. From the GCC Launcher, click **Reconnector**.

   The Welcome to the Reconnector window appears. (Figure 448)

Figure 448 Welcome window

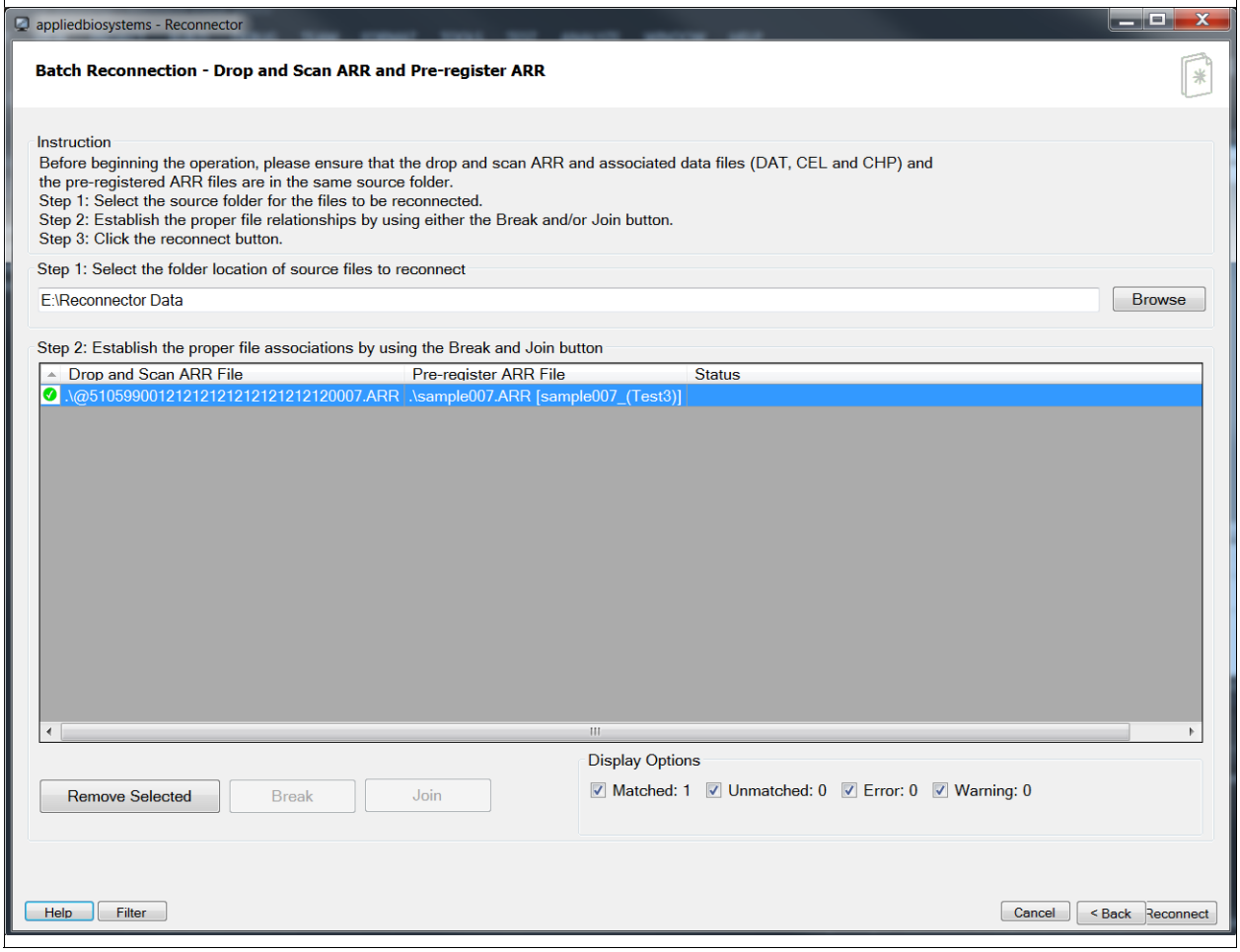


The Reconnect Drop and Scan Data Files and pre-registered ARR (batch operation) option (Figure 449) enables you to:

- Select the folder with the files you wish to merge. Please ensure that the drop and scan ARR and associated data files (DAT, CEL, and CHP) and the pre-registered ARR files are in the same source folder.
- Review and change the proposed relationships among the files in the folder.
- Reconnect the Drop and Scan data files with the pre-registered ARR files.

IMPORTANT! As a part of this operation the contents of the drop and scan ARR file will be merged with the pre-registered ARR file and the DAT, CEL, and CHP files will be renamed using the array name from the pre-registered ARR files.

Figure 449



Merging data files associated with drop and scan ARR and pre-registered ARR files

1. Make sure that the files you want to merge are all in the same folder, or in a sub-folder within the folder

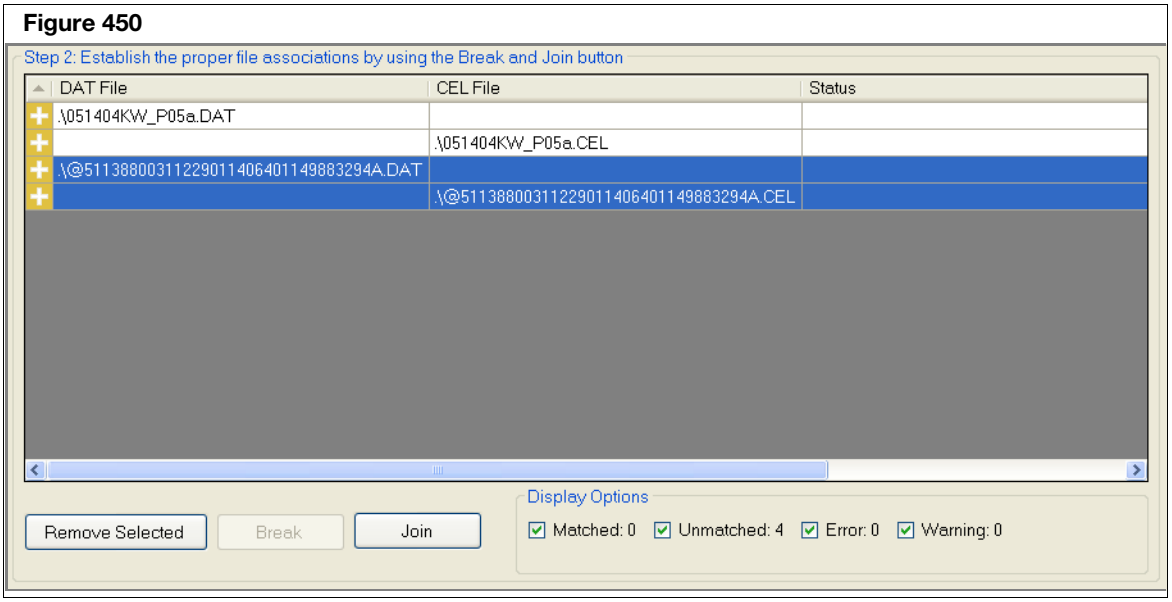
Selecting the folder

1. Enter the path in the select folder location box; or
2. Click **Browse**.

   The Browse for Folder window opens.
3. Navigate to the location of the folder, click to highlight it, then click **OK**.

   The Drop and Scan data files and pre-registered Sample (ARR) files in the folder and its sub-folders are displayed in a file list window. (Figure 450)

Figure 450



The file list window has four columns:

Status Icon	Unmatched: Indicates unmatched file Error: Indicates naming match between incompatible files Matched: Indicates match between compatible files. Warning: Indicates compatible files with tentative parent-child connections, but some information mismatch.
Drop and Scan ARR File	Sample (ARR) file created during Drop and Scan.
Pre-register ARR File	Sample (ARR) file created using sample registration functions of GCC Portal.
Status	Messages if files are not compatible.

IMPORTANT! Even though only the Drop and Scan ARR file is displayed in the window, the reconnect operation will connect all the associated data files (DAT, CEL, and CHP) with the pre-registered ARR file.

Click the check box(es) to select/deselect (show/conceal) these different display options:

Matched	Files with tentative parent-child connections.
Unmatched	Files with no tentative parent-child connections.
Error	Incompatible files with tentative parent-child connections.
Warning	Compatible files with tentative parent-child connections but some information mismatch.

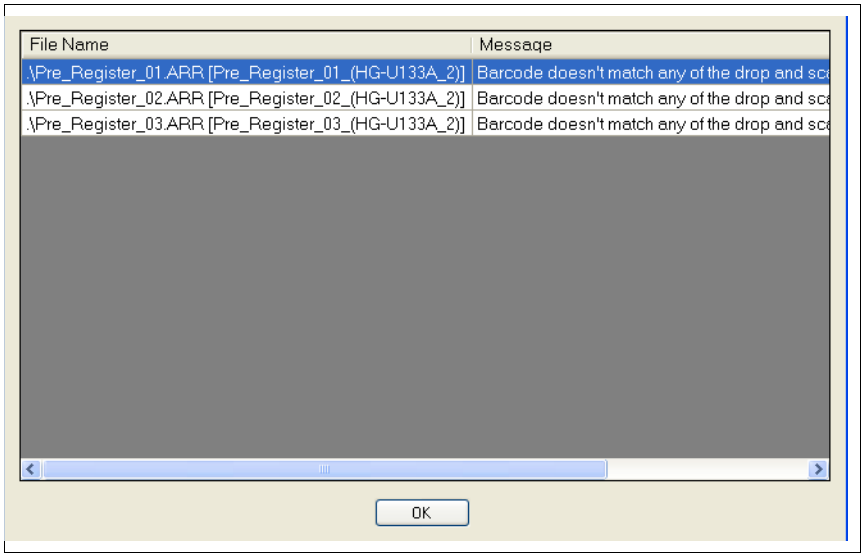
Use the bottom buttons to:

- **Remove Selected** - Remove selected/highlighted file(s).
- **Break** - Break current connections between files.
- **Join** - Join files that are not yet connected.

4. Click **Filter** to show a list of files that are not eligible for the merge operation. (Figure 451)

Click **OK** to close the Filter window.

Figure 451 Filter List



Breaking the tentative connection between two files

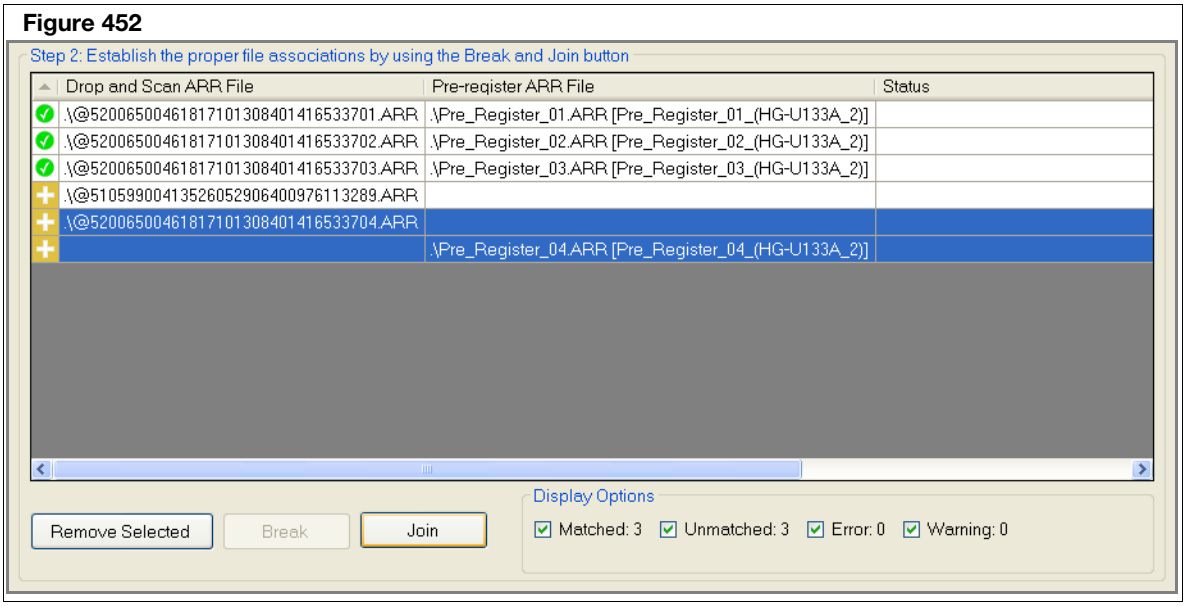
1. Click in the row with the files you want to break.
2. Click the **Break** button.

   Note: You can only break connections previously joined files.

Joining two unconnected files

1. Select the files you wish to join by holding down the Ctrl key while you click on each file. (Figure 452)

Figure 452

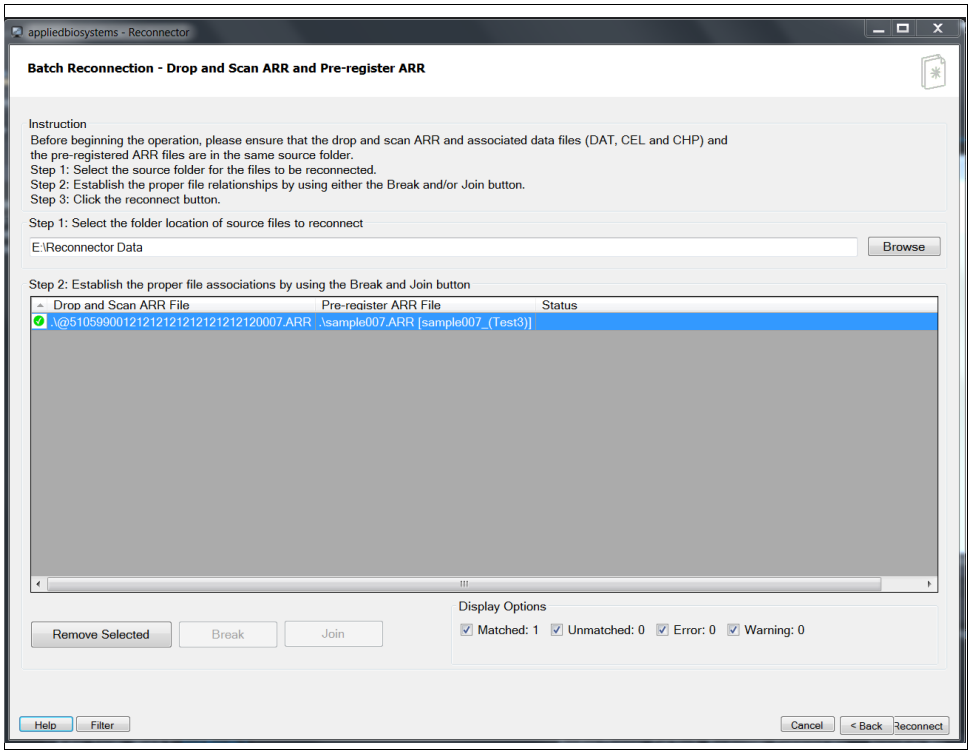


2. Click the **Join** button.

   Note: If the Join operation is not successful, an error message detailing the discrepancies appears. Acknowledge the message, then click **OK**.

   If the Join operation is successful, the new parent-child relationship is displayed in the file list. (Figure 453)

Figure 453 Batch Reconnection window

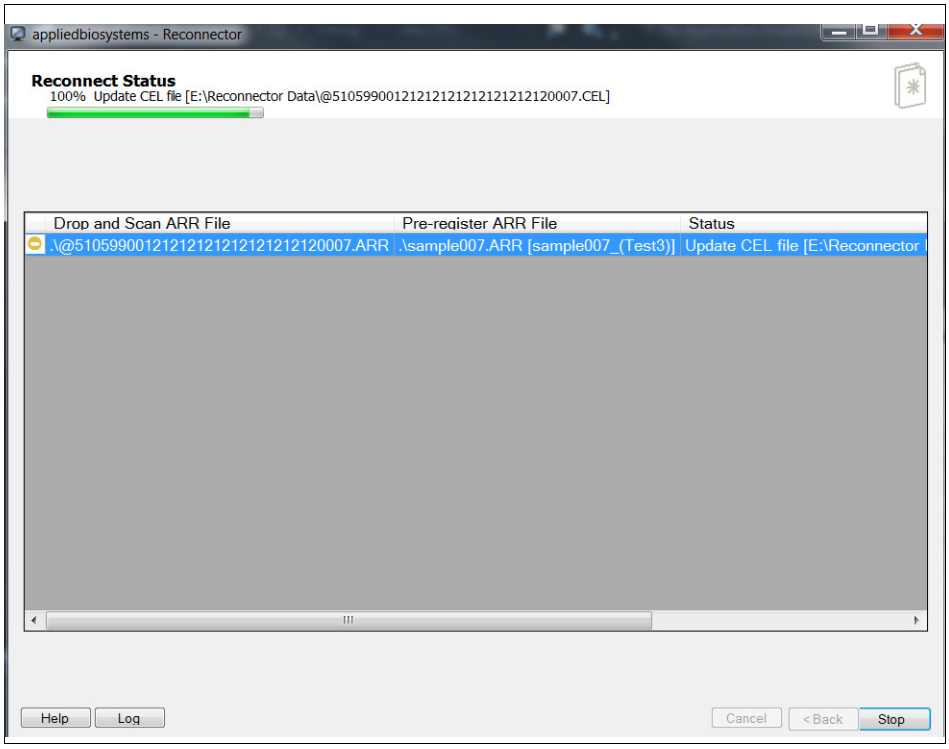


3. After joining is complete, click **Reconnect** to connect all matched files.
   The Reconnect Status window appears. (Figure 454)

Batch Merge Status

The Reconnect Status window displays the status of the different attempts at merging Sample (ARR) files.

Figure 454 Reconnect Status window



The list displays the files that have had their connections changed, with the following information:

Status Icon
- Unmatched: Indicates unmatched file
- Error: Indicates naming match between incompatible files
- Matched: Indicates match between compatible files.
- Warning: indicates compatible files with tentative parent-child connections, but some information mismatch.

Parent File Parent file.

Child File Child file.

Status Status of connect operation.

Click **Log** (bottom left) to open a file giving log information about the reconnect operations.